(K138N (N166D (A137G (A137G

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08-AUG-1988; 010706.
08-AUG-1988; FR-010706.
(GEORY) Georges M.
Georges M. Vassart G, Christophe D, Dumont J, Young M;
WPI; 90-093373/13.
Determn. of sex of ruminant embryos-by hybridisation assay using specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Discussion of the property of a 2.5 kb fragment of the Per gene of Drosophila. The motifs AcNGGN and/or TCAGGC (N=T, U, G, A, or C) or their complementary sequences are repeated in the probe. It is used in a hypridistation assay to determine the sex of runimant embryos. Either (i) Southern or (ii) Dot-blot techniques can be utilised and Y-chromosome shows up as intense signal either obscuring most of the hybridisation track in (i) or surrounding the dots in (ii). Significant results can be obtd. using samples of less than 50 ng weight.
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Polynucleotide sequence from the genome of Treponema pallidum.
Treponema pallidum infection; syphilis; Borrelia infection; animal;
Treponema pallidum.
W09859034-A2.
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New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
Mutant B
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Gaps: 0
Percent Identity: 52.632
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                                                                                                                                                                                                                   003665 standard; DNA; 2465 BP.
003665;
07-AUG-1989 (first entry)
Sequence homologous to Drosophila Per gene
Sex determination; ruminant embryos; ss.
FR2635116-A.
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X20561;
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                                                                                                                                        seq_name: N_Geneseq_36:003665
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Ratio: 2.933
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24-JUN-1997; US-050667
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US-08-653-294-31 x Q03665
                                                                                                                                                                                      seq_documentation_block:

DE Q03665 standard; DNA AC 003665 standard; DNA AUG-1989 (first DE Sequence homologous NA SEGS5116-A.

PD 09-FEB-1980; 010706.

PR 08-AUG-1988; 010706.

CC Drosophila. The motil complementary sequence complementary sequence
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N_Geneseq_36:Q10414
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N_Geneseq_36:Q10411
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Mutant protease gene (delta137
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Nhel-D fragment of DS6A genome
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Mycobacteriophage DSGA Nhel-D
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-Q=/cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.2
-Q=/cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.2
-Q=/cgn1_1/USPTO_spool/US08653294/runat_04022000_16000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000
-GAPEXT=4.000 -OGAPEXT=0.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP=6.000 -FGEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-TRANS=human40.cdi -LisT=45 -DOCALIGN=200 -THR_SCORE=pct
-ALIGN=15 -MODE=LOCAL -OUTFMT=Pfs -NORM=ext -MINLEN-0
-MAXLEN=1000000 -USER-US08653294 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
                                                                                                              About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Database sequences: 311585
Database length: 125096042
Search time (sec): 873.190000
OM of: US-08-653-294-31 to:
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Query: US-08-653-294-31
Query length: 20
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N_Geneseq_36:T93352
N_Geneseq_36:T93344
N_Geneseq_36:X14180
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N_Geneseq_36:Q06283
N_Geneseq_36:Q20766
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N_Geneseq_36:V45137
N_Geneseq_36:T93354
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N_Geneseq_36:Q13865
N_Geneseq_36:Q14235
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N_Geneseq_36:Q10416
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N_Geneseq_36:Q20765
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N_Geneseq_36:T39892
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N_Geneseq_36:X40398
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N_Geneseq_36:X37535
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N_Geneseq_36:T93353
                                                       Date: Feb 8, 2000
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Claim 1; Page 528-530; 1150pp; English.
X20500-21243 represent polynuclectide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrella infections in animals, and for the production of biosynthetic products such as enzymes. Sequence 4354 BP; 1148 A; 1183 C; 1084 G; 931 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag= e
note= "from human beta-globin (Splice acceptor)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1056. 1953
/*tag= j
/note= "promoter and 5' non-coding region from hamster DHFR gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-coding region from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .21

//arg- a

/note= "binding site for oligonucleotide

EBI-2133 (022519)"

.*tag- b

/*tag- b

/note= "CMV enhancer and promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interferon; O-glycosylation; beta-globin; IFNalpha 2C;
                                                                                                                                                                                                            Length: 14
Gaps: 0
Percent Identity: 64.286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= c
/ote= "CMV enhancer and promoter"
                                                                                                                                                                                                                                                                                                                                                                               5 IleargLeuAsnGluArgTyrArgLeuAlaIleArgLeuAsn 18 :::|||||||||||:::|||||||||||:: 80 CTGCGCTTAAACTCTCGCAGAAGACTGTCAATTCGTTTGGAC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= d
/note= "from CMV (Splice donor)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= g
/label= multi-cloning_site
923. .1055
/*tag= h
//note= from SV40"
                                                                                                                                                                                                                                                                                                                                                to: 4354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #36. .853
/*tag= f
/label= T7_promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag= i
'note= "promoter and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 namster DHFR gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "exon 1"
040. .2333
                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: X20561 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
ID Q20765 standard; DNA; 6062 BP.
AC Q20765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag= k
'label= DHFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . .1953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-APR-1992 (first entry)
pAD-CMV19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41. .805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62. .922
                                                                                                                                                                                                              44.00
3.385
92.857
                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: N_Geneseq_36:Q20765
                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-31 x x20561
                                                                                                                                                                                                            Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytomegalovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polya_signal
                                                                                                                                                                                              alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enhancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5'utr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon
   8000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LODACO SECTO SECTO
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contg. a suitable expression plasmid
Disclosure; Fig 7(A-D); 24pp; German
Disclosure; Fig 7(A-D); 24pp; German
Disclosure; Fig 7(A-D); 24pp; German
DAD-CANT9 includes CAW promoter, modified DHFR gene, splice donor and acceptor sites, Sv40 early adenylating signal, Sv40 origin, and mutitioning site. The 5'-non-coding region of human IFNalpha 2C-encoding CDNA was replaced with the non-coding region of human beta-globin mRNA using PCR. A PCR product of 0.64kb resulting from HindIII and XbaI restriction enzyme digests was isolated and ligated into appropriate restriction enzyme sites of plasmid pAD-CMV19. E.coli HB101 were transformed with the ligation prods. and an expression plasmid pAD-BD19-IFN secreting O-glycosylated human IFN-alpha 2C was identified. See also Q20764-66 and Q22517-29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JAN-1992.
10-JUL-1990; DE-021917.
10-JUL-1990; DE-021917.
10-JUL-1990; DE-021917.
HIMMLER A. Adolf G;
WPI: 92-0254857/04.
O-glycosylated alpha-interferon, used as medicament - isolated following secretion into conditioned medium of mammalian cells
                                                    /*tag= m
/note= "binding site for EBI-1857 (Q22522)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note- "binding site for EBI-2134 (022518)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "M13 intergenic region (M13ori)"
4423. .5283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LeuAlaIleArgLeuAsnGluArgTyrArgLeuAlaIleArgLeu 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 15
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                             pBluescript portion'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: Q20765 from: 1 to: 6062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= s
/label= beta-lactamase
6038. .6062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAY-1992 (first entry)
pAD-CMV19 expression vector.
Interferon; IFN; 0-glycosylation; ss.
                                                                                                                                                                               /note= "exons 2-6"
2822. .3474
/note= "intron 1"
2151. .2168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
                                                                                                                                                                                                                              /*tag= o
/label= DHFR
3475. .3812
/*tag= p
/label= SV40
                                                                                                                                                                                                                                                        DHFR
                                                                                                                                                                                                                                                                                                                                  SV40
                                                                                                                                /*tag= n
/label= DHFR
                                                                                                                                                                                                                                                                                                                                                            3813. .6055
/*tag= q
                                                                                                                                                                                                                                                                                                                                                                                                                                  3813. .4291
/*tag= r
                                                                                                      2344. .2821
                                                                                                                                                                                                                                                                                                                                                                                   /note= "pa'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
ID Q20732 standard; DNA; 6062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: N_Geneseq_36:020732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.143
93.333
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US-08-653-294-31 x Q20765
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us-08-653-294-31.rng

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promoter
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                                                                                                                                                                                                                                                                                         a
"binding region of EBI-2133 (Q20736)"
                                                                                                                                                                                                                                                                                                                                                                                                                 *tag- m
note- "binding region of EBI-1857 (Q20739)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "binding region of EBI-2134 (Q20735)"
                                                                                                      /*tag= d
/note= "CMV intron sequence (splice donor)'
                                                                                                                                                                                                                                                           *tag= i
'note= "promoter and 5' non-coding region
namster DHFR gene"
                                                                                                                                 ^*tag= e

objet= "human beta-globin intron sequence
splice acceptor)"
336. 853
                                    . .590
*tag= b
note= "cytomegalovirus enhancer and
                                                                                                                                                                                                  /*tag- g
/label= multi_cloning_site
// 23 1055
/*tag= h
/note= "SV40 poly(A) site"
1056 1953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - q
|- pBluescript_region
.4291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag= s
label= beta-lactamase
                                                                                                                                                                        *tag= f
label= T7_promoter
62. .922
cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "exons 2-6
822. .3474
                                                                                                                                                                                                                                                                                                                                                                                              note= "intron 1"
151. .2168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag= p
label= SV40_ori
                                                                                                                                                                                                                                                                                                                                                         note= "exon 1"
040. .2333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *tag= r
label= M13_ori
                                                                                                                                                                                                                                                                                                                               1954. .2039
/*tag= k
/label= DHFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JAN-1992.
06-JUL-1991; E01266.
10-JUL-1990; DE-021917.
12-NOV-1990; DE-035877.
(BOEH ) BOEHRINGER INGELHEIM.
                                                                                                                                                                                                                                                                                                                                                                              tag= 1
|abel= DHFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag= n
label= DHFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DHFR
                                                                                                                                                                                                                                                                                                                                                                                                                                      344. .2821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .6055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423. .5283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         038. .6062
                                                                                                                      41. .805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag=
label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag=
label=
                  /*tag=
/note=
Key
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                       polya_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9201055-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rep_origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rep_origin
                                                                                                                                                                promoter
                                                                                                                                                                                                                                                    promoter
                                      enhancer
                                                                 promoter
                                                                                             intron
                                                                                                                        intron
                                                                                                                                                                                                                                                                                                                                                                     intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3'utr
                                                                                                                                                                                                                                                                                          5'utr
                                                                                                                                                                                                                                                                                                                                exon
                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
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Tumour treatment and to understand mechanisms to rused in tumour treatment and to understand mechanisms to TNF action tumour treatment and to understand mechanisms to TNF action tumour treatment and to understand mechanisms to TNF action blackouse; Fig 6(1-4); Slpp; German.

Disclosure; Fig 6(1-4); Slpp; German.

In produce In the unithe of patients with uraemia and probes/primers were constructed from the determined amino acid sequence.

To produce a vector expressing a soluble form of TNF-binding protein, this plasmid was cut with Xmm1, amplified by PCR and the protein, this plasmid was cut with Xmm1, amplified by PCR and the manified DNA cut with BamHI and Econ; Inserted into pT7/T3 alpha-19 (BRL) cut with the same enzymes to recover pTNF-BP. This was cut with BamHI and Econ; and the recovered fragment inserted into pab-CMV1 to give the required plasmid padrNF-BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T 29-7AN-1991 (first entry)

E pAD-CMV1 contg. a Tumour Necrosis Factor-Binding Protein insert.

W Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;

N PAD-CMV1; SS.

N PAD-CMV1; SS.

N EP-39438-A.

24-0CT-1990;

C 21-APR-1999; DE-913101.

R 21-APR-1999; DE-913101.

R 21-APR-1999; DE-913101.

R 21-APR-1999; DE-913101.

R (BOBH ) BOEHRINGER INGEHEIMINT.

I HAUPTMANN R, Himmler A, Maurer-Fogy I, Stratowa C;

N NP1; 90-31997/43.
Adolf G, Himmler A, Ahorn HJ, Kalsner I, Maurer-Fogy I; 92-056870/07.
0-glycosylated alpha-interferon - used for treatment of viral of tumour diseases
Disclosure; Fig 7 (A-D); 104pp; English.
A DNA sequence encoding IFN-alpha may be inserted into pAD-CMV19 and the recombinant prod. used to transform cells of a multicellular organism, pref. a vertebrate. The cell supernatant is harvested and the O-glycosylated prod. recovered by known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ë
                                                                                                                                                                                                                 1448 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1174 CIGGCCATICACGIAAACAGAAGATICCGCCICAAGTICCGGITA 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LeuAlaIleArgLeuAsnGluArgTyrArgLeuAlaIleArgLeu 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1554 G;
                                                                                                                                                                                                                 1528 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 15
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                          Length: 15
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                 1506 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1565 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: Q20732 from: 1 to: 6062
                                                                                                                                                                                           See also Q20731-43 and Q20523-26.
Sequence 6062 BP; 1580 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1679 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID Q06283 standard; DNA; 6414 BP.
                                                                                                                                                                                                                                                                                          44.00
3.143
93.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.00
3.143
93.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seg_name: N_Geneseg_36:Q06283
                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-31 x Q20732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-31 x Q06283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6414 BP;
                                                                                                                                                                                                                                                                    alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
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                                                                                                                                                                             methods
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to: 6414

from: 1

to: Q06283

Align seg 1/1

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misc_feature
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                                                                                                                                                                 DE4021917-A
rep_origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enhancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    intron
                                                            cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . .
                                                                                                                                                                                                                          **tag= a
label= EBI-1733(022529)
fnote= "start of CMV enhancer-promoter (from CDM8)"
                                                                                                                                                                                                                                                                                    /*tag= b
//abel= EBI-1733(022529)
529. "start of CMV enhancer-promoter (from CDM8)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      **tag= n
'note= "end of DHFR gene (from psV2gptDHFR20)"
8832. .4169
                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag= e
note= "SV40 intron and poly-adenylation site
from CDM8)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14. .1412
**tag= f
**note= "SY40 intron and poly-adenylation site from CDM8)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /+tag- g
/note= "5' non-coding region and promoter of
hamster DHFR gene (from pSV2gptDHFR20)"
/+tag- h
/note= "5' non-coding region and promoter of
hamster DHFR gene (from pSV2gptDHFR20)"
                                                                                                                                                                                                                                                                                                                                                                                              *tag- d
| Tabel- multi-cloning_site
| mindIII-Xbal from EBI-1823,EBI-1829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               i,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "deletion between BglII and BamHI
'' non-coding region"
           /*tag= j
/label= mutation
/note= "A->T, disturbes PstI site"
/701. 3178
/*tag= k
/label= DHFR
/note= "exons 2-6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.abel = mutation
hote= "A->G, disturbing EcoRI site"
272. .3273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2311. .2396
/*tag= i
/label= DHFR
/note= "hamster DHFR: exon 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= o
/label= SV40_ori
/note= "from SV2gptDHFR20"
                                                                                                                                                                                                                                                                                                                                                /*tag= c
/label=_T7_promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= deletion
                                                                                                   seq_documentation_block:
ID Q20766 standard; DNA; 6414 BP.
                                                                                                                                              |-APR-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       . 1412
                                                                                                                                                                                                                                                                                                                                                                                558. .713
                                                                       seq_name: N_Geneseq_36:Q20766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_difference
                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polya_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rep_origin
                                                                                                                                                                 pAD-CMV1.
                                                                                                                                                                                                             promoter
                                                                                                                                                                                                                                                                         enhancer
                                                                                                                                                                                                                                                                                                                                   promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_rna
                                                                                                                                                                                                                                                                                                                                                                                                                                            intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5'utr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
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O-glycosylated alpha-interferon, used as medicament - isolated following secretion into conditioned medium of mammalian cells contq. a suitable expression plasmid blasmid pado-cmy 11(A-D); 24pp; German. Disclosure: Fig 11(A-D); 24pp; German. Plasmid pAD-CMV1 is formed from pCDM8, psv2gptDHFR20 and pBluescript SK+. The multi-cloning site is useful for the insertion of heterologous DNA, e.g. IFN. The plasmid is replicable in E.coli. See also 020764-66 and 025177-29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= c
/note= "binding region of EBI-1733 (Q20525), start
of CMV enhancer-promoter (from CDM8)"
632. .649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .21
A-tag a
/note= "binding region of EBI-1733 (Q20525), start
of CMV enhancer-promoter (from CDM8)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= e
/label= multi_cloning_site
/note= "HindIII-Xbal from EBI-1823, EBI-1829"
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= b
/note= "binding region of EBI-1733 (Q20525),
of CMV enhancer-promoter (from CDM8)"
                                                                                                                                                                  /*tag= r
/label= EBI-1729(Q22528)
/note= "end of pBluescript vector sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LeuAlaIleArgLeuAsnGluArgTyrArgLeuAlaIleArgLeu 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 15
Gaps: 0
Percent Identity: 60.000
*tag= p
/label= M13_ori
/note= "from pBluescript SK+"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 6414
                                                                                                  /*tag= q
/label=_beta_lactamase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O-glycosylation; ss
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= d
/label= T7_promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:

ID Q20733 standard; DNA; 6414 BP.

AC Q20733.

DT 19-MAY-1992 (first entry)

DE pAD-CMV1 expression vector.

KW Interferon; IFN; O-glycosylation

FH Key Location/qualifi.

FT misc_feature 1..21

/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: Q20766 from: 1
                                                                                                                                                                                                                                                                                                 10-JUL-1990; DE-021917.
(BOEH ) BOEHRINGER INGELHEI.
Himmler A, Adolf G;
WPI; 92-025485/04.
                                                                                                                                          6395. .6414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.00
3.143
93.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . .713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: N_Geneseq_36:Q20733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-31 x Q20766
                                                                                                                                                                                                                                                      16-JAN-1992.
10-JUL-1990; 021917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
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1616 T;

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1562 C;
                                                                                                                                                                                                                                                                      Location/Qualifiers
1. .767
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label = EBV ori P
2262. .2856
                                                                                                                    to: Q20733 from: 1
         1678 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label- pBR322
                                                                                                                                                                                                   seq_documentation_block:
ID Q43360 standard; DNA; 6623 BP
                                                                                                                                                                                                                                                                                      /label= CMV
68. .785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .6623
                                               44.00
3.143
93.333
                                                                                                                                                                               seq_name: N_Geneseq_36:Q43360
                                                                                       alignment_block:
US-08-653-294-31 x Q20733
           6414 BP;
                                                            Ratio:
Percent Similarity:
                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                        alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             rep_origin
                                                                                                                     Align seg 1/1
            Sequence
                                                                                                                                                                                                                                                                                 promoter
                                                                                                                                                                                                                                                                                                              promoter
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                                                                                                                                                                                                                                                                                                                                                                         intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3'utr
                                                                                                                                                                                                                                                                                                                                                                                                                5'utr
           g
                                                                                                                                                                                                             Disclosure: Fig 11 (A.E): 104pp; English.

This expression plasmid contains an intron sequence between the multi-cloning sequence and the poly(A) site. Variations may be made from pAD-CWYI, according to the amt. and positon of introns w.r.t. the multi-cloning site. For example, pAD-CWYI9 (Q20732) comprises only one intron between the CWV promoter and the multi-cloning site. A DNA sequence encoding IFN-alpha may be then be inserted into pAD-CWVI9 and the recombinant prod. used to transform cells of a multicellular organism, pref. a vertebrate. The cell supernatant is harvested and the 0-glycosylated prod. recovered by
note= "SV40 intron and poly(A) site (from CDM8)"
14. 1412
                                *tag= g
note= "SV40 intron and poly(A) site (from CDM8)"
                                                                                                                                                                                                                                                                                                                                                    *tag= o
note= "end of DHFR gene (from pSV2gptDHFR20)"
832. .4169
                                                                                       413. 2310

*tag= i
note= "promoter and 5' non-coding region of amster DHFR gene (from pSV2gptDHFR20)"
                                                                   note= "promoter and 5' non-coding region of master DHFR gene (from pSV2gptDHFR20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= s
/note= "binding region of EBI-1729 (Q20524),
end of pBluescript vector"
                                                                                                                                                                           /*tag= k
/label= mutation
/note= "A -> T, disturbing the PstI site of
DHFR intron 1"
                                                                                                                                                                                                                                                                      *tag= m
label= mutation
note= "A -> G, disturbing the EcoRI site"
                                                                                                                                                                                                                                                                                                             *tag= n
note= "deletion between BglII and BamHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JAN-1992.
06-JUL-1991: E01266.
10-JUL-1990: DE-021917.
12-NOV-1990: DE-035877.
(BOGH ) BOCHRINGER INCELHEIM.
Adolf G, Himmler A, Ahorn HJ, Kalsner I, Maurer-Fogy I;
WPI: 92-056870/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0-glycosylated alpha-interferon - used for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                           "from pBluescript SK+". 5640
                                                                                                                                                                                                                                                                                                                                                                             *tag= p
/label= SV40_ori
^^+e= "from pSV2gptDHFR20"
                                                                                                                                                                                                                                                                                                                                HFR 3' non-coding region
                                                           *tag= h
note= "promoter and 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag= r
label= beta-lactamase
                                                                                                                                                                                                                                                 note= "exons 2-6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        See also Q20731-43 and Q20523-26
                                                                                                                                                        'note= "exon 1"
516
                                                                                                                                                                                                                                                                                                                                                                                                                        *tag= q
label= M13_ori
                                                                                                                              2311. .2396 /
/*tag= j
/label= DHFR
                                                                                                                                                                                                                               *tag= 1
label= DHFR
                                                                                                                                                                                                                                                                                                    .3273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5395. .6414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                            note=
780. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                known methods
                                                                                                                                                                   misc_feature
                    polya_signal
                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                           misc_feature
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                                                                                                                                                                                                                                                                                                                                                                        rep_origin
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                                                  promoter
                                                                                        5'utr
                                                                                                                                exon
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10-JUN-1993.
25-NOV-1992; E02718.
25-NOV-1992; DE-138621.
6DEH DE-138621.
CZETNILOFSKY AP, HIMMLER A, STRATOWA C, Weyer U;
LAMCHE H, Schaefer R;
WPI; 93-197073/24.
Screening substances that modulate receptor-dependent signal transmission path - using test cells transformed with reporter gene and regulatory sequence sensitive to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Hygromycin B phosphotransferase gene
1913. .4161
                                                                                                                                                                                                                                                                   1558 G;
                                                                                                                                                                                                                                             3 LeuAlalleArgLeuAsnGluArgTyrArgLeuAlalleArgLeu 17
                                                                       Length: 15
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag- g
/label- HSV Thymidine kinase
/note= "with polyA signal"
2857. .312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label- HSV Thymidine Kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag- b
/4 label- T7
/4 s54
/*tag- c
/4 label- polycloning site
854 .1552
/*tag- d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= e
/label= Hamster DHFR gene
|737. .2261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label = Sv40 t intro
/note= "and polyA signal"
1553. .1736
                                                                                                                                                                                                         to: 6414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= k
/label= linker sequence
                                                                                                                                                                                                                                                                                                                                                                                                               13-5EP-1993 (first entry)
Sequence of circular plasmid pAHygCMV1
PCR, primer; oligonucleotide.
Synthetic.
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seq_name: N_Geneseq_36:x20551

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Transmission path - using test cells transformed with reporter gene and requiatory sequence sensitive to gene and requiatory sequence sensitive to gene and requiatory sequence sensitive to genes at 17 inositol-1,4,5-tripeptide and disacylgylycerine(s)

Example; Pages 107-112; 170 pp; German.

Example; Pages 107-112; 170 pp; German.

Franside for the expression of genes or CDNA under the franscription control of genes or cDNA under the for hygromycin B resistance were constructed from expression plasmids pah-CMV1 and pah-CMV2 (Ep-A 393 438) and path Genes (c et al 1965). Plasmid pahlygCMV1 contains the many features, given in FT. Plasmid pahlygCMV2 differs from pahlygCMV1 only in respect of the polycloning site. 'N' in q4380 denotes where the sequence printed in the patent application was illegible.

Sequence 6630 BP; 1655 A; 1704 C; 1628 G; 1643 T;
               Example: Pages 102-107; 170 pp: German.
Plasmids for the expression of genes or cDNA under the transcription control of CMV promoters/enhancer and selectable for hygromycin B resistance were constructed from expression plasmids pAD-CMV2 (EP-A 393 438) and pREBO (Sugden et al 1985). Plasmid pAHyGCMV1 contains the many features, given in FT. Plasmid pAHyGCMV2 differs from pAHyGCMV1 only in respect of the polycloning site. 'N' in q43360 denotes where the sequence printed in the patent application is illegible.
Sequence 6623 BP; 1651 A; 1701 C; 1626 G; 1640 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LeuAlalleArgLeuAsnGluArgTyrArgLeuAlalleArgLeu 17
inositol-1,4,5-tri:peptide and di:acyl:glycerine(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-NOV-1992; E02718.
25-NOV-1991; DE-138621.
(BOEH ) BOEHRINGER INGELHEIM INT GMBH.
Czernilofsky AP, Himmler A, Stratowa C, Weyer U;
                                                                                                                                                                                                                                                                                        Length: 15
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 60.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: Q43360 from: 1 to: 6623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: Q43361 from: 1 to: 6630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-588-1993 (first entry)
Sequence of circular plasmid pAHygCMV2
PCR: primer; oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seg_documentation_block:
ID Q43361 standard; DNA; 6630 BP.
                                                                                                                                                                                                                                                                                        44.00
3.143
93.333
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3.143
93.333
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                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-31 x Q43360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-31 x Q43361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lamche H, Schaefer R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 93-197073/24.
                                                                                                                                                                                                                                                                                          Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
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                                                                                                                                                                                                                                                                         alignment_scores:
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detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis (laim 1.) Page 483-487; ll50pp. English.
X20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, Treponema pallidum, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detection diseases related to Borrelia infections in animals, and for the production of blosynthetic products such as enzymes. Sequence 6993 BP; 1914 A; 2019 C; 1404 G; 1647 T;
                                                                                              DS-MX-1999 (first entry)
Polynucleotide sequence from the genome of Treponema pallidum.
Treponema pallidum infection; syphilis; Borrelia infection; animal;
enzyme production; ds.
Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers

1. .543

/*tag- a

/*product- IL-6_mutein
/note- "first 4 N-terminal amino acids are deleted
and Cys residues at positions 45, 51, 74
and 84 of wild-type IL-6 are substd. by
ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; R31996.
New cysteine-depleted interleukin-6 mutein - for promoting cell
differentiation (e.g. of B-cells), as antiinflammatory agents and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-1991; US-724698.
(IMCL-) INCLONE SYSTEMS INC.
(UVIC-) UNIV NORTH CAROLINA.
FOWLKES DM, SKelly SM, Snouwaert JN, Tackney CT;
WPI; 93-045433/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1993 (first entry)
-4aa IL-6 SSSS mutein.
Interleukin-6; mutant protein; pBgal/EK/cfIL-6; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 14
Gaps: 0
Percent Identity: 64.286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 IleArgLeuAsnGluArgTyrArgLeuAlaIleArgLeuAsn 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: X20551 from: 1 to: 6993
                                                                                                                                                                                                                                                                                                        30-DEC-1998.
23-JUN-1998.
24-JUN-1997; US-050667.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВР
seq_documentation_block:
ID X20551 standard; DNA; 6993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID Q34545 standard; DNA; 589
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3.385
92.857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-31 x X20551
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02-JUL-1992; U05612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 99-081273/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                        WO9859034-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         034545;
                                      HELL BERNESS OF STANDERS OF ST
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Example 1; Fig 2; 118pp; English.

Plasmid BPB91/Exforin-6 contains a DNA sequence which encodes a plasmid BPB91/Exforin-6 contains.

I usion protein comprising beta-galactosidase, followed by an enterokinase cleavage site, which is, in turn, followed by an enterokinase cleavage site, which is, in turn, followed by an enterokinase cleavage site, which is, in turn, followed by an enterokinase cleavage site, which is, in turn, followed by an enterokinase cleavage site, which is, in turn, followed by an enteroking the fire fraction of a the court of native IL-6 peptide sequence lacking the first 4 N terninal annot consider the preparation of various IL-6 muteins, either full-length considers in the preparation of various IL-6 muteins, either full-length considers (at positions 74 and 84) resulted in a mutein which retained IL-6 activity.

Sequence 589 BP; 193 A; 145 C; 134 G; 117 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D 23-CUL-1991; 724698.

R 02-JUL-1991; US-724698.

R 02-JUL-1991; US-724698.

A (JUL-1991; US-724698.

A (JUL-1991; US-907710.

A (JUNC-) IMCIONE YSTEMS INC.

A (JUNC-) UNIV NORTH CAROLINA.

P FOWLES DM, Skelly SM, Snouwaert JN, Tackney CT;

R WPI; 94-341061/42.

P PSDB: R72211.

P PSDB: R72211.

P PSDB: R72211

P PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         089359;
07-JUL-1995 (first entry)
Human interleukin-6 -(Alal), Ser45, Ser51, Ser74, Ser84 DNA.
Human interleukin-6; IL-6; -(Alal), Ser45, Ser51, Ser74, Ser84; SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 57.143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 0
Percent Identity: 57.143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LeuAlalleArgLeuAsnGluArgTyrArgLeuAlalleArg 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: Q34545 from: 1 to: 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _documentation_block:
Q89359 standard; DNA; 589 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.00
3.909
78.571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.00
3.909
78.571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-31 x Q34545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-31 x Q89359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5359034-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sed
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New nucleic acid encoding mutant IL-6 with two cys residues replaced

The more active than native process, useful e.g. as

The more active than native process, useful e.g. as

Immuno-therapeutic or anti-inflammatcry agents

This sequence represents the coding sequence for a interleukin-6 (IL-6)

This sequence represents the coding sequence for a interleukin-6 (IL-6)

This sequence represents the coding sequence for a interleukin-6 (IL-6)

This sequence represents the coding sequence for a interleukin-6 (IL-6)

This sequence represents the coding sequence for a interleukin-6 (IL-6)

This sequence represents the coding sequence for a interleukin-6 (IL-6)

This sequence represents the coding sequence for a interleukin-6 (IL-6)

The interpolation of the invention of IC-6 is simplified and be used for regulating factor (HSF). The mutein IL-6

The mutain of the action of B or I cells, megakaryocytes or multipotent

Codifferentiation of B or I cells. The muteins can also induce acute phase proteins in liver cell. The muteins can be used as immunotherapeutic

The foreign sequence of the Coding sequence of thrombocytopaenia, and anti-inflammatory agents, in the treatment of thrombocytopaenia, and anti-inflammatory agents, in the treatment of thrombocytopaenia, and anti-inflammatory agents, in the treatment of thrombocytopaenia, and a priminating 2 of the Cys residues, purification and isolation of IL-6

Is simplified, as only one Cys-Cys disulphide bond can form during oxidation. Due to this, yields of the mutein proteins are improved in comparison to wild type IL-6. By removing the hydrophobic N-terminus, the yield can be further improved. The IL-6 muteinly 250-400 times

The standard of the coding sequence of the sequence of the standard of the secondard of the second
                                                                                                                                                                                         seq_documentation_block:

ID T3982 standard; DNA; 589 BP.

T39892 standard; DNA; 589 BP.

T13982 standard; DNA; 589 BP.

T13982 standard; DNA; 589 BP.

DT 10-DEC-1996 (first entry)

Coding sequence for -4aa SSCC mutein of human Interleukin-6.

KW Toell; megakaryocyte; multipotent haematopoietic progenitor cell; BSF-2; W anti-inflammatory agent; thrombocytopaenia; bone marrow transplantation; interferon-beta-2; B-cell stimulation factor-2; 26 kDa protein; IFN-B2; KW B-cell hybridoma/plasmacytoma growth factor; HPGF; HGF; HSF;

KW hepatocyte stimulating factor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Snouwaert JN, Tackney CT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 14
Gaps: 0
Percent Identity: 57.143
                                              -4 aa interleukin-6 SSCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= b
/note= "optionally deleted"
to: 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
  Align seg 1/1 to: 089359 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the wild type IL-6.
e 589 BP; 193 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .540
/*tag= a
/product= ·
1. .72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUL-1991; US-724698.
02-JUL-1992; US-907710.
10-MAR-1994; US-209122.
(UYPR-) UNIV PRINCETON.
FOWLKES DM, SKelly SM, 9
WPI; 96-383669/38.
                                                                                                                                                seq_name: N_Geneseq_36:T39892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.909
78.571
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US-08-653-294-31 x T39892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                724698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; W05586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                that of
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37. .927 /*tag= a

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Weil; 95-260997/25.

Mentification and quantification of bacteria, fungi and bacterial identification and quantification of bacteria, fungi and bacterial antification and quantification of bacteria, fungi and bacterial claims is page 108; 167pp; English.

The present sequence represents an antibiotic resistance gene blaz (resistant to beta-lactams), and was used to design PCR primers (7050-51. The specification describes the use of probes and/or amplification primers which are specific, ubiquitous and sensitive for determining the presence and amount of nucleic acids from a bacterial antibiotic resistance gene and specific bacterial and fungal species in any sample suspected of containing the bacterial or fungal nucleic acids, where each of the nucleic acid or variant or part comprises a selected target region hybridisable with the probes or primers and detecting the presence of hybridised probes or amplified products as an indication of the presence of the specific bacterial or fungal species and bacterial antibiotic resistance genes. The methods and products can be detect and identify the bacterial and fungal species and genera and determine the bacterial resistance to antibiotics.

Sequence 846 BP; 356 A; 99 C; 135 G; 256 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human calcium signal modilating cyclophilin ligand coding sequence. Human calcium signal modulating cyclophilin ligand; DNA probe; calcium-activated pathway modulator drug screening; diagnosis; treatment; contraception; infertility; learning disorder; memory disorder; Escherichia coli; Saccharomyces cerevisiae; CHO; Jurkat; Chinese hamster ovary; H9C2(2-1); ds.
                                                                                                                                                                                                           Antibiotic resistance gene blaz for beta-lactams.
Detection; bacterial antibiotic resistance gene; bacteria;
fungal species; identification; beta-lactam; ds.
                                                     Length: 12
Gaps: 0
Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: V37110 from: 1 to: 846
                                  16
                                  3 LeuAlaIleArgLeuAsnGluArgTyrArgLeuAlaIleArg
                                                                                                                                                                                                                                                                                               14-MAY-1998.
04-NOV-1997; CA0829.
04-NOV-1996; US-743637.
(IDII-) IDI INFECTIO DIAGNOSTIC INC.
Bergeron MG, Ouellette M, Picard FJ, Roy PH; WPI; 98-286967/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 AsnGluArgTyrArgLeuAlaIleArgLeuAsnGlu 19
Align seg 1/1 to: T39892 from: 1 to: 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
ID T07329 standard; cDNA; 1391 BP.
                                                                                                                                         05-JUL-1996 (first entry)
                                                                                                                                                                                         04-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-31 x V37110/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio: 3.583
Percent Similarity: 100.000
                                                                                                      seq_name: N_Geneseq_36:V37110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: N_Geneseq_36:T07329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                  Enterococcus sp
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Location/Qualifiers

COS; Jurkat; (Homo sapiens.

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362 T;
                                                                                                                                                                                                                                                                                                                                                                                                         1194 AAGTTAGAGGAAAGGTACAGAATAGGAATTCTGATTAACAAGAAA 1150
                                                                                                                                                                                                                                                                                                                                                                                               6 ArgLeuAsnGluArgTyrArgLeuAlaIleArgLeuAsnGluArg 20
                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to reverse of: T07329 from: 1 to: 1391
                                                                                                                                                                                                                                                                                                                            Percent Identity: 46.667
                                                                                                                                                                                                                                                                      332 G;
                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                     280 C;
28-DEC-1995.
16-JUN-1995; U07752.
17-JUN-1994; US-261662.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Bram RJ, Crabtree GR;
WPI; 96-058511/06.
                                                                                                                                                                                                                                                                      417 A;
                                                                                                                                                                                                                                                                                                         43.00
3.071
93.333
                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-653-294-31 x T07329/rev
                                                                                                                                                                                                                                                                     1391 BP;
                                                                                                                                                                                                                                                                                                                    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                           Quality:
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                                                                                                                                                                                                                                                                       Sequence
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wed Feb

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qv02b02.x1 NCI_CGAP
SRN035KS Winter flo
qm21e02.x1 NCI_CGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index

Unpublished (1997)

On May 18, 1998 this sequence version replaced gi:3138601.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert Strausbergenih.gov

Coligo-dr track not found. Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B.

Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LIMI at:

Www-blo.linl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Subtraction: Two Approaches To Facilitate Gene Discovery Genome Research 6, 791-806.
                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 427)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                   seq_documentation_block:
LOCUS AW015295 427 bp mRNA EST 10-SEP-1999
DEFINITION UI-H-BIO-eap-d-02-0-UI.sl NCI_CGAP_Subl Homo sapiens cDNA clone
IMAGE:2709939 3', mRNA sequence.
 AI287354 c
AW013132 3
AI279828 c
99.07
103.52
125.05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .427
 134.58
134.24
132.77
                                                                                                                                                AW015295
AW015295.1 GI:5864052
                                                            seq_name: gb_est37:AW015295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLYA-NO.
                                                                                                                                                                                             human.
 gb_est25:AI287354
gb_est37:AW013132
gb_est25:AI279828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI492423 ti27g11.x1 NCI_CGAP_Ki
AI762057 w153a10.x1 NCI_CGAP_CC
AI437378 fb50h04.x1 zebrafish W
AI416006 fb30h04.y1 zebrafish W
AW147227 dal6c03.x1 normalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A1998122 701672303 A. thallana,
A099350 HS_5462_A2_D03_SP6E_RR_A177858 ea19b02.y1 Elimeria M5-A1755661 ea07b04.y1 Elimeria M5-A1755661 ea07b04.y1 Elimeria M5-A1755661 ea07b04.y1 Elimeria M5-A0305795 HS_2050_A1_B12_MR_CIT_A0579370 nbxb0084E04r_CUGI_R1ce_A0751248 HS_5574_B2_E09_SP6_RPC_A0591361 HS_5410_B2_E01_T7A_RPC_A0591361 HS_5410_B11_164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA773968 ac35a12.s1 Stratagene
AQ21534 HS_2259_B2_H06_MR CIT
AA454364 MBAFCXOF1173 Brugia me
A103506 EST212795 Normalized r
A0334845 HS_5018_A1_F09_T7 RPCI
A1738775 606049A10.x1 606 - Ear
AA263821 LD07093.5prime LD Dros
A1543580 SD10377.5prime SD Dros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALOS1558 Drosophila melanogaste
! AQ892181 HS_5339_B1_F08_SP6 RF
! C95817 C95817 Marchantia polymd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A1328939 a8a03ne.fl Neurospora
A0514060 HS_5184_A1_E05_SP6E RE
A0500194 V3327 mTn-3xHA/lac2
AV266473 AV266473 RIKEN full-le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI649944 486099E09.x1 486 - lea
AG008494 Homo sapiens genomic D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AV074366 AV074366 Mus musculus
AI070642 UI-R-C2-mv-g-10-0-UI.s
AI997515 701554353 A. thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW015295 UI-H-BIO-aap-d-02-0-U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yy29d12.s1 Soares meland
                                                                                               Command line parameters:
-MODEL-frame+_p2n.model -DEV-xlp
-Q-fcgnll_I/USPTO_spool/VS08653294/runat_04022000_160700_15770/app_query.fasta.2
-Q-fcgnll_I/USPTO_spool/VS08653294/runat_04022000_160700_15770/app_query.fasta.2
-DB-EST -QFWT=fastap -SUFFIX=rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPST=0.000
-GAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -PGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATHIX=blosum62 -TRANS=human40.cd1
-LIST=45 -DOCALIGN=200 -THR_SCORE=PCT -ALIGN=15 -MODE=LOCAL
-UNCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1
                                                          About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EScore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZSCORE
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1156.45
1153.27
1153.18
1150.54
1148.81
1147.32
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143.09
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133.67
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129.86
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Database sequences: 4538634
batabase length: 1887831982
Search time (sec): 7600.090000
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OM of: US-08-653-294-31 to:
                              6:23 AM
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                                                                                                                                                                                                                                                                                               Query: US-08-653-294-31
Query length: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_est37:AW015295
gb_est28 Al492423
gb_est27:Al492423
gb_est27:Al416006
gb_est40:AW147227
gb_est40:AW14773
gb_est33:AV074366
gb_est22:Al070642
gb_est22:Al070642
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gb_est32:AI757463
gb_est32:AI755661
gb_gssl1:AQ305795
gb_gssl4:AQ579370
gb_gssl4:AQ579370
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gb_gss13:AQ500194
gb_est41:AV266473
gb_est37:AI998122
                             Date: Feb 8, 2000
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gb_est34:AV139866
gb_est1:D15447
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gb_est32:AI738375
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gb_est28:AI512344
gb_est28:AI543580
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gb_est19:AA773968
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gb_est30:AI649944
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gb_gss1:CNS00881
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Sequence
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us-08-653-294-31.rst

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AI762057.1 GI:5177724
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US-08-653-294-31 x AI492423/rev
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                                                                                                                                                                       Quality:
                                                                                                                                                                                                         Percent Similarity:
                                                              97
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ORGANISM
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VERSION
KEYWORDS
                                                              BASE COUNT
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TITLE
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                                                                                   ORIGIN
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Contact: Robert Strausberg, Ph.D.
Tel: (3010 496-1550)
Tel: (3010 496-1550)
Tel: (3010 496-1550)
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDN Library Preparation: M. Bento Soares, Ph.D.
CDN Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker: Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NOT_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI492423 523 bp mRNA EST 30-MAR-1999
ti27g11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131748 3',
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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota: Primates; Catarrhini; Hominidae: Homo.

1 (bases 1 to 523)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                  to: 427
                                                                                                                                                                  Length: 18
Gaps: 0
Percent Identity: 66.667
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/db_xref="taxon:9606"
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/clone_lib="NCI_CGAP_Kid11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ww-bio.lln1.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: AW015295 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert Length: 731 Std Error: 0.00 Seq primer: -400P from Gibco High quality sequence stop: 453. Location/Qualifiers
                                                                57
TAG_LIB=NCI_CGAP_Pr22
TAG_TISSUE=prostate
TAG_SEQ=AAGIG"
                                                              161 g
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US-08-653-294-31 x AW015295/rev
                                                                  148 c
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Unpublished (1997)
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AI492423
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                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                    Quality:
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                                                           . 61
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                                                                                                                                                 alignment_scores:
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TITLE
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KEYWORDS
SOURCE
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/note-"Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_CO10 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block: 24 bp mRNA EST 24-JUN-1999
LOCUS AI762057 524 bp mRNA EST 24-JUN-1999
DEFINITION W153a10.x1 NCI_CGAP_CO16 Homo sapiens cDNA clone IMAGE:2393946 3'
Similar to contains TAR1.tl MER22 MER22 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 524)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Unpublished (1997)
On Jun 5, 1998 this sequence version replaced g1:3187034.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
(cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. 112 t
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Gaps: 0
Percent Identity: 66.667
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/clone_lib="NCI_CGAP_Co16"
/tissue_type="colon tumor, RER+"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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                                                                                            152 g
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High quality sequence stop: 4
Location/Qualiflers
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/tissue_type="26 somite embryos, adult livers, shield
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Ratio:
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JOURNAL
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
LOCUS A1437378 525 bp mRNA EST 09-MAR-1999
DEFINITION fb30h04.x1 Zebrafish WashU MPIMG EST Danio rerio CDNA 3' similar to
SW:PTEN_HUMAN 000633 PUTATIVE PROTEIN-TYROSINE PHOSPHATASE PTEN ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Zbrafish@watson.wustl.edu

CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
from a pool of 5,000 clones made from the same library (cloneins 1057416-1061255, and 1144584-1145311).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
193 c 190 g 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .525
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/db_xref="taxon:7955"
/clone_lib="zebrafish WashU MPIMG EST"
/sex="mixed"
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                                                                                                                                                                                                                                                                      Percent Identity: 66.667
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High quality sequence stop: 426
Location/Qualifiers
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A1437378.1 GI:4285423
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US-08-653-294-31 x AI762057/rev
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Fax: 314 286 1810
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Ratio:
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Exaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopteryg1; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopteryg1; Eleostel; Euteleostel; Ostariophys1; Cyptiniformes; Cyprincidea; Cyprinidae; Rasborinae; Danio.

I (bases I to 531)

Striation of Clark, M., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillar, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ratter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Washu Zebrafish EST Project 1998

Al Unpublished (1998)

On May 7, 1998 this sequence version replaced gi:3119070.

Contact: Stephen L. Johnson

Washington University School of Medicine

4444 Forest Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
LOCUS A1416006 531 bp mRNA EST 09-FEB-1999
DEFINITION 12 26brafish WashU MPIMG EST Danio retio CDNA 5' similar to SW:PTEN_HUMAN 000633 PUTATIVE PROTEIN-TYROSINE PHOSPHATASE PTEN ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TyrargleualalleargleuasnGluargTyrargleualalleargle
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Gaps: 0
Percent Identity: 52.941
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AI416006
AI416006.1 GI:4259510
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3.188
94.118
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US-08-653-294-31 x AI437378
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alignment_block:
US-08-653-294-31 x AW147227/rev
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Percent Similarity: 100.000
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                REFERENCE
AUTHORS
                                                                                             TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Mashington University Genome Sequencing Center Clone distribution: Genome Systems. St. Louis, Missouri (web address: www.genomesystems.com) (email contact: InfoGenomesystems.com) and Research Genetics, Huttsville, Alabama (web address: www.resgen.com) (email contact: infoGersen.com) and RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW147227 235 bp mRNA EST 30-NOV-1999 da16c03.x1 normalized Xenopus laevis gastrula Xenopus laevis cDNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                      /tissue_type="26 somite embryos, adult livers, shield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone XENOPUS_SOURCE_ID:Xlnga001n05 3', mRNA sequence.
AW147227
AW147227.1 GI:6195123
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/clone_lib="2ebrafish WashU MPIMG EST"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 531
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Gaps: 0
Percent Identity: 52.941
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                                                                                                                 stage embryos"
/lab_host="XL1-blue MRF"
Email: zbrafish@watson.wustl.edu
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US-08-653-294-31 x AI416006/rev
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119 c
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94.118
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Ratio:
Percent Similarity:
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REPERENCE 1 (bases 1 to 23)

AUTHORNS CONDEGO, S.L., Blumberg, B., Song, J., Clifton, S., Hiller, L., Packer, M. Matin, J., Wille, T., Undervood, Y., McCann, R., Terrer, B., Matin, J., Wille, T., Undervood, Y., McCann, R., Matin, J., Wille, T., Undervood, Y., McCann, R., Matin, J., Wille, T., Undervood, Y., McCann, R., Mathison, M., Mat
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ORGANISM

KEYWORDS

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mus.
Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
Etheses I to 287)
Scarinci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukunishi, Y., Funayama, T., Akahira, S., Akiyama, J., Forli, F., Ishikawa, T., Itoh, M., Izawa, M., Rawai, J., Kikuchi, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigamo, T., Niatuma, H., Sogabe, Y., Tominaga, N., Matanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Inpublished (1999)
On Dec 20, 1995 this sequence version replaced gi:1134354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 81-298-36-9145

Fax: 81-298-36-9098

Email: genome-researc.riken.go.jp

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))

Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
AV074366 287 bp mRNA EST 24-JUN-1999
AV074366 Mus musculus stomach C57BL/6J adult Mus musculus CDNA
clone 2210008P05, mRNA sequence.
AV074366 GI:5194194
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LOCUS A1070642 345 bp mRNA EST 05-JUL-1999
DEFINITION UI-R-C2-mv-g-10-0-UI.sl UI-R-C2 Rattus norvegicus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Mus musculus stomach C57BL/6J adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
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Gaps: 0
Percent Identity: 57.895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="2210008P05"
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/dev_stage="adult"
76 c 63 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-653-294-31 x AV074366/rev
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                                                                                                                                                                    Xenopus. S. Asenopus. S. Asenopus. S. Hillier, L., Shopus. J. (1) (bases 1 to 246)
Spape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Parson, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R. and May 1, 1997 this sequence version replaced gi:2059622.

Other_ESTs: dal6c03.x1
Contact: Stephen L. Johnson/WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by Bruce Blumberg
Library constructed by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
web page at: http://www.resgon.com/
Seg primer: -408PF from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers

Location/Qualifiers

1. 246

Action="Xenopus laevis"

Action="Xenopus laevis"

Action="Xenopus laevis"

Action="Xenopus laevis gastrula"

Action="In" normalized Xenopus laevis gastrula"

Atissue_type="gastrula (stages 10.5, 11.5 mixed)"

Atissue_type="gastrula (stages 10.5, 11.5 mixed)"

Anote="Vector: pBluescript SK-: Site_1: EcoRI: Site_2:

Anote="Vector: pBluescript SK-: Site_1: Sastrulae).

EcoRI-Anot cut CDNA was then ligated into Unizap-XR

(Stratagene) with EcoRI at the 5' end and XhoI at the 3' end. SS-ilbrary phagemids were prepared from the same library by end. SS-ilbrary phagemids were prepared from the same library by CR) to Cot-omega of 11. After removal of hybrids and excess driver by streptavidin sepharose chromatography, the ss-phagemids were made double stranded and electroporated into Top-10 F'. Original library contruction by Bruce Blumberg (Cho et al. 1991 Cell 67, 1111-1120). Mormalized by Jihwan Song (Song, Cho and Rlumberg unoughlish)
                                                                                             Amphibia;
Xenopodinae;
                                                                                          Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipldae;
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Gaps: 0
Percent Identity: 75.000
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                                   African clawed frog.
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Ratio: 4.000
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US-08-653-294-31 x AW147713
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                                                                   Xenopus laevis
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source

FEATURES

BASE COUNT

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US-08-653-294-31 x AI070642
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.ulowa.edu
The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult 12-Day-Embryo library. CDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics This clone is also available through the I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE
Seq primer: M13 Forward
POLYA-NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev. stage="adult" R-C2"
//dev. stage="adult" R-C3 | ibrary | is a subtracted library derived from the UI-R-C3 | ibrary, which is a subtracted library consisted of a mixture of individually taged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day embryo. The ragis a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C2) was constructed as follows: PCR amplified CDNA inserts from UI-R-C1 clones from within 3' SETS had been derived was used as a driver in a hybridization with the UI-R-C1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DHIOB bacteria (Life Technologies) to generate the UI-R-C2 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10, 20 10
                                                                                                                                                                                                                                                                                                1 (bases 1 to 345)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                          Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Sep 12, 1996 this sequence version replaced gi:1404937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps: 0
Percent Identity: 58.824
UI-R-C2-mv-g-10-0-UI 3', mRNA sequence.
AI070642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="UI-R-C2-mv-g-10-0-UI"
/clone_lib="UI-R-C2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 6 (9), 791-806 (1996)
97044477
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/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                   AI070642.1 GI:3396893
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Ratio:
Percent Similarity:
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AUTHORS
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                                                      ACCESSION
                                                                                VERSION
KEYWORDS
SOURCE
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/clone_1b="A. thaliana, Columbia Col-0, root-2"
/tissue_type="root"
/tissue_type="root"
/dev_stage="root"
/dev_stage="ro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seg_documentation_block:
LOCUS
LOCUS
DEFINITION 701554353 A. thallana, Columbia Col-0, root-2 Arabidopsis thallana
CDNA_clone 701554353, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thale cress.
Arabidopsis thallana
Bukaryota Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana Gene Expression MicroArray Unpublished (1999)
On Aug 23, 1999 this sequence version replaced gi:5761643.
Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4633 World Parkway Circle, St. Louis, MO 63134, USA
Tel: 877-577-2733
Fax: 314-427-3324
                                                                                                                                                                                                     3 LeuAlalleArgLeuAsnGluArgTyrArgLeuAlalleArgLeuAsnGl 19
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Gaps: 0
Percent Identity: 57.895
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Coultivar-"Columbia Col-0"
/db_xref="taxon:3702"
/clone="701554353"
to: 345
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Location/Qualifiers
1. .579
from: 1
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3.429
73.684
to: AI070642
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: Jwallacedu. Washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pleter@delpong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.hisc.washington.edu
Plate: 760 row: I column: 9
                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 507)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                      A0514060 507 bp DNA GSS 05-MAY-1999
HS_5184_A1_E05_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=760 Col=9 Row=I, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBACe3.6; Genomic sequence of BAC ends"
119 c 107 g 143 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="Plate=760 Col=9 Row=I"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence-tagged connectors: A sequence approach to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 19
Gaps: 0
Percent Identity: 47.368
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to reverse of: AQ514060 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"/db_xref="taxon:9606"
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                                                                                                                                  AQ514060.1 GI:4746351
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US-08-653-294-31 x AQ514060/rev
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2.765
89.474
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                     seq_documentation_block:
LOCUS AQ514060
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Ratio:
Percent Similarity:
                                                                                          genomic c
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                                                                                                                                                                                  human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                  DEFINITION
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MEDLINE
                                                                                                             ACCESSION
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                                                                                                                                                                                                                                                                                                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
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                                                                                                                                                                                                                                                                                                                                                      a8a03ne.fl Neurospora crassa evening cDNA llbrary Neurospora crassa cDNA clone a8a03ne 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="vector: pBlueScript SK-; Site_1: Xbal; Site_2:
ECORI; See: Bell-Perdersen,D., et al. PNAS 93:13096,1996.
5' end of cDNA cloned into Xbal site of pBluescript; 3'
end of cDNA cloned into ECORI site of pBluescript"
16 c 9 6 g 118 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seq primer: Universal Forward Primer
High quality sequence stop: 343.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="a8a03ne"
/clone_lib="Neurospora crassa evening cDNA library"
/tissue_type="tissue harvested following 22hr growth in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu Department of Chemistry and Blochemistry Advanced Center for Genome Technology, University of Oklahoma 620 Parrington Oval, Norman, OK 73019, USA Tel: 405 325 4912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurospora crassa.
Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pyrenomycetes; Sordariales;
                                                                                                                                     385 Arcceccrecaagaecegreecercregacaragecegaaaceaecee 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ArgLeuAlaIleArgLeuAsnGluArgTyrArgLeuAlaIleArgLeuAs
                                                                  to: 579
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Gaps: 0
Percent Identity: 68.750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 484)
Zhu, H., Lai, H., Kupfer, D., Dunlap, J.C.
Two Neurospora crassa EST Databases
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. 484
/organism="Neurospora crassa"
/strain="Strain 30-7 (bd; A)"
/db_xref="taxon:5141"
                                                                  from: 1
                                                                to reverse of: A1997515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AI328939.1 GI:4065498
alignment_block:
US-08-653-294-31 x AI997515/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-653-294-31 x AI328939/rev
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3.615
81.250
                                                                                                                                                                                                                                                                                                seq_name: gb_est26:AI328939
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                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS AI328939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                  295 CTATCGA 289
                                                                                                                                                                                                        nGluArg 20
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                                                                Align seg 1/1
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

DEFINITION

18

ACCESSION

to: 507

BASE COUNT ORIGIN

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Quality:
Ratio:
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JOURNAL
COMMENT
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pHSS6-Sal; A yeast genomic DNA library leakth.pdf. leakthg mitochondrial DNA) was prepared in pHSS6-Sal; genomic DNA was size-fractionated (DNA of roughly 2-3 kb in length) prior to cloning. This library was ubsequently mutagenized with a mTn-3xHA/Lacz minitransposon containing lacz, URA3, and tet resistance."
                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycetales;
Saccharomycetacee; Saccharomyces.

1 (bases 1 to 533)
1 (bases 1 to 533)
1 (bases 1 to 534)
1 (bases 1 to 534)
1 (bases 1 to 535)
1 (bases 1 to 536)
1 (ba
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Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Radota, K., Ragawa, I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AV266473 271 bp mRNA EST 05-NOV-1999
AV266473 RIKEN full-length enriched, adult male testis (DH10B) Mus
musculus cDNA clone 4930518A01 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         house mouse.
Mus musculus musculus instanta; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 271)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene Disruption
L Unpublished (1999)
On Feb 19, 1999 this sequence version replaced g1:4143976.
On Feb 19, 1999 this sequence version replaced g1:4143976.
Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 9949
Fax: 203 432 6161
Email: anuj. Kumarevale.edu
te of mTn-3xHA/lacz insertion.
Seq primer: GGCCTTCTTTGGAGTAC
Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:4932"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .533 /organism="Saccharomyces cerevisiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 14
Gaps: 0
Percent Identity: 64.286
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                                                                                                                                                             Saccharomyces cerevisiae
AQ500194
AQ500194.1 GI:4705016
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92.857
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US-08-653-294-31 x AQ500194
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                                                                                                                            baker's yeast.
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LOCUS AV266473
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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                                            VERSION
KEYWORDS
SOURCE
        ACCESSION
                                                                                                                                                                                                                                                                             REFERENCE
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Meal.C., Corea T., Miki.R., Misuno Y., Wakamirah. Odan.R., Odanki.Y., Odanki.Y., Shibata Y., Shilata K., Shibata K., Shibata Y., Shilata K., Shibata K., Shibata K., Shibata Y., Shilata Y., Takahahi.F., Tataon W., Tominada N., Tominada Y., Wathiki.A., Wathinabe, S., Zhammira.R., Takahahi.Y., Taminahi.F., Tataon Y., Tominahi.Y., Taminahi.P., Taminahi.P., Taminahi.R., Taminahi.P., Taminahi.P., Taminahi.R., Taminahi.P., Taminahi.P., Taminahi.R., Taminahi.P., Taminahi.P.,
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18 nGluArg 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L., Turner, C., Krikorian, S., Elder, L. and Hanson, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                         A1998I22 330 bp mRNA EST 08-SEP-1999 7016/2303 A. thaliana, COlumbia Col.0, rosette-1 Arabidopsis thaliana CDNA clone 701672303, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi:3189440.
Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.
Pharmaceuticals, Inc.
Acid World Parkway Circle, St. Louis, MO 63134, USA
Tel: 877-577-2733
Fax: 314-427-3324
Email: service@genomesystems.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 others
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Gaps: 0
Percent Identity: 52.632
                                                                                                                                                                                                                  169 GCTGTAAGAGTAAATGCTAGGTATCGAGTTGCTGTCACCCTC 210
                                                                                                                                                                   4 AlaileArgLeuAsnGluArgTyrArgLeuAlaileArgLeu 17
                                                                                 to: 271
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70 c 68 c
                                                                                 to: AV266473 from: 1
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1 (bases 1 to 330)
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US-08-653-294-31 x AI998122
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                                                                                 Align seg 1/1
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JOURNAL
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AUTHORS
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KEYWORDS
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to: 330

from: 1

Align seg 1/1 to: A1998122

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2 ArgleuAlalleArgleuAsnGluArgTyrArgLeuAlalleArgLeuAs 18
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200 GCTCAGG 206

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February 8, 2000, 04:05:44; Search time 133.56 Seconds (without alignments) 4.434 Million cell updates/sec

US-08-653-294-32

133 1 WDRETQICKAKAQIDRENLRIALRY 25 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

188963 Total number of hits satisfying chosen parameters:

188963 seqs, 23686106 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

A_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ptide fo	HLA-B2702 CTL modu	HLA-B2702.60-84. C	Peptide B2702.60-8	Peptide fragment o	HLA-B2702 CTL modu	HLA-B2705.60-84. C	Sequence of the hu	Sequence encoded b	latin	Human HLA-B27 alph	Peptide fragment o	HLAB38 CTL modulat	HLAB38.6084. Comps	HLA-B7.60-84. Comp	e of HI	Seq	e of HLA	HLA-Bw53 exon. HLA	seg	E	702	Human HLA-B27 alph	Peptide fragment o	HLA-Bw62 CTL modul	HLA-Bw62.60-84. Co	Peptide fragment o	Š	HLA-Bw46.60-84. Co	⊣	HLA-C exon Cb-1. H	cancer a	fragment	HLA-B35 antigen. H
SUMMARIES		4.1	m	ഗ	ന	-	R83091	R95417	P70590	P70155	R83071	W58992	R48286	R83093	R95422	R95431	R03142	Y06801	R03144	R12463	P80911	R92912	W33795	W58993	R41207	R83073	R95419	_	m	ഹ	-	N	X07033	-	\sim
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HLA-C exon Cb-2. H Human HLA-B27-(62- Human MHC 1 alpha Probe FlO-encoded HLA B27 hypervaria MHC Class I-derive MHC-I peptide Dk-(Human MHC 1 alpha Peptide Eragment o HLA-B2702/05 CTL m
R12466 R71443 R71443 R71443 P83149 R80266 R20116 R71420 R411420 R411420 R41244
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366 174 245 345 145 125 255 100 100
4444444444 8777900000444 04490000000000000000000000000
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                                           Example 13; Page 32; 80pp; English.
R83061-R83085, R83090-R83096 and R93907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HLA-B3702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-NOV-1996 (first entry)
HLA-B2702.60-84.
HLA-B2702.60-84.
That, PV4: alphal-helix, human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
- using Class I B75-84 MHC antigen of the recipient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 25;
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ilarity 100.0%; Pred. No. 4.1e-14;
Conservative 0; Mismatcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 133; DB 1;
100.0%; Pred. No. 4.1e-14;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI: 95-194027/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 WDRETQICKAKAQTDRENLRIALRY 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R95416 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25; Conservative
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Best Local Similarity
Matches 25; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                   25 AA;
     donor hosts
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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Gaps

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Query Match Best Local Simi Matches 25;

Length 25;

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treating autoimmune diseases

Example 1: Page 19: 41pp; English.

Peptides Wi3784-98 and Wi3778-9 were assayed for their immunomodulating activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or creaminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (C-terminal amidated compound comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = (D, S or N; aa79 = R or E; aa80 = I or N; aa10 = R or E; aa81 = a hydrophobic or small amino acid; aa82 = R or E; aa83 = G or R; and as represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprises amino acid sequences related to a Class I HIA-B alphal domain (positions 79-84). They can be used to inhibit cyctoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in cresponse to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, consultation with antigenic because the products can also be consultative or the products can also be
                                                                                                                                                                                                                                                                                                                      19-JUN-1998 (first entry)
Peptide B2702.60-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosupressant drug; CTL activation; transplantation; autoAmmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R41221;
15-WAR-1994 (first entry)
Peptide fragment of HiA-B2705 antigen.
Human leukocyte antigen; HiA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic T lymphocyte; modulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-NOV-1997.
22-MAY-1995.
24-MAY-1996. US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
(STRD ) UNIV LELAND STANFORD JUNIOR.
WPI; 98-Ulow R, Clayberger C, Krensky AM;
WPI; 98-Ulow G, Uloyberger C, Krensky AM;
WPI; 98-Ulosof G, William G, Linary G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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100.0%; Pred. No. 4.1e-14;
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25-FBE-1993; 001758.
02-FMR-1992; US-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                                                                                                                                                  W33794 standard; peptide; 25 AA
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1 WDRETQICKAKAQTDRENLRIALRY
                                     1 WDRETQICKAKAQTDRENLRIALRY
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Best Local Similarity
Matches 25; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rejection.
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This is a superior of the proteins of the may inhibit cytolytic activity and differentiation of CTLS.

Example: Rage 9: 29pp: English.

Example: Rage 9: 29pp: English.

Example: Page 9: 20pp: Englis
                       HIA-B2705.60-84.

HIA-B2705.60-84.

HIA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;

T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;

B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Such DNA, antigen or antibody
Disclosure; Page 5: 5pp; German.
The DNA may be used as a hybridisation probe for detecting the HLA
B27 gene, eg for assessing susceptibility to rheumatic disorders
such as ankylosis spondylitis, or may be used to transform cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA coding for antigen HLA B27 - and diagnostic reagents contg.
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88.7%; Score 118; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 8.1e-12;
Matches 22; Conservative 1; Mismatches 2; Indels
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Sequence of the human histocompatibility antigen HLA B27
Rheumatic disorder; genetic screening; diagnosis;
ankylosing spondylltis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BEHW ) BEHRINGWERKE AG.
Riethmuller G, Meo T, Weiss E, Szots H;
                                                                                                                                                                                                                                18-MAY-1995.
10-NOV-1994, U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                             cytolysis; antigen presenting cell.
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P70590;
                                                                                                                                                                                                                                                                                                                                              Krensky AM;
     (first entry)
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28-NOV-1985; DE-542024.
21-DEC-1985; DE-545576.
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N-PSDB; N70935.
                                                                                                                                                                                                                                                                                                                                           Clayberger C, Kr
WPI; 95-194027/25
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R83061-R83085, R83090-R83096 and R93907-F92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HIA-B3702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
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HIA-B2702 CTL modulating peptide (B2702.60-84).
Cytotoxic T lymphocyte: CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
                                                                               modulating cytotoxic T-lymphocyte activity towards targets
Example 13; page 39; 61pp; English.
The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
activity, either by inhibition or stimulation. It can be used for
inhibiting CTL toxicity in transplantations, for inducing CTL
inhibiting CTL coxicity in transplantations, for inducing CTL
infection. The peptide can also be used for identifying CTLs which
bind to it and removing subsets of CTLs from a T-cell composition.
This peptide is derived from the HLA-B2705 antigen and corresponds
to the amino acid positions 60-84 of that antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Clayberger CA, Krensky AM;
WPI; 93-303134/38.
New peptide(s) based on Class I HLA antigen domains - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.7%; Score 118; DB 1; Length 25; 88.0%; Pred. No. 8.1e-12; ive 1; Mismatches 2; Indels
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12-OCT-1995.
05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22
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Best Local Similarity 88.0
Matches 22; Conservative
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Best Local Similarity 88.0
Matches 22; Conservative
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Sequence

host

R95417;

RESULT R95417 ID R AC R

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Gaps

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21 AA;
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                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                        Query Match
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CLT modulating peptide #5.
Cytocoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy;
                                                                                                                                                                                                                                                                                                                                                                              DNA coding for human histocompatibility antigen HIA-B 27 - useful for diagnosis and antigen and antibody prodn.

Disclosure: p6: 13pp; German.

THE DNA may be used to detect the HLA-B 27 gene (opt. mutated) in human genetic material. The HLA-B 27 may be used to detect anti-HLA-B 27 antibodies in human serum. The antibodies may be used to detect anti-HLA-Germine HLA-B 27 levels in human serum, eg for diagnosis of rheumatic disorders, esp. ankylosing spondylitis.
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
for prodn. of HLA B27. The HLA B27 may be used to detect HLA B27 antibody in human serum, or to produce mono- or polyclonal HLA B27 antibodies for use in immunoassay. Sequence 337 AA;
                                                                                                                                                                                                                             03-APR-1991 (first entry)
Sequence encoded by genomic DNA encoding human histocompatibility
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.7%; Score 118; DB 1; Length 362; 88.0%; Pred. No. 1.6e-10; Live 1; Mismatches 2; Indels
                                                                    Length 337;
                                                        Score 118; DB 1; Length 35
Pred. No. 1.5e-10;
                                                                                                                                                                                                                                                                                                                                                   Szots H, Weiss E, Dorner C, Lang M, Meo T, Riethmuller G; WPI: 87-171469/25.
N-PSDB; N70225.
                                                                                                                                                                                                                                                             Ankylosing spondylitis; rheumatic disorder; diagnosis.
                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                          60 WDRETQICKAKAQTDREDLRTLLRY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                          P70155 standard; protein; 362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'label - Asn, Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Ala, Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label= Ile, Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R83071 standard; peptide; 26 AA.
                                                                    88.7%;
88.0%;
                                                                 Query Match 88.7%
Best Local Similarity 88.0%
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22; Conservative
                                                                                                                                                                                                                                                                                                                                          (BEHW ) BEHRINGWERKE AG
                                                                                                                                                                                                                                                                                               24-JUN-1987.
21-NOV-1986; 116139.
01-JAN-1985; DE-542024.
21-DEC-1985; DE-545576.
                                                                                                                                                                                                                   (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 22; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_difference 18
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                                                                                                                                                                                                                                                  antigen HLA-B 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9526979-A1.
                                                                                                                                                                                                                                                                         Homo sapiens.
EP-226069-A.
                                                                                                                                                                                                                  10-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-0CT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        class I MHC
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R83071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
R83071
AC R83071
AC R83071.
DE T-MAY.
DE T-MAY.
DE CYLCHOOK
KW ALMHUNOS
KW ALMHUNOS
KW ALMHUNOS
FF KEY
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P70155
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Treatment and diagnosis of HLA-dependent autoimmune disease - using peptide(s) derived from HLA-B27 or human keratin VI, e.g. for peptide(s) derived from HLA-B27 or human keratin VI, e.g. for Claim 2: Page 9: 57pp; German.

CC HLA-B27 or human keratin IV and are used in methods for diagnosis and/or treatment of HLA (human leucocyte antigen)-dependent autoimmune diseases. Such peptides have implications in the treatment of cases of Class I and II-associated autoimmune diseases, especially non-HLA-B27 diseases (iritis, uveitis, psoriasis and rheumatic diseases such as arbitis, psoriatic arthritis or Juvenile rheumatic diseases such as arbitistered intravenously, subcutaneously or intramuscularly, or to be administered intravenously, subcutaneously or intramuscularly, or to the mucosa (orally, or as nasal or pulmonary spray). This method results in antigens that are more specific than complete protein antigens, so provide a more exact classification of disease, and thus a more specific treatment. In the case of keratin-derived peptides, they also have better solubility. Compared with complete proteins, peptides are easier to prepare, do not require recovery from natural tissue or recombinant methods of production, have better storage stability when dry, are less contains and prepared methods of production, have required required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 9; 80pp; English.
R83061-R83085, R83090-R83096 and R82907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs) of the patient.
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Human HLA-B27 alpha-1 domain (aa. 60-80) peptide B27PA.

Human leucocyte antigen; HLA; alpha-1 domain; alpha-2 domain; HLA-B27;

Keratin VI; diagnosis; treatment; HLA-dependent autoimmune disease;

Class I-associated autoimmune disease; iritis; uveitis; psoriasis;

Class II-associated autoimmune disease; rheumatic disease; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                  Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.2%; Score 112; DB 1; Length 26; 84.0%; Pred. No. 7e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ankylosing spondylitis; antigen; regulator.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 WDRETQICKAKAQTDRENLRIALRY 25
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Matches 21; Conservative
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18-SEP-1997; E05124.
18-SEP-1996; DE-038108.
                                                                                                                 Clayberger C, Krer
WPI; 95-358582/46.
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WO9812221-A1.
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1 WDRETQICKAKAQTDRENLRIALRY 25
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                                                                                                                                                                                                                                                                                              12-NOV-1996 (first entry)
                                                                                                                           Query Match
Best Local Similarity 80.0
Matches 20; Conservative
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Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                  R95422;
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27-FEB-1993: U01758.

28-FEB-1993: U01758.

29-MRR-1992: US-844716.

20-MRR-1992: US-844716.

21 Clayberger CA, Krensky AM;

WHI: 39-301314/38.

New peptide(s) based on class I HLA antigen domains - used for modulating cytotoxic T-1ymphocyte activity towards targets

Example 13: Page 39: Glpp: English.

The peptide is used to modulate cytocxic T-1ymphocyte (CTL)

Cativity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL

Cativity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which conditions to it and removing subsets of CTLs from a T-cell composition.

This peptide is derived from the HLA-B38 antigen and corresponds to the amino acid positions 60-84 of that antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLAB38 CTL modulating peptide (B38.6084).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLAB38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 13; Page 32; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                     Gaps
                                                                                                                                                                            15-MAR-1994 (first entry)
Peptide fragment of HLA-B38 antigen.
Human leukccyte antigen, HLA, peptide; transplantation; neoplasia;
parasitic disease; cytotoxic T lymphocyte; modulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clayberger C, Krensky AM, Parham P; WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 106; DB 1; Length 25; Pred. No. 5.6e-10; Mismatches 5; Indels
          Length 21;
         Score 109; DB 1; I
Pred. No. 1.6e-10;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR
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82.0%; Scc..
100.0%; Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R83093 standard; peptide; 25 AA.
                                                                                                                                                     R48286 standard; peptide; 25
                                                                          1 WDRETQICKAKAQTDRENLR 20
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80.0%;
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                                                            1 WDRETQICKAKAQTDRENLR
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Best Local Similarity 80.09
                     Similarity 100.
20; Conservative
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05-APR-1995; U04349.
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HLAB38 CTL m
         Query Match
Best Local
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                      Best Loca
                                                                                                                           RESULT 12
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While Stranger's comparising lymphoid surface membrane proteins - which may will by 1940L/LY.

Tompsons. comparising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example: Page 9: 29p; English.

R95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the HLAB38.6084. These sequences can be used to isolate the protein p74 from a T-ceil lyaste. P74 is a T-ceil surface membrane protein associated with T-ceil activation in mammalian T-ceils, and is also immunologically cross reactive with the heat shock protein HSc70. P74 is found in a ceils. P74 can be isolated by lysis of a suitable ceil with an amphoteric detergent, and then passed through an affinity column collist. P74 can be isolated by lysis of a suitable ceil with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide.

Compositions comprising the extracellular fragment of P74 combined with CAT-ceils, by combining them with the extracellular portion of P74, and determining the amount of binding between the candidate compound and p74.

Containing T-ceils and antigen presenting cells (APCS), by adding to the mix the extracellular portion of P74, in an amount sufficient to compete containing of the P74 ligand.
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HIAB38. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an WHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLAB38.6084.
HLAB38.6084.
HLAB38.6084.
HLAP, p74. alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic T lymphocyte; CIL; differentiation;
cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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80.0%; Pred. No. 5.6e-10;
"Homatches 5;
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80.0%; Pred. No. 5.6e-10;
ive 0; Mismatches 5;
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10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
(Clayberger C, Krensky AM;
WPI; 95-194027/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 WDRETQICKAKAQTDRENLRIALRY 25
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us-08-653-294-32.rag

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will solidate the manual surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example: Page 12: 29pp; English.

Example: Page 13: 20pp; English.

Example: Page 13: 20pp; English.

Example: Page 13: 20pp; English.

Example: Page 14: 20pp; English.

Example: Page 15: 20pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete
                                                                                                                                                                          HLA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with p74 for the binding of the p74 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                      10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRO) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI: 95-194027/28
R95431
ID R95431 standard; peptide; 25 AA.
                                                                                                                (first entry)
                                                                                                         12-NOV-1996
HLA-B7.60-84
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Query Match 78.2%; Score 104; DB 1; Length 25; Best Local Similarity 95.0%; Pred. No. 1.1e-09; Matches 19; Conservative 1; Mismatches 0; Indels
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1 WDRETQICKAKAQTDRENLR 20

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1 WDRETQICKAKAQTDRESLR 20

Search completed: February 8, 2000, 04:05:44 Job time: 9361 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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 protein search, using sw model OM protein

Run on:

February 7, 2000, 18:04:40; Search time 111.22 Seconds (without alignments) 10.603 Million cell updates/sec

US-08-653-294-32 133 1 WDRETQICKAKAQTDRENLRIALRY Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

142080 seqs, 47169319 residues Searched:

hits satisfying chosen parameters: Total number of

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

PIR_62:* Database :

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES		ISSASON DE PROCESSION DE PROCE	0167 class I	MHC clas	MHC HLA-B27-	MHC c	human lymph	MHC C	MHC HLA-B27		class I	class I	9 class I	71 class I	class I	class I	HLA-	5 MHC clas	class I	class I		HLA-B al	class	MHC clas	I61861 MHC HLA-B44.2 chai	I84486 transmembrane glyc	MHC class I h	38509 MHC class I	A45834 MHC class I histoc	· control control
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	en	354	354	359	338	362	362	362	362	362	362	362	355	355	363	363	274	362	362	354	362	355	362	362	362	362	362	273	362	
de	$_{\rm ch}$	93.2	m	90.2	88.7	88.7	88.7	88.7	88.7	85.7	85.7	85.7	。	ö	80.5	。	φ.	75.9	δ.	ω.		ď.	'n		ς.		ς.			
	Score	124	124	120	118	118	118	118	118	114	114	114	107	107	107	107	106	101	101	86	98	96	96	96	96	96	96	92	95	
	Result No.		7	e	7	S	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	

MHC class I histoc HIA-AWA4 protein - HIA-AWA4 protein - MHC class I histoc MHC class I histoc MHC class I histoc class I histoc MHC class I histoc Class I histocompa class I histocompa	
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## ALIGNMENTS

SULT 1	9308	class I histocompatibility antigen – pygmy chimpanzee (fragment)	C;Species: Pan paniscus (pygmy chimpanzee, bonobo)	Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 23-Jul-1999	C;Accession: 159308
RESULT	I59308	class	C; Spe	C; Dat	C; Acc

C. Accession: 159308
R; McAdam, S.N.; Boyson, J.E.; Llu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Wat Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A; Title: A uniquely high level of recombination at the HLA-B locus.
A; Reference number: 159308; MUID: 94286544
A; Accession: 159308
A; Accession: 159308
A; Molecule type: MRNA
A; Residues: 1-354 <RES>
A; Cross references: EMBL: U05575; NID: 9454767; PIDN: AAAS0178.1; PID: 9454768
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology

Gaps ö Length 354; Indels Query Match 93.2%; Score 124; DB 2; Le Best Local Similarity 92.0%; Pred. No. 9.4e-12; Matches 23; Conservative 1; Mismatches 1;

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76 WDRNTQICKAQAQTDRENLRIALRY 100 셤

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Class I histocompatibility antigen - pygmy chimpanzee (fragment)
Class I histocompatibility antigen - pygmy chimpanzee, bonobo)
C;Species: Pan paniscus (pygmy chimpanzee, bonobo)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C;Caccession: 18016
R;McAdam, S. N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Wat Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Reference number: 159308; MUID:94286544
A;Reference number: 159308; MUID:94286544
A;Residues: 1-354
A;Residues: 1-354
A;Residues: 1-354
CRES>
A;Cross-references: EMBL:U05578; NID:9454773; PIDN:AAA50181.1; PID:9454774
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

Gaps ö Length 354; Query Match 93.2%; Score 124; DB 2; Length 35 Best Local Similarity 92.0%; Pred. No. 9.4e-12; Matches 23; Conservative 1; Mismatches 1; Indels

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A; Molecule type: mRNA
A; Residues: 1-139, 'H', 141-362 < CDAM>
A; Residues: 1-139, 'H', 141-362 < CDAM>
A; Cross-references: EMBL: 233453; NID: 9486652; PIDN: CAA83876.1; PID: 9486653
B; Ezquerra, A.; Bragado, R.; Vega, M.A.; Strominger, J.L.; Woody, J.; Lopez de Castro
Biochemistry 24, 1733-1741, 1985
A; Title: Primary structure of papain-solubilized human histocompatibility antigen HLA
A; Reference number: A90493; MUID: 85226361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          restriction analysis of a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLA-B27 genomic exon sequences isolated from
equence_revision 28-Apr-1995 #text_change 22-Jun-1999
.25092; B25092; A94087; S34180; S44942; A90493; B24741; I55965;
'; Doerner, C.; Lang, M.; Riethmueller, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.Szoets, H.; Riethmueller, G.; Welss, E.; Meo, T.
Proc. Natl. Acad. Sci. U.S.A. 83, 1428-1432, 1986
A;Ftle: Complete sequence of HLA-B27 cDNA identified through the characterization (A). Reference number: A94087; MUID:86149317
A;Accession: A94087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Molecule type: protein A; Molecule type: protein A; Molecule type: 25-25, F2, 267-295 < EZQ>
R; Rojo, S.; Aparicio, P.; Bragado, R.; Lopez de Castro, Proc. Natl. Acad. Sci. U.S.A. 82, 7394-7398, 1985
Proc. Natl. Acad. Sci. U.S.A. 82, 7394-7398, 1985
A; Title: Estructural analysis of an HIA-B27 functional variant: identification of A; Reference number: A94070; MUID:86042671
A; Accession: B24741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             may generate polymorphism in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-362 <SEE>
A;Cross-references: GB:X03665; NID:932250; PIDN:CAA27302.1; PID:g871297
A;Acces:this allele is designated B*27051 (formerly 27W)
A;Accession: B25092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A. Residues: 1-100, 'N', 102-103, 'IA', 106-362 <SE2>
A. Cross-references: GB:X03664; NID:g32236; PIDN:CAA27301.1; PID:g871296
A. Note: this allele is designated B*2702 (formerly 27K)
                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                         gene:
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A;Residues: 1-100,'S',102-<u>137,'</u>D',139,'Y',141-175,'E',177-362 <VIL>
                                                                                                                                                                                                                                                                                                                                                                      Ala
                                                                                                    A TITLE: Organization, NOUS, NOTE 1985

A TITLE: Organization, sequence and expression of the HLA-B27 gen A, Teference number: S07441; MUID:86138405

A, Reference number: S07441; MUID:86138405

A, Rolecule type: DNA

A, Residues: 1-362 < WHEL:
A, SCOSS = references: EMBL: X03945

A, NOTE: the authors translated the codon GAC for residue 61 as Ali
A, Note: this allele is designated B*27052 (formerly 27W)

R, Seemann, G. H.A.; Rein, R.S.; Brown, C.S.; Ploegh, H.L.

EMBO J. 5, 547-552, 1986

A, Title: Gene conversion-like mechanisms may generate polymorphisi
A, Reference number: A91061; MUID:86220133
                                                                                                                                                                                                                                                                                                                                                                          as
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submitted to the EMBL Data Library, May 1994
A;Description: Identification of a novel HLA-B27 subtype by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Molecule type: protein
A; Residues: 86-100, N', 102-103, IA', 106-107;171-181 <VEG>
K; Coppin, H.L.; McDevitt, H.O.
J. Immunol. 137, 2168-2172, 1986
A; Title: Absence of polymorphism between HLA-B27 genomic of A; Reterence number: 155965; MUID:87009855
A; Accession: 155965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 25-205, 'v', 207-362 <S20>
A;Cross-references: GB:M12678
A;Note: this allele is designated B*27052 (formerly 27W)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reference number: S34180 ;Accession: S34180 ;Accession: S34180
              C;Date: 13-Aug-1986 #sequence_revision 28-Apr
C;Accession: S07441; A25092; B25092; A94087;
R;Weiss, E.H.; Kuon, W.; Doerner, C.; Lang, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Cross-references: EMBL:X73578
A:Note: this allele is designated B*2706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ty Vilches, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Map position: 6p21.3
A; Map position: 6p21.3
A; Introns: 22/1; 112/1; 204/1; 296/1; 335/1; 346/1
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterodimer; transmembrane protein; transplantati
E; 1-21/Domain: signal sequence #status predicted <SIG>
F; 2-35/9/Product: class I histocompatibility antigen HLA alpha chain #status predicted <F; 22-304/Domain: extracellular #status predicted <EXT>
F; 22-111/Domain: alpha-1 <EXI>
                                                                                                                       hur
                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA Sharesters: 1-359 CAML.
A; Residues: 1-359 CAML.
A; CTOSS-references: GB:J00191; GB:V00526; NID:9187600; PIDN:AAA36218.1; PID:9386873
C; Comment: The seven exons correspond approximately to the domain structure of this chai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Homo sapiens (man)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C; Accession: 156116
B; Choo, S. Y.; Fan, L.A.; Hansen, J.A.
J. Immunol. 147, 174-180, 1991
A; Title: A novel HIA-B27 allele maps B27 allospecificity to the region around position A; Reference number: 156116; MUID:91268545
A; Accession: 156116
A; Status: preliminary: translated from GB/EMBL/DDBJ
                                                                                                                       (clone pHLA 12.4) -
                                                                                                                                                                                                                                                  R;Malissen, M.; Malissen, B.; Jordan, B.R.
Proc. Natl. Acad. Sci. U.S.A. 79, 893-897, 1982
A;Title: Exon/intron organization and complete nucleotide sequence of an HLA gene.
A;Reference number: A02189; MUID:82151002
A;Accession: A02189
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MHC class I histocompatibility antigen HLA-B27 alpha chain precursor - human
C:Species: Homo saplens (man)
                                                                                                                MHC class I histocompatibility antigen HLA alpha chain precursor (clone pHLA C;Species: Homo sapiens (man)
C;Species: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHC HLA-B27-HS - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul_1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
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C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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F:335-359/Domain: intracellular #status predicted <INT>
F:107/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:224-280/Disulfide bonds: #status predicted
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Pred. No. 4e-11;
2; Mismatches 1; Indels
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Pred. No. 7.7e-11;
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A;Molecule type: mRNA
A;Residues: 1-338 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :112-203/Domain: alpha-2 <EX2>
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88.0%;
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88.0%;
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Best Local Similarity 88.0
Matches 22; Conservative
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Best Local Similarity
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UH0541

Class Instrocompatibility antigen Gogo-B0103 heavy chain precursor - lowland gorilla class Instrocompatibility antigen Gogo-B0103 heavy chain precursor - lowland gorilla (Species: Gorilla gorilla (lowland gorilla)

C.Species: Gorilla gorilla (lowland gorilla)

C.Species: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999

C.Accession: JH0541

F.Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.

J. Exp. Med: 174, 1491-1509, 1991

A.Title: Gorilla class I major histocompatibility complex alleles: comparison to huma A; Reference number: JH0534; MUID: 92078860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C;Accession: 154289
R;Choo, Z; X; X; X; Juloh, T; Orr, H.T; Hansen, J.A.
Hum. Immunol. 21, 209-219, 1988
A;Title: Molecular analysis of the variant alloantigen HLA-B27d (HLA-B*2703) identifi
A;Recession: 154289; MUID:88227491
A;Accession: 154289
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Alecule type: DNA
                                                                                                                                                                                                      A;Cross-references: EMBL:X73578; NID:g975658; PIDN:CAA51980.1; PID:g975659
C;Genetics:
                                                                                                                                                                                                                                                                                                A;Cross-references: GDB:120048; OMIM:142830
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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A;Map position: 6p21.3
A;Introns: 25/1: 115/1; 207/1; 299/1; 338/1; 349/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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X;Residues: 1-362 <LAMP.
A;Cross-references: EMBL:X60254; NID:g22869; PIDN:CAA42806.1; PID:g22870
A;Experimental source: EBV-transformed B cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M54883; NID:g187663; PIDN:AAA59616.1; PID:g187664
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 118; DB 2; L6
Pred. No. 8.2e-11;
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A;Title: Nucleotide sequence of HLA-B*2706.
A;Reference number: 137515; MUID:94102824
A;Accession: 137515
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 WDRETQICKAKAQTDRENLRIALRY 25
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88.0%;
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Matches 22; Conserv
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                                                                                                                                    A; Molecule type: mRNA
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                                                                                                                                                                      A; Residues: 1-362
                                                                                                                                                                                                                                                                        A; Gene: GDB: HLA-B
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A. Map position: 6p21.3-6p21.3
A. Map position: 6p21.3-6p21.3
A. Map position: 6p21.3-6p21.3
A. Introns: 25/1.114/1. 207/1; 299/1; 338/1; 349/1
A. Introns: 25/1. 114/1; 207/1; 299/1; 338/1; 349/1
C. Superfamily: class I histocompatiblity antigen; immunoglobulin homology
C. Keywords: ankylosing spondylitis; duplication; glycoprotein; heterodimer; transmembran F: 124/Domain: signal sequence #status predicted <SIG>
F: 25-36/Product: class I histocompatibility antigen HIA-B27 alpha chain #status predict F: 25-307/Domain: extracellular #status predicted <EXT>
F: 25-114/Domain: alpha-1 <EXI>
                                                                                                                                                                                                                                                                                  C;Comment: This allele for HLA-B correlates with the development of ankylosing spondylit C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               restriction analysis of a cytotox
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C; Species: Homo sapiens (man)
C; Species: O2-Ju1-1996 #sequence_revision 02-Ju1-1996 #text_change 23-Ju1-1999
C; Accession: 137486 #sequence_revision 02-Ju1-1996 #text_change 23-Ju1-1999
C; Accession: 137485 #sequence_revision 02-Ju1-1996 #text_change 23-Ju1-1999
D: Immunol: 153, 3093-3100, 1994
A; Title: Identification of a novel HLA-B27 subtype by restriction analysis of a cytoto A; Reference number: 137485; WUID:94375872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHC class I histocompatibility antigen HLA-B*2706 alpha chain precursor - human
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C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 23-Jul-1999
C;Accession: 137515
R;Vilches, C.; de Pablo, R.; Kreisler, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-362 <RES>
A;Cross-references: EMBL:233453; NID:9486652; PIDN:CAA83876.1; PID:9486653
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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             A;Cross-references: GB:M14013; NID:g187743; PIDN:AAA59643.1; PID:g187744 R;Blasczyk, R.; Weber, M.; Salama, A. submitted to the EMBL Data Library, January 1995 A;Reference number: S52291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;115-206/Domain: aipha-2 <EX2>
F;220-285/Domain: immunoglobulin homology <IMM>
F;220-285/Domain: transmembrane #status predicted <TMM>
F;308-331/Domain: transmembrane #status predicted <TMM>
F;310/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;125-188,227-283/Disulfide bonds: #status experimental
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88.0%; Pred. No. 8.2e-11;
tive 1; Mismatches 2;
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A;Molecule type: mRNA
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Immunogenetics 39, 219, 1994
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                                                                                                                                                               A; Accession: $52291
A; MoLecule type: DNA
Residues: 116-192 <BLA>
A; Cross-references: EMBL:X83737
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A; Residues: 25-298 <RES>
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Best Local Similarity
Matches 22; Conserv
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C;Superfamily: class I histocompatibility antigen; immunoglobulin homology C;Keywords: transmembrane protein F;1-24/Domain: signal sequence #status predicted <SIG> F;1-24/Domain: signal sequence #status predicted <SIG> F;25-362/Product: class I histocompatibility antigen heavy chain, Gogo-B0102 #status F;25-114/Domain: alpha-1 <ALl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Pan troglodytes (chimpanze)
C;Species: Pan troglodytes (chimpanze)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C;Accession: I80169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: mRNA
A,Residues: 1-355 <RES>
A;Cross-references: EMBL:U05580; NID:g454777; PIDN:AAA50183.1; PID:g454778
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      class I histocompatibility antigen - chimpanzee (fragment)
                                                                                                                                                       F:115-206/Domain: alpha-2 <AL2>F:207-208/Domain: alpha-3 <AL3>F:207-285/Domain: alpha-3 (AL3)F:220-285/Domain: intracellular #status predicted <INT>F:299-362/Domain: intracellular #status predicted <INT>
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Pred. No. 4.1e-09;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                     Score 114; DB 2; 1
Pred. No. 3.5e-10;
1; Mismatches 2;
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84.0%;
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Best Local Similarity 88.0%;
Matches 22; Conservative
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84.0%;
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Matches 21; Conservative
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Best Local Similarity
Matches 21; Conserv
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A; Residues: 1-355 <RE
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A.Residues: 1-362 <LAM>
A.Roross-references: EMBL:X60255; NID:g22865; PIDN:CAA42807.1; PID:g22866
A.Experimental source: EBV-transformed B cell
C.Genetics: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
C.Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Reywords: transmembrane protein
C; Reywords: transmembrane protein
F:1.24/Domain: signal sequence *status predicted <SIG>
F:1.24/Domain: signal sequence *status predicted version heavy chain, Gogo-B0101 *status pre
                                                                          pre
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                                                                    Gogo-B0103 #status
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J. Exp. Med. 174, 1491-1509, 1991
A;Title: Gorilla class I major histocompatibility complex alleles: comparison
A;Reference number: JH0534; MUID:92078860
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C; Keywords: transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-362/Product: class; Inistocompatibility antigen heavy chain,
F;25-114/Domain: alpha-1 <ALI>
F;215-206/Domain: alpha-2 <ALI>
F;207-298/Domain: alpha-3 <ALI>
F;207-288/Domain: munoglobulin homology <IMM>
F;220-385/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                         Length 362;
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                                                                                                                                                                                                                                                                                                      Score 114; DB 2; L
Pred. No. 3.5e-10;
1; Mismatches 2;
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Pred. No. 3.5e-10;
1; Mismatches 2
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Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
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88.0%;
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Best Local Similarity 88.0%;
Matches 22; Conservative
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Best Local Similarity 88.0°
Matches 22; Conservative
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R; Lawlor, D.A.;
J. Exp. Med. 174
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Length 355;

Wat

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Gaps

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Length 362;

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class I histocompatibility antigen - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C;Accession: 18017]
R;McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Wat Proc. Natl. Acad. Scl. U.S.A. 91, 5893-5897, 1994
A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Reference number: 159308; MUID:94286544
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A;Cross-references: EMBL:U05582; NID:q454781; PIDN:AAA50185.1; PID:g454782
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
  Gaps
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Pred. No. 4.1e-09;
.; Mismatches 3;
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WDRETQICKAKAQTDRENLRIALRY
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Job time: 22207 sec
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C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Superfamily: class I histocompatibility antigen ch39 alpha chain #status predicted
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-14/Domain: alpha-1 #status predicted <EXI>
F:25-14/Domain: alpha-1 #status predicted <EXI>
F:115-206/Domain: alpha-1 #status predicted <EXI>
F:210-285/Domain: immunoglobulin homology <IMM>
F:307-332/Domain: intransmembrane #status predicted <IVM>
F:333-363/Domain: intransmembrane #status predicted <IVM>
F:110/Alinding site: carbohydrate (Asn) (covalent) #status predicted
F:110-188,227-283/Disulfide bonds: #status predicted
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1.25-363/Product: class I histocompatibility antigen alpha chain #status predicted <MAT>
1.25-384/Domain: extracellular #status predicted <EXT>
1.20-285/Domain: immunoglobulin homology <IMM>
1.299-338/Domain: transmembrane #status predicted <TMM>
1.339-363/Domain: intracellular #status predicted <IMM>
1.339-363/Domain: intracellular #status predicted <IMT>
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Rambo J. 7, 2765-2774, 1988
A:Title: Nuclectide sequences of chimpanzee MHC class I alleles: evidence for trans-spec
A:Reference number: S01171; MUID:89030641
                                                                                                                                       C; Species: Pan troglodytes (chimpanzee)
C; Species: Pan troglodytes (chimpanzee)
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 23-Jul-1999
C; Accession: S07113; 136957
R; Lawlor, D.A.; Ward, F.E.; Ennis, P.D.; Jackson, A.P.; Parham, P.
Nature 335, 268-271, 1988
A; Title: HA-A and B polymorphisms predate the divergence of humans and chimpanzees.
A; Reference number: S06424; MUID:88319000
A; Rocession: S07113.
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    chimpanzee

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Pred. No. 4.2e-09;
1; Mismatches 3; Indels
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Pred. No. 4.2e-09;
1; Mismatches 3; Indels
                                                                                                        antigen Ch39 alpha chain precursor
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A;Residues: 1-363 <LAM>
R;Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
J. Immunol. 142, 3937-3950, 1989
A;Title: Diversity and diversification of HLA-A,B,C alleles.
A;Reference number: 136956; MUID:89235215
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Best Local Similarity 84.0%;
Matches 21; Conservative
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C; Keywords: transmembrane protein
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Best Local Similarity
Matches 21; Conserv
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;Residues: 1-363 <RES>
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GenCore version 4.5
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- protein search, using sw model OM protein

Run on:

February 8, 2000, 01:26:01; Search time 68.63 Seconds

(without alignments)
10.879 Million cell updates/sec

US-08-653-294-32

Perfect score:

1 WDRETQICKAKAQTDRENLRIALRY 25 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

82229 seqs, 29864866 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

SwissProt_38:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	15	HLAH_HUMAN	1B20_HUMAN	1B14_HUMAN	1B16_HUMAN		- 1	1B01_GORGO	- 1	1B03_GORGO	1B01_PANTR	1B47_HUMAN	1B53_HUMAN	1B05_HUMAN	1B41_HUMAN	1B42_HUMAN	1B49_HUMAN	1B52_HUMAN	1B54_HUMAN	1A23_HUMAN	1A24_HUMAN	1A32_HUMAN	1A25_HUMAN	1B40_HUMAN	1B60_HUMAN	1B61_HUMAN	1B62_HUMAN	1A04_GORGO	1B07_HUMAN	1B08_HUMAN	1B29_HUMAN	1B31_HUMAN	1B45_HUMAN	1B02_HUMAN
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home	P30493 homo sapien P30494 homo sapien	Щ О Н О	home	P06140 oryctolagus	P13751 pan troglod
1B39_HUMAN 1B55_HUMAN	1B56_HUMAN 1B57_HUMAN	1B58_HUMAN 1B59_HUMAN	1B32_HUMAN HA1A_RABIT	HAIB_RABIT	1802_PANTR
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63.	63.2	93.9	60 59	59.	57.
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35 36	37	3 9 9 9 9	<b>4</b> 1 <b>4</b> 2	43	4.5

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE: 86042671.

VEGA M.A., EZQUERRA A., ROJO S., APARICIO P., BRAGADO R.,

LOPEZ DE CASTRO J.A.;

Structural analysis of an HLA-B27 functional variant: identification
of residues that contribute to the specificity of recognition by
cytolytic T lymphocytes.";

Proc. Natl. Acad. Sci. U.S.A. 82:7394-7398(1985).

-! FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
-! SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 86220133.
SEEMANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.L.;
"Gene conversion-like mechanisms may generate polymorphism in human class I genes.";
EMBO J. 5:547-552(1986).
                                                 01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALPHA CHAIN
PRECENSOR (B-27K) (827.2).
                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                         SECUTION N.A.
PARHAM P., ARNETT K.L., ADAMS E.J.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                    362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM: PF00047; 19:1.
PFAM: PF00129; MHC_I: 1.
MHC I: Transmembrane; Glycoprotein; Signal.
SIGNAL
                    PRT;
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EMBL; X03667; CAA27301.1; JOINED.
EMBL; L38504; AAA69724.1; -.
PIR; B25092; HLHUBK.
HSSP; P03989; 1HSA.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 86-107 AND 171-181.
                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MICROGLOBULIN).
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1B15_HUMAN
ID 1B15_HUMAN
AC P10317;
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BY SIMILARITY.
BY SIMILARITY.
5E610F63 CRC32;
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                                                                                   2; Mismatches
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Best Local Similarity 88.0'
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1B20_HUMAN
ID 1B20_HUMAN
CARBOHYD
DISULFID
SEQUENCE
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HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALPHA CHAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 82151002.
MALISSEN M., MALISSEN B., JORDAN B.R.;
"Exon/intron organization and complete nucleotide sequence of an
                                                                                                                                                                                                                                                                                                    HIAH HUMAN STANDARD; PRT; 362 AA.
P01893;
21-JUL-1996 (Rel. 01, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
115-DEC-1899 (Rel. 39, Last annotation update)
116-DEC-1899 (Rel. 39, Last annotation update)
116-DEC-1999 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 79:893-897(1982).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
-!- THE IMMUNE SYSTEM. COULD BE THE PRODUCT OF A PSEUDOGENE.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                      Length 362;
                                                                                                                                                                                             Indels
          B-27 B*2702 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                     100.0%; Score 133; DB 1; 100.0%; Pred. No. 5.1e-13;
                                                           CONNECTING PEPTIDE
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                                                                                              BY SIMILARITY.
BY SIMILARITY.
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                                                                                   CYTOPLASMIC TAIL.
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ALPHA CHAIN H.
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PIR; A02189; HLHU12.
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HSSP; P03989; 1HSA.
MIM; 142800; -
PROSITE; PS00290; IG_MHC; 1.
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PFAM: PF00129: MHC_I: 1.
BFAM: PF00129: MHC_I: 1.
SIGNAL TANSMEMBY AB 24
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362 AA;
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Matches 25; Conser
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MEDLINE; 91268545.

CHOO Y.S., FAN L.A., HANSEN J.A.;

CHOO Y.S., FAN L.A., HANSEN J.A.;

A novel HLA-B27 allele maps B27 allospecificity to the region around position 70 in the alpha 1 domain.";

J. Immunol. 147:174-180(1991).

-! FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.

-! SUBUNT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                Gaps
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01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2707 ALPHA CHAIN
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
Length 362;
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MIM; 142830; -. PSO0290; IG_MHC; 1.
PPAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_1; 1.
DOWAIN 1 90 EXTRACELLULAR ALPHA-1.
DOWAIN 1 91 EXTRACELLULAR ALPHA-2.
DOWAIN 1 183 274 EXTRACELLULAR ALPHA-3.
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      Score 120; DB 1;
Pred. No. 4.8e-11;
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88.0%; Pred. No. 9e-11;
11ve 1; Mismatches
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RESULT
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                                                              23-0CT-1986 (Rel. 02, Created)
13-AuG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOPEZ DE CASTRO J.A.; Primary structure of papain-solubilized human histocompatibility
                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 25-300.
MEDLINE; 92405152.
MADDEN D.R., GORGA J.C., STROMINGER J.L., WILEY D.C.;
"The three-dimensional structure of HLA-B27 at 2.1-A resolution suggests a general mechanism for tight peptide binding to MHC.";
                                                                                                                                                                                                                                                            MEDLINE; 86149317.
SZOETS H., RIETHMUELLER G., WEISS E., MEO T.;
"Complete sequence of HLA-B27 cDNA identified through the
characterization of structural markers unique to the HLA-A, -B,
                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 25-295.
MEDILINE: 8226561.
EZQUENRA A: BRAGADO R., VEGA M.A., STROMINGER J.L., WOODY J.,
LOPEZ DE CASTRO J.A.;
                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE; 86138405.
WEISS E.H., KUON W., DOERNER C., LANG M., RIETHMUELLER G.;
"Organization, sequence and expression of the HLA-B27 gene: a molecular approach to analyze HLA and disease associations.";
Immunobiology 170:367-380(1985).
                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE IMMUNE SYSTEM.
--- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROCLOBULIN).
--- DISEASE: THIS PROTEIN CORRELATES WITH THE DEVELOPMENT OF ANXYLOSING SPONDYLITIS.
                                                                                                                                                                                                                                                                                                            -C allelic series.";
Proc. Natl. Acad. Sci. U.S.A. 83:1428-1432(1986)
                                           361 AA.
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PIR; A25128; HLHUB2.
PIR; S07441.
PPB; 1HSA; 15-OCT-92.
MIM; 142830; -.
                                                                                                                                                                                                                                                                                                                                                                                                        antigen HLA-B27.";
Biochemistry 24:1733-1741(1985).
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SEQUENCE OF 25-361 FROM N.A.
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                                           STANDARD;
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Cell 70:1035-1048(1992)
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P03989;
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                  HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal; 3D-structure.
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Pred. No. 9.6e-11;
1; Mismatches 2; Indels
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Best Local Similarity 88.0%;
Matches 22; Conservative 1
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ID 1B16 P
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                  SEQUENCE FROM N.A. MEDLINE; 86220133
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                                                                                                             CLASS I HISTOCOMPATIBILITY ANTIGEN,
          ol-NOV-1990 (Rel. 16, Last sequence update)
01-FBB-1995 (Rel. 31, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2703 ALPHA CHAIN
PRECURSOR (B-27D).
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01-WAR-1989 (Rel. 10, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2705 ALPHA CHAIN
PRECURSOR (B-27W) (B27.1).
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                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
                                                                                                                                                                      THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 118; DB 1; Length 362;
Pred. No. 9.6e-11;
1; Mismatches 2; Indels
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B-27 B*2703 ALPHA CHAIN.
EXTRACELJULAR ALPHA-1.
EXTRACELJULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_1; 1.
PFAM; PR01129; MHC_1; 1.
PFAM; PR01129; MHC_1; 1.
SIGNAL.
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01-NOV-1990 (Rel. 16, Last seq
01-FEB-1995 (Rel. 31, Last ann
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                                                                  Homo sapiens (Human).
                                                                                                                                                                                          MICROGLOBULIN).
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Best Local Similarity
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                                                                                                       SEQUENCE FROM N.
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                                                                                                                                                                                                                                                                                                                                  MEDLINE; 95148615.

ROGNAN D., SCAPOZZA L., FOLKERS G., DASER A.;

"Rational design of nonnature pertides as high-affinity ligands for the HLA-BR-2705 human leukocyte antigen.";

Proc. Natl. Acad. Sci. U.S.A. 92:753-757(1995).

- PROCION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.

-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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B-27 B*2705 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
SEEMANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.L.;
"Gene conversion-like mechanisms may generate polymorphism in human
Class I genes.";
EMBO J. 5:547-552(1986).
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                                                                                                                                                                             WEISS E.H., KUON W., DOERNER C., LANG M., RIETHWUELLER G.; "Organization, sequence and expression of the HLA-B27 gene: a molecular approach to analyze HLA and disease associations."; Immunobiology 170:367-380(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 118; DB 1; Length 362;
Pred. No. 9.6e-11;
1; Mismatches 2; Indels
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PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal; 3D-structure.
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73243566 CRC32;
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                                                                                                                                                                                                                                                                                          [3]
3D-STRUCTURE MODELING OF 115-206.
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88.0%;
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PROSITE; PS00290; IG_MHC; 1.
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PDB, 1ROH, 30-SEP-94.
PDB, 1ROI, 30-SEP-94.
PDB, 1ROJ, 30-SEP-94.
PDB, 1ROL, 30-SEP-94.
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                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 86138405.
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362 AA

1B19_HUMAN

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                                                                                                                                                                                                                                                                                                                                                                                                                    LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.,
LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.,
"Gorilla class I major histocompatibility complex alleles: comparison
"Gorilla class I major histocompatibility complex alleles: comparison
to human and chimpanzee class I.",
J. Exp. Med. 174:1491-1509(1991).
-1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
-1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GGGO-B0101 ALPHA CHAIN PRECURSOR.
GOTILLA GOTILLA (LOWLand gorilla, Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
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Best Local Similarity 88.0
Matches 22; Conservative
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ID 1802_GORGO
AC P30380;
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P30379;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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B-27 B*2706 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1 (BY SIMILARITY).
EXTRACELLULAR ALPHA-2 (BY SIMILARITY).
EXTRACELLULAR ALPHA-3 (BY SIMILARITY).
CONNECTING PEPTIDE (BY SIMILARITY).
BY SIMILARITY.
CYTOPLASMIC TAIL (BY SIMILARITY).
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RUDWALEIT M., BOWNESS P., WORDSWORTH P.;
RUDMALEIT M., BOWNESS P., WORDSWORTH P.;
Fhe nucleotide sequence of HLA-B*2704 reveals a new amino acid substitution in exon 4 which is also present in HLA-B*2706.";
Immunogenetics 43:160-162(1996).
-: FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMONE SYSTEM.
                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2706 ALPHA CHAIN
PRECURSOR.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 9.6e-11;
1; Mismatches 2; Indels
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VILCHES C., DE PABLO R., KREISLER M.;
"Nucleotide sequence of HLA-B*2706.";
Immunogenetics 39:219-219(1994).
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PFAM; PF00129; MHC_I; 1.
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01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
01-APR-1993 (Rel. 25, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN PRECURSOR.
Gorilla gorilla (Lowland gorilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
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                                                                                                       Length 362;
                                                                                                     85.7%; Score 114; DB 1; Length 36
88.0%; Pred. No. 3.9e-10;
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SWISS-PROT entry is copyright. It is produced through a collaboration
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88.0%;
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                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMED GUESTALLON the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAWIOR D.A., WARREN E., TAYLOR P., PARHAM P.; "Gorilla class I major histocompatibility complex alleles: comparison to human and chimpanzee class I.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN; GOGO-B0103 ALPHA CHAIN PRECURSOR.
GOTILLA GOTILLA (LOW-Hand GOTILLA)
ELNARYOTA: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrihii; Hominidae; Gorilla.
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                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
CLASS I HISTOCOMPATIBILITY ANTIGEN,
GOGO-BO102 ALPHA CALN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                       J. Exp. Med. 174:1491-1509(1991).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS THE IMMUNE SYSTEM.
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                                                                                                                        -:- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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3CF119AD CRC32;
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PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
1 24 BY SIMILARITY.
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PROSITE; PS00290; 3
 SEQUENCE FROM N.A.
               MEDLINE; 92078860
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SEQUENCE
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CHAIN

1B03_GORGO ID 1B03_G

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between the Swiss Institute of Bioinformatics and the EMBL outstation—
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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EMBO J. 7:2765-2774(1988).
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01-JAN-1990 (Rel. 13, Last sequence update)
01-AR-1993 (Rel. 25, Last annotation update)
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN PRECURSOR
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-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                         Glycoprotein; Signal.

4 BY SIMILARITY.
2 CLASS I HISTOCOMPATIBILITY ANTIGEN, GGGO-B0103 ALPHA CHAIN.
4 EXTRACELLULAR ALPHA-1.
6 EXTRACELLULAR ALPHA-2.
8 EXTRACELLULAR ALPHA-3.
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Eutheria, Primates, Catarrhini, Hominidae, Pan.
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MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
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Pred. No. 3.9e-10;
1; Mismatches 2;
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BY SIMILARITY.
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EMBL; M22793; AAA59645.1; JOINED.
EMBL; M22794; AAA59645.1; JOINED.
                                                                                                                                                                                                                                                                                                    1 WDRETQICKAKAQTDRENLRIALRY 25
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Best Local Similarity 80.0%;
Matches 20; Conservative (
                              EMBL; M24037; AAA02950.1; -.
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115
207
310
334
110
125
362 AA;
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M22796;
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P30490;
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DOMAIN
TRANSMEM
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DISULFID
SEQUENCE
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CARBOHYD
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EMBL;
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or send an email to license@isb-sib.ch).
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
HLA CLESS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVISION TO 78.
MEDLINE: 93056529.
HILDEBRAND W.H., MADRIGAL J.A., BELICH M.P., ZEMMOUR J., WARD F.E., WILLIAMS R.C., PARHAM P.;
"Serologic cross-reactivities poorly reflect allelic relationships in the HLA-B12 and HLA-B21 groups. Dominant epitopes of the alpha 2
                                                                                                                      CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN.
B-1 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-3.
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-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                    Score 107; DB 1; Length 359;
Pred. No. 4.5e-09;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDILINE: 89235215.
PARHAM P., LAWLON D.A., LOMEN C.E., ENNIS P.D.;
"Diversity and diversification of HLA-A,B,C alleles.";
J. Immunol. 142:3937-3950(1989).
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BY SIMILARITY.
BY SIMILARITY.
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Y SIMILARITY.
5395FFC9 CRC32;
                           EMBL; X13115; CAA31507.1; -.
PIR; S03537; S03537.
HSSP; P03989; IHRA.
PROSITE: PS00290; IG_MHC; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
NOW TER 
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                                                                                                                                                                                                                                       40173 MW;
                                                                                                                                                                                                                                                                    80.5%;
84.0%;
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Best Local Similarity 84.0 Matches 21; Conservative
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106
359 AA;
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REVISION TO
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P30487;
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TRANSMEM
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DISULFID
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CARBOHYD
SEQUENCE
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
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HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K., TAKIGGOLI M.;
"ARKIGGOLI M.;
"HLA-B51 and HLA-Bw52 differ by only two amino acids which are in the helical region of the alpha I domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                              B-49(B-21) B*4901 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 101; DB 1; Length 362;
Pred. No. 3.7e-08;
0; Mismatches 5; Indels
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-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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MIM; 142830; -.
PPROSTIE; PS00290; IG_MHC; 1.
PFAM; PF00047; 4g; 1.
PFAM; PF00129; MHC_I; 1.
MHC_I; Transmembrane; Glycoprotein; Signal.
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Homo sapiens (Human)
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MICROGLOBULIN).
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Best Local Similarity
Matches 19; Conserv
  MICROGLOBULIN)
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P30481;
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DISULFID
SEQUENCE
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CARBOHYD
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SIGNAL
CHAIN
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15.JUL-1998 (Rel. 36, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-13 B*1301 ALPHA CHAIN
PRECURSOR (B13.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
THE IMMUNE SYSTEM.
-:- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-BLOOD;
MEDLINE; 96053518.

LIN L., TOKUNAGA K., NAKAJIMA F., ISHIKAWA Y., KASHIWASE K.,
TANAKA H., KUWATA S., SIDELTSEVA E., AKAZA T., TADOKORO K.,
SHIBATA Y., CHANDANAYINGYONG D., JUJI T.;
"Both HLA-B*1301 and B*13102 exist in Asian populations and arsociated with different haplotypes.";
Hum. Immunol. 43:51-56(1995).
                                                                                                                                                                                                                                                                                                             ö
                                                                                                                          HLA CLASS I HISTOCOMFALLELL...
BW-57, B-5201 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZEMMOUR J., ENNIS P.D., PARHAM P., DUPONT B.; "Comparison of the structure of HLA Bw47 to HLA-B13 and its relationship to 21-hydroxylase deficiency."; immunogenetics 27:281-287(1988).
                                                                                                                                                                                                                                                                                       Length 362;
                                                                                                                                                                                                                                                                                     Score 101; DB 1; Length 36
Pred. No. 3.7e-08;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE: 89232215.
PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
"Diversity and diversification of HLA-A,B,C alleles.";
J. Immunol. 142:3937-3950(1989).
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 38436FE8 CRC32;
                    PIR; B30345; B30345.
PIR; B30548; B30548.
HSSP; P30491; JAIM.
MIM; 142830; --
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; ig; 1.
PFAM; PF00129; MHC_I; 1.
MHC_I; Transmebrane; Glycoprotein; Signal.
SIGNAL
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EMBL; M22797; AAA59645.1; JOINED
EMBL; M22798; AAA59645.1; JOINED
PIR; B30345; B30345
PIR; B30548; B30548.
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
                                                                                                                                                                                                                                                                                     75.9%;
                                                                                                                                                                                                                                                     40521
                                                                                                                                                                                                                                                                                    Query Match 75.9°
Best Local Similarity 80.0
Matches 20; Conservative
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                                                                                                                                                                                                                                         227
362 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                  1805_HUMAN
ID 1805_HUMAN
AC P30461;
                                                                                                                                                                                                                             DISULFID
DISULFID
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation for Entry European Bioinformatics Institute. There are no restrictions on its use by non-profil institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-44(B-12) B*4402 ALPHA CHAIN
PRECURSOR (B44.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-13 B*1301 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunol. 142:3937-3950(1989).
FUNCITON: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO STREET EMMUNE SYSTEM.
SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;;
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE; 89235215.
PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
"Diversity and diversification of HLA-A,B,C alleles.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 96; DB 1; Lengran No. 2.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY.
28B67875 CRC32;
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76.0%;
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EMBL; M19757; AAA52657.1; -.
EMBL; D50291; BAA08822.1; -.
HSSP; P30491; IAIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 142830; -.
PROSITE; PS00290; IG_MHC; 1.
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PFAM; PF00129; MHC_I; 1.
MHC_I: Transmembrane; G1
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1841_HUMAN
1D 1840_HIMAN
1D 1.4PR
DT 01.4PR
DT 01.4PR
DT 15.4DR
DT 01.4PR
DT 15.4DR
DT 01.4PR
DT 15.4DR
DT
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Search completed: February 8, 2000, 01:26:01 Job time: 1561 sec

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Gaps

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Query Match 72.2%; Score 96; DB 1; Length 362; Best Local Similarity 76.0%; Pred. No. 2.1e-07; Matches 19; Conservative 0; Mismatches 6; Indels

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095528

029941 031602 019607 019608 019609 019610

OM protein

Run on:

Searched:

Database

Result No.

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O19189;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TIEMBLrel. 12, Last annotation update)
MHC CLASS I HISTOCOMPATIBILITY ANTIGEN-B (HLA-B-27KSH) (FRAGMENT).
HLA-B.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE-LEUKOCYTE;
PETERSDORF E.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
EMBL, 142830;
MIM; 142830;
PFOMIS, PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            095524 PRELIMINARY; PRT; 354 AA.
095524;
01-FEB-1997 (TYEMBLEEL: 02, Created)
01-FEB-1997 (TYEMBLEEL: 02, Last sequence update)
01-NOV-1999 (TYEMBLEEL: 12, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 133; DB 7;
Best Local Similarity 100.0%; Pred. No. 2.1e-13;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1
133 AA; 15491 MW; 3A3BC802 CRC32;
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                                         Homo sapiens (Human)
MHC I.
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Q95527 pan paniscu
Q46697 gorilla gor
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                                                                                                                                                     February 8, 2000, 19:16:17; Search time 176.54 Seconds
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                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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1 WDRETQICKAKAQTDRENLRIALRY 25
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    sp_rodent:*
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Listing first 45
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Maximum DB seq length: 1000000
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Gaps

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Length 133; Indels

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
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Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.2%; Score 120; DB 7; Length 90; 88.0%; Pred. No. 1.5e-11; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 39
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Pred. No. 1.3e-11;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRIMSLEY C., MATHER R.A., OBER C.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF022172; AAC99794.1; -.
PFAM; PF00129; MHC_I; 1.
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BLASCIXK R., WEBER M., SALAWA A.;
SUBMILTED (JAN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X83127; CAA58689.1; -
FEMBL; XB3727; CAA58689.1; -
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019193;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HIGHORPATIBILITY ANTIGEN ALPHA 1 DOMAIN (FRAGMENT).
HOMEO Sapiens (Human).
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                                       01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
MHC CLASS I ANTIGEN HIA-H ORTHOLOG (FRAGMENT).
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90 90
90 AA; 10689 MW; 5E5F2495 CRC32;
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Best Local Similarity 88.0%;
Matches 22; Conservative
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39 39
39 AA; 4748 MW;
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Matches 22; Conserv
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NON_TER
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019193
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AC 01:
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                                                                                                                                                                                                                           STRAIN-LOREL;
MEDLINE; 94286544.
MCDLINE; 94286544.
MCADAM S.N., BOYSON J.E., LIU X., GARBER T.L., HUGHES A.L.,
BONTROP R.E., WATKINS D.I.;
"A uniquely high level of recombination at the HLA-B locus.";
Proc. Natl. Acad. Sci. U.S.A. 91:5893-5897(1994).
EMBL: 400575; AAASO178.1;
PROSITE; PS00290; IG_MHC; 1.
PROMITE; PS00290; IG_MHC; 1.
PPAM: PF00129; MHC_I; 1.
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MEDLINE: 9428644.
MCADAM S.N., BOYSON J.E., LIU X., GARBER T.L., HUGHES A.L.,
BONTROP R.E., WATKINS D.I.;
"A uniquely high level of recombination at the HLA-B locus.";
Proc. Natl. Acad. Sci. U.S.A. 91:5893-5897(1994).
EMBL; U05578; AAA50181.1; --
PROSTE; PS00209: IG_MHC; 1.
HLA-B.
Pan paniscus (Pygmy chimpanzee) (Bonobo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Pan.*haria: Primates; Catarrhin1; Hominidae; Pan.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Pred. No. 1.4e-11;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 93.2%; Score 124; DB 7; Length 354; Best Local Similarity 92.0%; Pred. No. 1.4e-11; Matches 23; Conservative 1; Mismatches 1; Indels
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER 1 1 SEQUENCE 354 AA; 39227 MW; 5D75939D CRC32;
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Best Local Similarity 92.0%;
Matches 23; Conservative 1
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095527;
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ID 046697
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MEDLINE: 86149317.
MEDLINE: 86149317.
MEDLINE: 86149317.
MEDLINE: BOLY BOLY SETHWULLER G., WEISS E., MEO T.;
"Complete sequence of HLA-B27 cDNA identified through the characterization of structural markers unique to the HLA-A, -B, and allelic series.";
Broc. Natl. Acad. Sci. U.S.A. 83:1428-1432(1986).
EMBL; MI2678; AAAS9614.1;
                                                                                        [1]
SEQUENCE FROM N.A.
MEDLINE; 87009855.
COPPIN H.L., MCDEVITT H.O.;
COPPIN H.L., MCDEVITT H.O.;
"Absence of polymorphism between HLA-B27 genomic exon sequences isolated from normal donors and ankylosing spondylitis patients.";
J. Immunol. 137:2168-2172(1986).
EMBL; M14013; AAA59643.1; -.
HSSP; P10318; 1ROG.
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                          Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Mammalia,
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 274;
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Best Local Similarity 88.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 1; Mismatches 2; Indels
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Last annotation update)
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Pred. No. 9.2e-11;
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359 AA; 40042 MW;
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88.0%;
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PROSITE; PS00290; IG_MHC; 1.
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PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
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PFAM; PF00129; MHC_I; 1.
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sapiens (Human).
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274 2
274 AA;
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Best Local Similarity
Matches 22; Conserv
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SEQUENCE
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029693;
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Q29693
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        STIME STANDORS STANDO
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                                                                                                         MEDLINE; 92337445.
HIGGINS C.M., LUND T., SHIPLEY M.E., EBRINGER A.,
SADOWSKA-WROBLEWSKA M., CRIER R.K.;
Ankylosing spondylitis and HLA-B27: restriction fragment length
polymorphism and sequencing of an HLA-B27 allele from a patient with
ankylosing spondylitis.";
Ann. Rheum bis 51:855-862(1992).
EMBL; S39758; CAB27364.1;
PFAM: PF00129; MHC_L; 1.
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     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 118; DB 7; Length 90;
Pred. No. 3e-11;
1; Mismatches 2; Indels
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STEINER N.K., HURLEY C.K., KOESTER R.P.;
"NOVEL-HLA-B allele.";
Submitted (1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF072763; AAC25779.1;
EMBL; AF072763; AAC25779.1;
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I ANTIGEN (FRAGMENT).
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
MHC CLASS I HLA-B27 M (FRAGMENT).
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90 90
90 AA; 10571 MW; F22CCB4E CRC32;
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Best Local Similarity 88.0%;
Matches 22; Conservative
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Matches 22; Conservative
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PFAM; PF00129; MHC_I; 1.
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SEQUENCE FROM N.A.
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TISSUE-BLOOD;
HASEGAWA T., SUGAHARA Y., MORIYAMA Y., NANZAI H., OGAWA A., TAWARA K.,
KONDO S., TOKUNGAR K.;
"Molecular characterization of a novel HLA-B27 allele.";
Submitted (JAN-1996) to the EMBL/Genbank/DDBJ databases.
EMBL; D83043; BAA11753.1; -.
HSSP; P10318; JRO3.
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF000429; MHC_1: 1.
SEQUENCE 362 AA; 40441 MW; 1D8099BC CRC32;
                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 118; DB 7; Length 362;
Pred. No. 1.2e-10;
1; Mismatches 2; Indels
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Pred. No. 1.2e-10;
1; Mismatches 2; Indels
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EMBL: AF026218; AAC42275.1; -.
HSSP; P10318; 1R0G.
                                 Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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 362 AA
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 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEURYNCK K.L., BAXTER-LOWE L.A.; "B27052 W496D.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 AA; 40486 MW;
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88.0%;
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Best Local Similarity 88.0%;
Matches 22; Conservative
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12,
                              01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-NOV-1999 (TrEMBLrel. 12,
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Best Local Similarity 88.0
Matches 22; Conservative
 PRELIMINARY;
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PFAM; PF00129; MHC_I; 1.
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01-NOV-1998 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
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HLA-B.
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                                                                                    HLA-B PROTEIN.
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SEQUENCE
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046693
ID 046693
AC 046693
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078189
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MEDLINE; 94375872.
DEL PORTO P., D'AMATO M., FIORILLO M.T., TUOSTO L., PICCOLELLA E., SORRENTINO R.;
                                                                                                                                                                    MEDLINE; 96134006.

REDMALDELT M., BOWNESS P., WORDSWORTH P.;

RUDMALDELT M., BOWNESS P., WORDSWORTH P.;

Substitution in exon 4 which is also present in HLA-B*2706.";

Immunospenetics 43:160-162(1996).

EMBL; U27608; AAC50444.1; --

HSSP; P10318; IROG.

PROSITE; PS002309; IG_MHC; 1.

PRAM: PF000129; MHC_1; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                          Length 362;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I ANTIGEN.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HUMAN LYMPHOCYTE ANTIGEN HLA-B27.
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ilarity 88.0%; Pred. No. 1.2e-10;
Conservative 1; Mismatches 2;
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HSSP, P10318; 1ROG.
PROSITE; PS00290; IG_MHC; 1.
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Best Local Similarity
Matches 22; Conserv
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                                                                         Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                     STRAIN=ROSS;
GRIMSLEY C., MATHER K.A., OBER C.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF022168; AAC99790.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=EVE;
GRINGLEY C., MATHER K.A., OBER C.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF022169; AAC27911.; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                046694 PRELIMINARY; PRT; >v co. 046694; 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-MAY-1999 (TrEMBLrel. 10, Last annotation update) MHC CLASS I ANTIGEN HLA-H ORTHOLOG (FRAGMENT).
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
MHC CLASS I ANTIGEN HLA-H ORTHOLOG (FRAGMENT).
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NON_TER 90 90
SEQUENCE 90 AA; 10707 MW; EE865717 CRC32;
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90 90
90 AA; 10707 MW; EE865717 CRC32;
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Search completed: February 8, 2000, 19:16:17 Job time: 21504 sec

60 WDRNTQICKAQAQTERENLRMALRY 84

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4287 i X03945 Human gene for HLA-B
6553 i AR008238 Sequence 1 from pa
271 i AF022168 Pan troglodytes 1so
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RVAEQLRAYLEGECVEWLRRYLENGKETLQR"
                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (14-DEC-1994) Effie Petersdorf, Human Immunogenetics,
Fred Hutchinson Cancer Research Center, 1124 Columbia, Seattle, WA
                                                                                     HSU18659 399 bp mRNA PRI 30-APR-1995 Human MHC class I HLA-B mRNA (HLA-B-27KSH allele) exons 2 and 3, partial cds. U18659.1 GI:790214
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/HLA-B-27KSH) that differs from the published B-2702
/HLA-B-27KSH) that differs from the published B-2702
/phenotype="HLA-B-27"
/replace="t"
a 119 c 145 g 48 t
                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 399)
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Gaps: 0
Percent Identity: 100.000
 1.2e-10
1.9e-10
8.8e-12
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/note-"HLA-B-27KSH allele"
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1. .399
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1. .399
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Unpublished
 335.04
331.40
355.58
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/gene="HLA-B"
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Petersdorf, E.
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Ratio: 5.320
Percent Similarity: 100.000
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US-08-653-294-32 x HSU18659
                                                     seg_name: gb_pr2:HSU18659
                                                                                                                                                                                                                                    Petersdorf, E.
                                                                            seg_documentation_block:
LOCUS HSU18659
DEFINITION Human MHC Cla
                                                                                                                                                                                                                                                                                                                                         98104, USA
                                                                                                                                                                     human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
gb_pr1:HSHLAB27
gb_pat:AR008238
gb_pr4:AF022168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 variation
                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                   ORGANISM
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                                                                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                         REFERENCE
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JOURNAL
                                                                                                                                 ACCESSION
                                                                                                                                            VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                            E01341 Genomic DNA encoding HI
M12967 Human MHC class I HLA-E
S39758 HLA-B27 (HLA-B*2705)=hi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233453 H.saplens mRNA for hums M12678 Human HLA-B27 mRNA, cor M54883 Human MC class I HLA-1 E01341 Genomic DNA encoding H
                                                                                                      -MODEL-frame+_p2n.model -DEV-x1p
-Q-Gqq1_J/USPTO_2002/US0865329/runat_04022000_160701_15779/app_query.fasta.2
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-MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000 -QGAPOP-4.500
-GAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500 -FGAPOP-6.000
-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-DELEXT-7.000 -START-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -ALIGN-15 -MODE-LOCAL
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-NCPU-6 -ICPU-3 -NO_XLPXY -WAIT -THREADS-1
                                                    About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7e-11
7e-11
7e-11
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36-09
36-12
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340.80
337.62
304.33
355.83
351.53
358.74
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346.70
345.66
345.45
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346.79
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346.79
    GenEmbl:*
                                                                                                                                                                                                                                                                                    Database: GenEmbl:*
Database sequences: 821193
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Search time (sec): 10176.920000
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                          Date: Feb 8, 2000 10:25 PM
                                                                                                                                                                                                                                              Search information block:
Query: US-08-653-294-32
Query length: 25
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92-pri HSHLAKI

92-pri PPU05575

92-pri HSHLABHBB

92-pri HSHLABHBB

92-pri HSHLABHBB

92-pri HSP022163

92-pri HSP022164

92-pri HSP022165

92-pri HSP022165

92-pri HWMHCTRAN

92-pri HWMHCTRAN

92-pri HWMHCTRAN

92-pri HWMHCZYO

92-pri HWMHZZYO

92-pri HSHLABZYY

92-pri HSHLABZYY

92-pri HSHLABZYY

93-pri HSHLABZYY
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Sequence
gb_pr2:HSU18659
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Ratio: 5.320
Percent Similarity: 100.000
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US-08-653-294-32 x HUMHLABC
                                                                                                                                                                                                                                                                                               seq_name: gb_pr1:HSHLAK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human.
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AUTHORS
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FEATURES
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SDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDRTFQKWAAVVVPSG
EEORYTCHVQHEGLPKPLTLRWEPSSQSTVPIVGIVAGLAVLAVVVIGAVVAAVMCRR
KSSGGKGGSYSQAACSDSAQGSDVSLTA"
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RIALRYYNQSEAGSHTLQNMYGCDVGPDGRLLRGYHQDAYDGKDYIALNEDLSSWTAA
                                                                                                                                                                                  HUMHLABC 1089 bp mRNA PRI 11-JUL-1995
Homo sapiens (clones 18.1, 18.2, 19.2) MHC class I HLA-B*2702 mRNA,
complete cds.
                                                                                                                                                                                                                                                         L38504
L38504.1 GI:886270
cell surface glycoprotein; class I gene;
integral membrane protein; major histocompatibility complex.
Homo sapiens (clone: B18.1) cDNA to mRNA; Homo sapiens (clone:
18.2) cDNA to mRNA; and Homo sapiens (clone: 19.2) cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                     34 TGGGACCGGGAGACACAGATCTGCAAGGCCAAGGCCACAGACTGACCGAGA 83
                                                                                                                                                                                                                                                                                                                                                                                                                          Tobases 1 to 1089)
Parham, P., Arnett, K.L. and Adams, E.J.
On the nucleotide sequences of B*2702 and B*2705
Unpublished (1995)
Location/Qualifiers
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/clone="19.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="HLA-B*2702"
74. 343
/gene="HLA-B*2702"
344. 619
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/gene="HLA-B*2702"
1055. >100
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                                                                                             17 uAsnLeuArgIleAlaLeuArgTyr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                               seq_name: gb_pr2:HUMHLABC
                                                                                                                                                                                    seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217
                                                                                                                                                                                                         LOCUS
DEFINITION
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AUTHORS
TITLE
JOURNAL
FEATURES
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join(79. 151,280. 549,793. 1068,X03667.1:6. 281,
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x03667.1:1299. .>1639)
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KSSGGKGGSYSQAACSDSAQGSDVSLTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1241)
Seemann, G. H., Rein, R. S., Brown, C. S. and Ploegh, H. L.
Gene conversion-like mechanisms may generate polymorphism in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(79. .151,280. .549,793. .1068,X03667.1:6. .281,
X03667.1:373. .489,X03667.1:930. .962,X03667.1:1069.
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Locus HSHLAKI 1241 bp DNA PRI 28-JAN-1997
DEFINITION Human class I MHC gene HLA-B27K exons 1-3 (BRUG cell line).
ACCESSION X03664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  380 bp of intron III missing. Sequence continued in X03667. Location/Qualifiers
                                                                                                                                                                                                                      X03664.1 GI:32236 class I antigen; major histocompatibility antigen; major histocompatibility complex; signal peptide.
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                  to: 1089
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EMBO J. 5 (3), 547-552 (1986)
86220133
                                                                                                                                                                                                                                                                                                                                                                                   300 GAACCIGGGATCGCGCTCCGCTAC 324
                                                                                                                                                                  from: 1
                                                                                                                                                                                                                                                                                                                                  17 uAsnLeuArgIleAlaLeuArgTyr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="HLA-B27K"
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447

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BASE COUNT

25

Length:

Quality: 133.00

alignment_scores:

ORIGIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (25-JAN-1994) Jonathan E. Boyson, Watkins Unit, Wisconsin
Regional Primate Research Center, 1220 Capitol Court, Madison, WI
53715, USA
                                                                                                                                                                                                                                                                                                                                                                                                               PPU05578 1065 bp mRNA PRI 08-0CT-1994 Pan paniscus class I histocompatibility antigen Papa-B (Papa-B-02 allele) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 1065)
McAdam, S.N., Boycon, J.E., Liu, X., Garber, T.L., Hughes, A.L., Bontrop, R.E. and Watkins, D.I.
A uniquely high level of recombination at the HLA-B locus Proc. Natl. Acad. Sci. U.S.A. 91 (13), 5893-5897 (1994)
                                                                                                                                                                   Length: 25
Gaps: 0
Percent Identity: 92.000
Gaps: 0
Percent Identity: 92.000
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                                                                                                                            from: 1
                                                                                                                                                                                                                                                           17 uAsnLeuArgileAlaLeuArgTyr 25
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Pan paniscus
                                                                                                                            Align seg 1/1 to: PPU05575
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Ratio: 4.960
Percent Similarity: 100.000
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Percent Similarity: 100.000
                                                               alignment_block:
US-08-653-294-32 x PPU05575
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US-08-653-294-32 x PPU05578
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                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_pr1:PPU05578
                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS PPU05578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boyson, J.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-JAN-1994) Jonathan E. Boyson, Watkins Unit, Wisconsin Regional Primate Research Center, 1220 Capitol Court, Madison, WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="VLLLLSAALALTETWAGSHSMRYFDTAVSRPGAGEPRFITVGTV
ODDOFVRREDSDAASPREBRARWEGGGEFWRNNTQICKAGAOTORERILRIALRYN
OSEAGSHTLQRWYGCDVGPDGRLLRGYSGSAYDGKDYTALNEDLSSWTAADTAAQITO
RKWEAARVAEGLRAYLEGLCVEWLRRYLEBNGKETLQRADPPRTHVTHPISDHSAAQITO
RKWAGRYPBETITLTWQROGEDOTODTELVETRRAGDPRTHVTHPISDHEATLR
VQHEGLPEPLILRWEBSSGSTIPIVGTVAGLAVVYTGAVVAAVWCRRKSSGGKGG
SYSQAASSDSAQGSDVSLTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPU05575 1065 bp mRNA PRI 08-OCT-1994
Pan paniscus class I histocompatibility antigen Papa-B (Papa-B-03 allele) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1 (bases I to 1065)
McAdam, S.N., Boyson, J.E., Liu, X., Garber, T.L., Hughes, A.L., Bontrop, R.E. and Watkins, D.I.
A uniquely high level of recombination at the HIA-B locus Proc. Natl. Acad. Sci. U.S.A. 91 (13), 5893-5897 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="class I histocompatibility antigen"
/protein_id="AAA50178.1"
/db_xref="G1:454768"
                                                                                                                                                                                                                                                                                                         1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                               Percent Identity: 100.000
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                                                                                                                                                                                                                                       from: 1 to: 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Pan paniscus"
/isolate="Lorel"
/db_xref="taxon:9597"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <1. .1065
/gene="HLA-B"
/note="HLA-B-03 allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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/gene="HLA-B"
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Boyson, J.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U05575.1 GI:454767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pygmy chimpanzee.
Pan paniscus
                                                                               Quality: 133.00
Ratio: 5.320
Percent Similarity: 100.000
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                                                                                                                                                                                                                                     Align seg 1/1 to: HSHLAK1
                                                                                                                                                                     alignment_block:
US-08-653-294-32 x HSHLAK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_pr1:PPU05575
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LOCUS
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53715, USA
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                                                               alignment_scores:
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL MEDLINE REFERENCE AUTHORS

TITLE JOURNAL

FEATURES

gene CDS BASE COUNT

DEFINITION

ACCESSION

DEFINITION ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS

TITLE

JOURNAL REFERENCE

AUTHORS

TITLE JOURNAL

FEATURES

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Homos sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 250)
1 (bases 1 to 250)
Molecular evolution of HLA-B locus in a small population amerindian community: The Nukak-Maku
                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (07-07-1996) A. Rojas-Munoz, National Institute Of
Health, Immunogenetics, Avenida El Dorado, Carrera 50, Santafe De
Bogota / Zona 6, COLOMBIA
                                                                                                                 10-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS AF022159 255 bp DNA PRI 05-JAN-1999
DEFINITION Homo sapiens isolate 026 MHC class I antigen HLA-H (HLA-H)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .250
/organism="Homo sapiens"
/isolate="Isabel-26"
/isolate="from amerindian community Nukak-Maku"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 TGGGACCGGAACACACAGATCTGCAAGGCCCAGGCACAGACTGAACGAA 213
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                                                                                               HSHLABHBB 250 bp DNA PRI H.saplens HLA-B gene, exon 2, HB(b) allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 120.00 Length: 25
Ratio: 4.800 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 88.000
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                                                                                                                                                                                         HLA-B gene; human leukocyte antigen.
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/tissue_type="blood"
/cell_type="white"
/lab_host="E.coli TG1"
/clone="cHBC2(b)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="allel HB(b)"
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14. .250
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114 GAACCTGCGGATCGCGCTCCGCTAC 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="HLA-B"
<14. .>250
/gene="HLA-B"
                                                                                                                                                                      Y08693.1 GI:1619288
                                                                                                                                                                                                                                                                                                                                                          Unpublished
2 (bases 1 to 250)
Rojas-Munoz,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /number=2
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US-08-653-294-32 x HSHLABHBB
                                                          seg_name: gb_pr1:HSHLABHBB
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                                                                                               seq_documentation_block:
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                                                                                                                                                                                                             human.
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                                                                                                                                 DEFINITION
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1 (bases I to 250)
Rojas-Munoz, A., Mendez, I. and Yunis, I.
Molecular evolution of HIA-B locus in a small population amerindian community: The Nukak-Maku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (07-0CT-1996) A. Rojas-Munoz, National Institute Of
Health, Immunogenetics, Avenida El Dorado, Carrera 50, Santafe De
Bogota / Zona 6, COLOMBIA
Location/Qualifiers
                                                                                                                                                                                                                                                                  10-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/isolate="Nancy-28"
/isolate="from amerindian community Nukak-Maku"
//isolate="faxon:9606"
/chromosome="6"
                                                      HSHLABHBA 250 bp DNA PRI
H.saplens HLA-B gene, exon 2, HB(a) allele.
Y08692
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Gaps: 0
Percent Identity: 88.000
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                                                                                                                                                                                                                                                                                                                 Y08692.1 GI:1619287
HLA-B gene; human leukocyte antigen.
                   Align seg 1/1 to: PPU05578 from: 1 to: 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="blood"
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/lab_host="E.coll TG1"
/clone="cHBC1(a)"
/clone="cHBC2(A)"
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/gene="HLA-B"
/note="allel HB(a)"
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/gene="HLA-B".
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2 (bases 1 to 250)
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Percent Similarity: 100.000
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US-08-653-294-32 x HSHLABHBA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rojas-Munoz, A.
                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS HSHLABHBA
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alignment_scores:

BASE COUNT ORIGIN

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Quality:
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                                                                                    TITLE
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2 (bases 1)
2 (bases 1)
3 (bases 1)
3 (bases 1)
4 (bases 2)
5 (bases 3)
6 (bases 4)
6 (bases 4)
7 (bases 4)
                                                                                                                                      Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 255;

Grimsley,C., Mather,K.A. and Ober,C.

HIA-H: a pseudogene with increased variation due to balancing selection at neighboring loci

Mol. Biol. Evol. 15 (12), 1581-1588 (1998)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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LOCUS AF022161 271 bp DNA PRI 05-JAN-1
DEFINITION Homo sapiens isolate 068 MHC class I antigen HLA-H (HLA-H)
ACCESSION AF022161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
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Gaps: 0
Percent Identity: 88.000
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/codon_start=1
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pseudogene, partial sequence.
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AF022159.1 GI:2655062
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/gene="HLA-H"
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/gene="HLA-H"
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Percent Similarity: 100.000
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US-08-653-294-32 x AF022159
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2 (bases 1 to 271)
2 (bases 1 to 271)
3 (crimsley,C., Mather,K.A. and Ober,C.
Direct Submission
Submitted (03-SEP-1997) Fred Hutchinson Cancer Research Center,
1100 Fairvlew Ave. N., M374, Seattle, WA 98109, USA
Location/Qualifiers
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases I to 271)
Grimsley, C., Mather, K.A. and Ober, C.
HIA-H: a pseudogene with increased variation due to balancing
selection at neighboring loci
Mol. Biol. Evol. 15 (12), 1581-1588 (1998)
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Homo sapiens isolate 138 MHC class I antigen HLA-H (HLA-H)
pseudogene, partial sequence.
AF022163.1 GI:2655066
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                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/isolate="068"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
/note="African-American individual"
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Gaps: 0
Percent Identity: 88.000
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/note="MHC class I antigen HLA-H"
/codon_start=1
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/gene="HLA-H"
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/gene="HLA-H"
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LOCUS AF022163
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2 (bases 1 to 271)
Grimaley,C., Mather,K.A. and Ober,C.
Direct Submission
Submitted (03-SEP-1997) Fred Hutchinson Cancer Research Center,
1100 Fairview Ave. N., M374, Seattle, WA 98109, USA
Location/Qualifiers
1. .271
/organism="Homo sapiens"
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Grimeley/C., Mather,K.A. and Ober,C.

Direct Submission

Submitted (03-SEP-1997) Fred Hutchinson Cancer Research Center,

1100 Fairview Ave. N., M374, Seattle, WA 98109, USA

Location/Qualifiers
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1 (bases 1 to 271)
Grimsley,C., Mather,K.A. and Ober,C.
HIA-H: a pseudogene with increased variation due to balancing selection at neighboring loci
Mol. Biol. Evol. 15 (12), 1581-1588 (1998)
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LOCUS AF022164 271 bp DNA PRI 05-JAN-1.
DEFINITION Homo sapiens isolate 156 MHC class I antigen HLA-H (HLA-H)
pseudogene, partial sequence.
ACCESSION AF022164
VERSION AF022164.1 GI:2655067
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                                                                                                                                                                                       /note="African-American individual"
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Ratio: 4.800 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 88.000
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/gene="HLA-H"
/note="MHC class I antigen HLA-H"
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/chromosome="6"
/map="6p21.3"
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/gene="HLA-H"
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/gene="HLA-H"
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/number=2
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US-08-653-294-32 x AF022163
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1 (bases) tanged, the following of the following of the following of the following the following the following the following local mol. Biol. Evol. 15 (12), 1581-1588 (1998) 99083456 2 (bases I to 27) (crimsley,C., Mather,K.A. and Ober,C. Direct Submission Submitted (03-5EP-1997) Fred Hutchinson Cancer Research Center, 1100 Fairylew Ave. N., M374, Seattle, WA 98109, USA Location/Qualifiers
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class I antigen HLA-H (HLA-H)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/chromosone="6"
/map="6p21.3"
/note="African-American individual"
                                                                       /map="6p21.3"
/note="African-American individual"
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Gaps: 0
Percent Identity: 88.000
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//note="MHC class I antigen HLA-H"
//codon_start=1
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/organism="Homo sapiens"
/isolate="156"
                                    /db_xref="taxon:9606"
/chromosome="6"
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LOCUS AF022165 271 bp DNA
DEFINITION Home sapiens isolate 175 MHC
pseudogene, partial sequence.
ACCESSION AF022165.1 GI:2655068
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/gene="HLA-H"
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/gene="HLA-H"
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US-08-653-294-32 x AF022164
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Grimaley,C., Mather,K.A. and Ober,C.
Direct Submission
Submitted (03-SEP-1997) Fred Hutchinson Cancer Research Center,
1100 Fairview Ave. N., M374, Seattle, WA 98109, USA
1. .271
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 27)
Grimsley,C., Mather,K.A. and Ober,C.
HLA-H: a pseudogene with increased variation due to balancing selection at neighboring loci
Mol. Biol. Evol. 15 (12), 1581-1588 (1998)
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LOCUS AF022166 271 bp DNA PRI 05-JAN-1999
DEFINITION Home sapiens isolate 219 MHC class I antigen HLA-H (HLA-H)
ACCESSION AF022166
VERSION AF022166.1 GI:2655069
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                                                                                                                                                                                                                      Length: 25
Gaps: 0
Percent Identity: 88.000
                                       <1. .>270

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                                                                                                                                                    35
                                                                                                                                                                                                                                                                                                                     to: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
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Percent Similarity: 100.000
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US-08-653-294-32 x AF022165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_pr4:AF022166
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                                                                                                                                                    53
                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                   BASE COUNT
ORIGIN
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AUTHORS
TITLE
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JOURNAL
                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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SOURCE
                                        CDS
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84 c 91 g 37 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA PRI 05-JAN-1999
Shamba MHC class I antigen HLA-H ortholog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z. (bases 1 to 271)
GrimsLey,C., Mather,K.A. and Ober,C.
Direct Submission
Submitted (03-SEP-1997) Fred Hutchinson Cancer Research Center,
1100 Fairview Ave. N., M374, Seattle, WA 98109, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gorilla.

Gorilla gorilla

Gorilla gorilla

Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Primates; Catarrhini; Hominidae; Gorilla.

1 (Dases I to 271)

Grimaley, C., Mather K.A. and Ober, C.

HLA-H: a pseudogene with increased variation due to balancing selection at neighboring loci

Mol. Biol. Evol. 15 (12), 1581-1588 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                     178 TGGGACCGGAACACACAGATCTGCAAGGCCCAGGCACAGACTGAACGAGA 227
                                                                                                                                                                                                                                                                                                                                                                                          1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                               Length: 25
Gaps: 0
Percent Identity: 88.000
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/isolate="Shamba"
/db_xref="taxon:9593"
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;
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LOCUS
AF022172
LOCUS
DEFINITION GOTILIA gorilla isolate ShancesIn (HLA-H) gene, partial cds.
ACCESSION AF022172
VERSION AF022172.1 GI:2655079
                                                                                       91
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/pseudo
<1. .>271
/gene="HLA-H"
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/gene="HLA-H"
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84 c
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Ratio: 4.800
Percent Similarity: 100.000
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US-08-653-294-32 x AF022166
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Length:

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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata: Mammalla; Eutheria: Primates: Catarrhini; Hominidae; Homo.
1 (bases 1 to 1096)
2 Eammour, J., Koller, B.H., Ennis, P.D., Geraghty, D.E., Lawlor, D.A., Orr. H.T. and Parham, P.
HIA-AR, an inactivated antigen-presenting locus related to HLA-A.
Implications for the evolution of the MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ....1096
1. .1096
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Ab_xxef="taxon:9606"
Ab_xxef="taxon:9606"
LCL721
                                                                                                                                                                                                                                                                                                                     14-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Authorin copy of sequence [1] kindly submitted by J. Zemmour, 14-FEB-1990.
                                                                                                                                           1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                  Gaps: 0
Percent Identity: 88.000
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Percent Identity: 88.000
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LOCUS HUMMHCAR3 1096 bp DNA
DEFINITION HUMBU MIC HLA-AR gene, inactive antigen.
ACCESSION M32106
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/pseudo
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                                                                                                          Align seg 1/1 to: AF022172 from: 1 to: 271
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major histocompatibility complex.
Homo sapiens DNA.
Homo sapiens
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334 c 362 g
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Ratio: 4.800
Percent Similarity: 100.000
Quality: 120.00
Ratio: 4.800
Percent Similarity: 100.000
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US-08-653-294-32 x HUMMHCAR3
                                                               alignment_block:
US-08-653-294-32 x AF022172
                                                                                                                                                                                                                                                                      seq_name: gb_pr2:HUMMHCAR3
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90229758
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ACCESSION
VERSION
KEYWORDS
SOURCE
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AUTHORS
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COMMENT
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Human secreted protein 5' ES Human nel-related protein t Mus musculus SOCSIO gene. S Human nel-related protein t Human secreted protein 5'

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Such DNA, antigen or antibody
Claim 2; Page 4; 5pp; German.
The DNA may be used as a hybridisation probe for detecting the HLA
B27 gene, e.g. for assessing susceptibility to rheumatic disorders
such as ankylosis spondylitis, or may be used to transform cells
for prodn. of HLA B27. The HLA B27 may be used to detect HLA B27
antibody in human serum, or to produce mono- or polyclonal HLA B27
sequence 1026 BP; 213 A; 307 C; 344 G; 162 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:

ID N70225 standard; DNA; 3874 BP.

AC N70225
DT 03-APR-1991 (first entry)
DE Sequence of genomic DNA encoding human histocompatibility antigen
DE HIA-B 27.
                                                                                                                                                                                                                        10-AFR-1991 (first entry)
Sequence encoding the human histocompatibility antigen HLA B27
Rheumatic disorder; genetic screening; diagnosis;
ankylosing spondylitis; ss.
Homo saplens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA coding for antigen HLA B27 - and diagnostic reagents contg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 TGGGACCGGGAGACACAGATCTGCAAGGCCAAGGCACAGACTGACCGAGA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ankylosing spondylitis; rheumatic disorder; diagnosis;
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 118.00 Length: 25
Ratio: 5.130 Gaps: 0
nilarity: 92.000 Percent Identity: 88.000
    322
2448
2649
3198
13.93
176.22
194.51
246.19
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                                                                                                                                                                                                                                                                                                                                                                                                        04-JUN-1987.
28-NOV-1985; 542024.
28-NOV-1985; DE-542024.
21-DEC-1985; DE-545576.
(BEHW ) BEHRINGWERKE AG.
RAETHMULLER G, MGO T, Weiss E, SZOUS H;
WPI: 87-157893/23.
P-PSDB; P70590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ĥ
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518. .590
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                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .1026
128.96
109.17
108.40
106.56
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                                                                                                                                                                    N70935 standard; DNA; 1026 BP. N70935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 GGACCTGCGGACCCTGCTCCGCTAC
  seq_name: N_Geneseq_36:N70935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: N_Geneseq_36:N70225
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US-08-653-294-32 x N70935
                                                                                                                                                           seq_documentation_block
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  N_Geneseq_36:X40673
N_Geneseq_36:V01882
N_Geneseq_36:V38678
N_Geneseq_36:V01883
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DE3542024-A.
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                                                                                                                                                                                    1026 Sequence encoding the human hill 1026 Sequence of genomic DNA encoding 1187 In 1872 Consensus sequence. De 1086 Sequence encoding HAA-BW52 and 1089 HIA-BW52 gene for production C 1086 Sequence encoding HAA-BS1 anti 1088 HIA-BW52 gene for production C 1089 HIA-BW52 gene for production C 1089 HIA-BW53 exon. HIA-BW53 gene, 4059 HIA-BW53 exon. HIA-BW53 gene, 11089 HIA-BW53 exon. HIA-BW53 gene, 1101 HIA-C gene, 11089 HIA-BW53 exon. HIA-BW53 gene, 11089 HIA-BW53 exon. HIA-BW53 gene, 11089 HIA-BW53 exon. HIA-BW53 gene, 11089 HIA-BW542 Exon. Graphor Caxon GD-2. HIA-C gene, 11089 HIA-BW53 exon. HIA-BW53 gene, 11089 HIA-BW54 exon. Graphor Carbonic-anhydrase cDNA. Clone 11095 Carbonic-anhydrase cDNA. Clone 11095 Carbonic-anhydrase cDNA. Clone 11095 Carbonic-anhydrase cDNA. Clone 11096 CARBONIC-Anhydrase cDNA. Cl
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Acetobacter cdg2 operon. Polyn
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                                                                                                                                                                         - MODEL-frame-f_D2n.model - DEV-xlp
- Q=/cgnl_1/USPTO_spool/USO8653294/runat_04022000_160701_15807/app_query.fasta.2
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-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000
-GAPEXT=0.000
-GERPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
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-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM-ext -MINLEN=0
-MAXLEN 1000000 -USER=USO8653294 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
                                                                                         About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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    OM of: US-08-653-294-32 to: N_Geneseq_36:*
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Database sequences: 311585
Database length: 125096042
search time (sec): 873.190000
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search information block:
Query: US-08-653-294-32
Query length: 25
                                                                                                                                                           Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strd
                                              Date: Feb 8, 2000 7:31
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N_Geneseq_36:142166
N_Geneseq_36:148977 +
N_Geneseq_36:004524 +
N_Geneseq_36:004524 +
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N_Geneseq_36:T61639
N_Geneseq_36:001822
N_Geneseq_36:005701
N_Geneseq_36:005701
N_Geneseq_36:005934
N_Geneseq_36:012114
N_Geneseq_36:012114
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N_Geneseq_36:V34403
N_Geneseq_36:V34181
N_Geneseq_36:T29389
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N_Geneseq_36:N80603
N_Geneseq_36:T21345
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N_Geneseq_36:Q92069
N_Geneseq_36:Q92066
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N_Geneseq_36:T86375
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N_Geneseq_36:Q70152
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N_Geneseq_36:N60080
N_Geneseq_36:V04901
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N_Geneseq_36:Q25977
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N_Geneseq_36:V19941
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Sequence
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indicative of a predisposition to SNSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: N_Geneseq_36:Q01822
                                                                                                                                                                                                                                                                  Quality: 118.00
Ratio: 5.130
nilarity: 92.000
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Quality: 101.00
                                                                                                                                                                                                                                                                                                                      US-08-653-294-32 x T61639
                                                                         WPI; 97-192924/17
                                                                                                                                                                                                                                                                                       Percent Similarity:
           WO9709450-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                          alignment_scores:
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                                                                                                                                                                                                                                                                                                            aliqnment_block:
                                                                Iyan DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
DNA coding for human histocompatibility antigen HLA-B 27 - useful for diagnosis and antigen and antibody prodn.

for diagnosis and antigen and antibody prodn.

for diagnosis and antigen and antibody prodn.

THE DNA may be used to detect the HLA-B 27 gene (opt. mutated) in human genetic material. The HLA-B 27 may be used to detect anti-HLA-B 27 antibodies in human serum. The antibodies may be used to determine HLA-B 27 lavels in human serum, e.g. for diagnosis of rheumatic disorders, esp. ankylosing spondylitis.

Sequence 3874 BP; 751 A; 1094 C; 1171 G; 858 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIA B27 consensus sequence.
HIA B27; seronegative spondylarthropathy; ankylosing spondylitis;
Reiter's syndrome; arthritis; acute anterior uveitis; diagnosis;
ss; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /noce= "3' flanking region diagnostic for genetic predisposition to SNSA" 4770. 4556
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/note= "HLA-B27 3' flanking region, downstream
                                                                                                                                                                                                                                                                                                                                                                                                       /note= "3' flanking region diagnostic for predisposition to SNSA"
                                                                                                               01-JAN-1985; DE-542024.
21-DEC-1985; DE-545576.
(BEHW ) BEHRINGWERKE AG.
Szots H, Weiss E, Dorner C, Lang M, Meo T, Riethmuller G;
WPI; 87-171469/25.
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"absence of cytosine at this site
                                                                                                                                                                                                                                                                                                           Length: 25
Gaps: 0
Percent Identity: 88.000
                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: N70225 from: 1 to: 3874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3' untranslated region"
4112. .4556
/*tag= b
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3968. .6653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     946 GGACCTGCGGACCCTGCTCCGCTAC 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                17 uAsnLeuArgIleAlaLeuArgTyr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID T61639 standard; DNA; 6553 BP.
        /*tag= d
2450. .2566
/*tag= e
3149. .3041
/*tag= g
/*tag= g
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Ratio: 5.130
nilarity: 92.000
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US-08-653-294-32 x N70225
                                                                                                       116139
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Percent Similarity:
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                                                                                            24-JUN-1987.
21-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                 EP-226069-A
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                     intron
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Detecting pre-disposition to seronegative spondylarthropathies - Trom the absence of a C residue at a specific position in the from the absence of a C residue at a specific position in the 3'-flanking region of the HLA B27 allele Gametic predisposition to seronegative spondyloarthropathies (SNSA) is detected by determining the absence of a cytosine nucleotide in the 3' flanking region (see also T61647-48) of an HLA-B gene at a position corresponding to nucleotide 4495 of the HLA-B37 consensus caquence given in T61639. Probes and primers (see also T61640-46) chased on this region can be used in diagnostic assays to detect the genetic predisposition to SNSA, and permit the distinction of B27+ individuals who are resistant to SNSA, and permit the distinction of B27+ individuals who are resistant to SNSA, romal individuals who are susceptible (but as yet unaffected) to such diseases. Sequence 6553 BP; 1443 A; 1619 C; 2017 G; 1474 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA for class 1 human leucocyte antigens and derived probes and transformed cells, useful for DNA typing, as immunogens etc.
Claim 2: ppil-12: 23pp: English.

The HLA class I DNA can be used a source of probes for use in DNA typing. Transformed cells, which are useful as immunogens, can be obtained by introducing these DNAs into eucaryotic cells.
Sequence 1086 BP; 333 A; 335 C; 358 G; 170 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 25
Gaps: 0
Percent Identity: 88.000
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Sequence encoding HLA-Bw52 antigen.
Probe; HLA class I DNA; immunogen; ss.
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1. .1086
/*tag= a
13-MAR-1997.
11-AUG-1996; U13256.
01-SEP-1995; UG-522942.
(CEDA-) CEDARS SINAI MEDICAL CENT.
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10-AuG-1999

11-AuG-1988; JP-200758.

(OLYU) Olympus Optical Co., Ltd.

Kano K, Takiguchi;

WPI: 90-046289/07.

P-PSDB: R03142.
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ID 001822 standard; DNA; 1086 BP.
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us-08-653-294-32.rng

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The spleen lymphocytes were fused with myeloma cells (P3x63-Ag8.653). Hybridomas producing antibodies were selected. Sequence 1089 BP; 223 A; 336 C; 359 G; 171 T;
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Allotype specific monoclonal anti- HLA antibodies prodn. - using hybridomas derived from transgenic animals carrying HLA gene and immunised with HLA antigen of different allotype Disclosure; Fig 1 A-G; 20pp; English.
The human HLA-BW52 gene was introduced into mouse L cells and then these cells used to immunise one of the transgenic mice (see Q05693).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           005701;
03-JAN-1991 (first entry)
HIA-BW52 gene for production of monoclonal antibodies.
Alloptype specific monoclonal anti-HIA antibodies; hybridomas;
transgenic animals; HIA-BW52 gene; ss.
                                                                                                                                                                                                                         vaps: 0
Percent Identity: 80.000
                                                                                                                                                                       from: 1 to: 1086
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120. .895
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896. .1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID Q05701 standard; DNA; 1089 BP.
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22-AUG-1990.
07-FEB-1999; 102424.
08-FEB-1999; JP-029313.
(OLYU ) OLYMPUS OPTICAL KK.
Takiguchi M;
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1043. .1089
/*tag= g
/number=7
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/*tag= f
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/number=1
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/*tag= b
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4.391
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                                                                                  alignment_block:
US-08-653-294-32 x Q01822
Ratio:
Percent Similarity:
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Length: 25 Gaps: 0 Percent Identity: 80.000

101.00 4.391 92.000

Quality: Ratio:

alignment_scores:

Percent Similarity:

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Transgenic non-human mammalian HLA-Bw 52 gene - useful for analysis of expression of gene structure, and prodn. of malysis of expression of gene structure, and prodn. of malysis of expression of gene structure, and prodn. of passes of bisclosure; Fig 1; 8pp; Japanese.

Disclosure; Fig 1; 8pp; Japanese.

Disclosure; Fig 1; 8pp; Japanese.

The sequence shows the exon 2 alpha-1-domain of the human leukocyte antigenes by pref. rat or mouse, or their ancestors at the primary developmental biological step via transplantation into the zygote or embryo to generate transgenic non-human mammals incorporating the non-human mammals contg. HLA-Bw 52 are useful for the analysis of expression of the gene, its structure, and prodn. of mouse models of cuman disease.

See also 02916672.

Sequence 270 BP; 59 A; 88 C; 86 G; 37 T;
                                                                                                                                                                                                                                                                                                                                                                           029167;
029167;
09-MAR-1993 (first entry)
HIA-BW 52 exon 2 alpha-1 domain.
Human leukocyte antigen; transgenic; germ cells; somatic cells;
expression; ss.
                                                                                                                                         1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 25
Gaps: 0
Percent Identity: 80.000
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Sequence encoding HLA-B51 antigen.
Probe; HLA class I DNA; immunogen; ss.
BP354580-A.
                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID 029167 standard; DNA; 270 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-1990; 207329.
03-AUG-1990; JP-207329.
(OLYU ) OLYMPUS OPTICAL CO.
WPI; 92-342893/42.
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ID 001834 standard; DNA; 1086
                                                                                                                                                                                                                                                                                                   seq_name: N_Geneseq_36:Q29167
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Ratio: 4.348
nilarity: 92.000
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alignment_block:
US-08-653-294-32 x Q05701
                                                                to: 005701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-653-294-32 x Q29167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                   Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       001834;
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D 14-FEB-1990.

F 10-AuG-1988; JP-200758.

R 11-AuG-1988; JP-200758.

I Amon K, Takiguchi;

R WPI; 90-046289/07.

New DRA for class I human leucocyte antigens and derived probes and transformed cells, useful for DNA typing, as immunogens etc.

T transformed cells, useful for DNA typing, as immunogens etc.

Claim 1: Page 11: 23pp; English.

Claim 1: Page 11: 23pp; English.

The HLA class I DNA cells, which are useful as immunogens, can be useful as immunogens, can be cotaling these DNAs into eucaryotic cells.

Sequence 1086 BP; 224 A; 334 C; 356 G; 172 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-37N-1991 (first entry)
03-37N-1991 (first entry)
HLA-B51 gene for production of monoclonal antibodies.
Alloptype specific monoclonal anti-HLA antibodies; hybridomas;
transgenic animals; HLA-B51 gene; ss.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.00 Length: 25
4.130 Gaps: 0
92.000 Percent Identity: 76.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: Q01834 from: 1 to: 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="alpha 3-domain"
396. .1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="alpha 1-domain'
344. .619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="alpha 2-domain'
620. .895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID Q05693 standard; DNA; 1089 BP.
AC Q05693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-AUG-1990.
07-FEB-1990; 102424.
08-FEB-1999; JP-029313.
(OLXU ) OLXMPUS OPTICAL KK.
Takiguchi M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= e
/number=5
1013. 1042
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /number=6
1043. .1089
/*tag= g
/number=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .73
/*tag= a
/number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= b
/number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= c
/number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= d
/number=4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74. .343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: N_Geneseq_36:Q05693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-653-294-32 x Q01834
                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intron
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        DDA
PETT - LEGIT - LEG
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N USAL OLY OLY DATA SPICAL KK.

DR (OLUT) OLY MAPROS PETCAL KK.

DR P-PSDB; R12463.

PT HLA-BW53 gene, DNA probe and transformant cells - used for immunisation, identifying specificity of antiserum etc.

PT immunisation, apart of the sequence can be used to identify comprising part of the sequence can be used to identify can imals and prodn of monoclonal antibodies specific for the can imals and prodn. of monoclonal antibodies specific for the companies.

CC animals and prodn. of monoclonal antibodies specific for the cCC animals and interpretation of specific for the sequence of the sequence of interpretation of specific for the sequence of the sequence of interpretation of specific for the sequence of the sequence of interpretation of specific for the sequence of the specific for the sequence of the sequence of the specific for the specific for the sequence of the specific for t
         Allotype specific monoclonal anti- HLA antibodies prodn. - using hybridomas derived from transgenic animals carrying HLA gene and immunised with HLA antigen of different allotype busic with HLA antigen of different allotype busic busic busic has an HLA-BSI gene was injected into fertilised mouse eggs and then these introduced into the uterus of a pseudo pregnant mouse. The young were tested to ensure incorporation of the gene into the produces, and one of them mated 3 times with a normal male to produce 16 young, seven of which carried the HLA-BSI gene. The transgeneic offspring were immunised with HLA antigen. The spleen lymphocytes were fused with myeloma cells. Hybridomas producing antibodies were selected.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human leukocyte antigen; probe; major histocompatibility complex;
MHC; class I; ss.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                           173 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 25
Gaps: 0
Percent Identity: 76.000
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Gaps: 0
Percent Identity: 75.000
                                                                                                                                                                                                                                                                                                                                                                                                           357 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: Q05693 from: 1 to: 1089
                                                                                                                                                                                                                                                                                                                                                                                                           335 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualiflers
1..1089
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 GAACCTGCGGATCGCGCTCCGCTAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 uAsnLeuArgIleAlaLeuArgTyr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
ID 012114 standard; DNA; 1089 BP.
AC 012114;
                                                                                                                                                                                                                                                                                                                                                                                                           224 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-AUG-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.00
4.130
92.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: N_Geneseq_36:Q12114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.00
4.130
92.000
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US-08-653-294-32 x Q05693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-32 x Q12114
                                                                                                                                                                                                                                                                                                                                                                                                        1089 BP;
90-255479/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                0057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J03112487-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                See also
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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Align seg 1/1

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/*tag= a
/note= "Rous sarcoma virus LTR promoter domain, derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression vector; pHLA-B7/beta-2 microglobulin; heavy human HLA-B7; light beta-2 microglobulin; class I major histocompatibility complex; MHC; bicistronic mRNA; human leukocyte antigen; HLA; covalently closed circular DNA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "murine encephalomyocarditis CAP-independent translational enhancer (EMCV-CITE); taken from nucleotides 255-843 of cloned EMCV genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= e
/note= "encodes putative HLA-B7 heavy chain mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 It is a non-coding regulatory sequence functioning as an internal entry point for the eukaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for the Schmidt-Rupin strain nucleotides 8673-9146. This region also includes a 56 bp region of a synthetic oligonucleotide which modifies this regulatory sequence to effect a higher level of expression of downstream sequences. The oligonucleotide removes a polyadenylation signal sequence originally found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLA-B7 heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= g
/note= multiple cloning site, forms a junction
between the HLA-B7 sequence and the EMCV-CITE
sequence, and is used to facilitate subcloning"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= c
/note= "HLA-B7 heavy chain open reading frame"
                                                                                                                                                                                                                                   2634 TGGGACCGGAACACACAGATCTACAAGGCCCAGGCACAGACTGACCGAGA 2585
                                                                                                                                                                                                             1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note- "encodes putative signal peptide HLA-B7 heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label- consensus_Kozak_signal_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag= f
note= "3' untranslated sequence of
                                                                                                                                                                          to: 4059
                                   Length: 20
Gaps: 0
Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pHLA-B7/beta-2 microglobulin expression vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .n the RSV DNA sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                          to reverse of: Q75974
                                                                                                                                                                                                                                                                                                                                                                                                                       Q75973 standard; cDNA; 4965 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .. .1853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chain mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . .1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        535. .606
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-AUG-1995 (first entry)
                                                                                                                alignment_block:
US-08-653-294-32 x Q75974/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . .534
                                                       4.421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide"
                                                                                                                                                                                                                                                                                                                                                                  seq_name: N_Geneseq_36:Q75973
                                     84.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                            2584 GAGCCTGCGG 2575
                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block
                                                                                                                                                                                                                                                                                      17 uAsnLeuArg 20
                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                     alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
                                                                                                                                                                          Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                           075973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3'utr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rbs
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI: 95-036494/05.
WPI: 95-036494/05.
New vectors for gene therapy, partic for tumours - comprising genetic material encoding one or more cistron(s) which express immunogenic or therapeutic peptide(s) immunogenic or therapeutic peptide(s) immunogenic or therapeutic peptide(s).
This HLA-B7 antigen encoding plasmid was developed to incorporate many advantageous features, eg. the kanamycin resisitance gene. The eradication of two open reading frames encoding portions of SV40 viral proteins lowers the risk of tumourigenicity. The vector may also operate as a cassette into which cistrons may be inserted and removed at will for the transcription and subsequent translation of peptides of interest.
                                                                                                                                                                                                                                                                                23-AUG-1995 (first entry)
pHLA-B7 expression vector.
percession vector; pHLA-B7; beavy human HLA-B7; bicistronic mRNA;
light beta-2 microglobulin; class I major histocompatibility complex;
MHC; human leukocyte antigen; HLA; covalently closed circular DNA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "kanamycin resistance gene open reading frame;
the gene is taken from the transposable element
TU903"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The vector is used partic. for the treatment of neoplastic disease, eg. melanoma, and provides enhanced gene delivery and expression in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note "Rous sarcoma virus 3' LTR promoter region"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/note= "pBR322 backbone contg. bacterial origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1000 T;
                                                         1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  untranslated region of HLA-B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ...ce= "SV40 polyA signal sequence"
complement (1412, .1560)
/*tan= 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1033 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "HLA-B7 open reading frame" complement (2886. .3415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 t intron"
.1794)
to: 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (1410. .1177)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1051 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "pBR322 backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (1795. .2880)
                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= c
/note= "SV40 polyA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "SV40 small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (1561.
                                                                                                                                                  300 GAACCTGCGGATCGCGCTCCGCTAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heavy chain mRNA"
                                                                                                              17 uAsnLeuArgIleAlaLeuArgTyr 25
from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "HLA-B7
                                                                                                                                                                                                                                                 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        replication"
355. 1170
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               975 A;
                                                                                                                                                                                                                       _documentation_block:
Q75974 standard; cDNA; 4059
Q75974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .4059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-DEC-1994.
27-MAY-1994; U06069.
07-UNN-1993; US-074344.
(UNMI ) UNIV MICHIGAN.
(VICA-) VICAL INC.
Lew D, Marquet M, Nabel
                                                                                                                                                                                       seq_name: N_Geneseq_36:Q75974
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to: Q12114
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misc_feature

Synthetic.

polya_signal

intron

3'utr

cgs

NEW WENT THE FETT THE

ltr

misc_feature

WO9429469-A

Sequence

the

oţ

US-08-653-294-32 x Q75973

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PPR 22-DEC-1994; U06069.

PPR 27-MAY-1994; U06069.

PR 07-JUN-1993; US-074344.

ROW-1994; US-074344.

A (URMI ) UNIV MICHIGAN.

PA (VICA-) VICAL INC.

PA (VICA-) VICAL INC.

PA (VICA-) VICAL INC.

PA (WAT) 1994; US-076494.

PE Lew D, Marquet M, Nabel EG, Nabel GJ;

New vectors for gene therappy, partic for tumours - comprising

PT (Ind. Marguet M, Partic Periods)

PT New vectors for gene therappy, partic for tumours - comprising

PT (Ind. M) Properties on more cistron(s) which express

PT New vectors for gene therappy, partic for tumours - comprising

PT (Ind. M) Properties on more cistron(s) which express

PT (Ind. M) Properties in English.

PR New vectors for gene therappy, partic for tumours - comprising

PT (Ind. M) Properties in English.

PR New vectors for gene therappy, partic for the plasmid by the case of the margines of a class I major hisotocompatibility complex (MFC) antigen of the plasmid is designed to express these two proteins via a bicistronic mRNA in class arcoma Virus (RSV) promoter sequence deriv. from the 3' long terminal repeat. Permination of transcription is dependent upon the polyadenylation signal sequence deriv. from the bovine growth hormone gene. Eukaryotic cell translation of the heavy chain is regulated by the CITE. Finally the replication of the plasmid in bacterial cells is controlled by the presence of a bacterial origin of creplication. The vector is used partic. for the treatment of mopplastic cell disease, eg. melanoma, and provides enhanced gene delivery and expression of the plasmid controlled by the presence of a bacterial origin of the company case of the plasmid or the controlled by the presence of a bacterial origin of the company and expression the company or company case of the company case o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note- "bovine growth hormone 3'UTR and transcriptional terminator; it starts at a blunt-ended BglI site within the 3'UTR of the mRNA coding sequence"
                      mol. It enables the translational start codon of the beta-2 microglobulin, downstream of the HLA-B7 stop codon on this biscistronic mRNA to be recognised by the ribosome"
2480. 2880. 2880. /*tag= 1 //ote="encodes beta-2 microglobulin; this cDNA is deriv. from chimpanzee (differs to the human cDNA by only 4 bases)"
2840. 2846.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= o
/*tag= 
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/note= "pBR322 backbone contg. bacterial origin of
replication, it represents nucleotides 2244-3193"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "synthetic linker to facilitate cloning complement (3151. .3967)
ribosomal subunits when located within a mRNA
                                                                                                                                                                                                                                                                                                                                                                                     /*tag= j
/note= "3' untranslated region of the beta-2
microglobulin mRNA"
2847. 2870
/*tag= k
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "synthetic linker"
'UTR .3111
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3112. .
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Length: 20 Gaps: 0 Percent Identity: 80.000

84.00 4.421 95.000

Quality:

alignment_scores:

Ratio: Percent Similarity:

alignment_block:

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19-MAY-1998 (first entry)
Human Class I non-classical HLA gene exon 2 consensus DNA.
Human leukocyte antigen class I gene; non-classical HLA; allele testing;
donor; tissue matching; recipient; graft rejection; class typing; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIA-C gene, DNA probe and transformant cells - for immunisation of animals and monoclonal antibody development.
Claim 1; Page 1; 13pp; Japanese.
Probes comprising part of the sequence can be used to identify class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HIA-C animals and prodn. of monoclonal antibodies specific for the HIA-C sequence 1101 BP; 211 A; 337 C; 377 G; 176 T;
                                                                                                                                                                                                                                                                        HLA-C ezon Cb-1.
Human leukocyte antigen; probe; major histocompatibility complex;
MHC; class I; ss.
Homo sapiens.
                                                      1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
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Gaps: 0
Percent Identity: 70.000
to: 4965
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                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .1101
/*tag= a
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ID V02693 standard; DNA; 268 BP.

AC V02693; Standard; DNA; 268 BP.

DT 19-MAY-1998 (first entry)

DE Human Class I non-classical HLA

KW Human Elekocyte antigen class I

KW donor; tissue matching; recipien

OS Homo sapiens.

PN W0972365-A1.

PD 03-JUL-1997.

PF 04-JAN-1996; U00362.
from: 1
                                                                                                                                                                                                                              Q12116 standard; DNA; 1101 BP. Q12116;
                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAY-1991.
22-SEP-1989; 247695.
22-SEP-1989; UP-247695.
(OLVU) OLYMPUS OPTICAL KK.
WPI; 91-182989/25.
P-PSDB; R12465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.00
4.375
80.000
                                                                                                                                                                                seg_name: N_Geneseg_36:Q12116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: N_Geneseq_36:V02693
to: Q75973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: 012116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-32 x Q12116
                                                                                                                               seq_documentation_block:
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                                                                                                          17 uAsnLeuArg 20
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
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 Align seg 1/1
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300 GAGCCIGCGG 309
         alignment_scores;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viologia is a consensus sequence of the human leukocyte antigen (HLA) Class 102633 is a consensus sequence of the human leukocyte antigen (HLA) Class I non-classical HLA genes exon 2, which is used in a novel method for lesting a tissue sample to determine the allelic type of a HLA class I gene in the sample. The HLA Class I gene is selected from among HLA-A, be and -C genes. The method comprises of treating the tissue sample to obtain nucleic acid polymers suitable for amplification then combining these polymers with a first primer which hybridises with a different portion of the HLA Class I gene and a second primer which hybridises with a different portion of the HLA Class I gene under conditions suitable for amplification to obtain an amplified product. The product is then evaluated to determine the allelic type of the HLA-Class I gene. The method is useful for tissue matching HLA class I antigens between donors and recipients and hence for preventing graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human leukocyte antigen; probe; major histocompatibility complex; MHC; class I; ss.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI: 91-182991/25.
P-PSDB; R12464.
P-PSDB; R12464.
P-PSDB; R12464.
P-PSDB; R12464.
P-PSDB; R12464.
P-PSDB; R12464.
Immunising animals, for developing monoclonal antibody.
Claim 1: Page 1; 11pp; Japanese.
Probes comprising part of the sequence can be used to identify Class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HLA-B35 antigen. See also J03112485 and J03112487.
Sequence 1089 BP; 221 A; 336 C; 359 G; 173 T;
04-JAN-1996; WO-U00362.

(SLOK ) SLOAN KETTERING INST CANCER RES.

(Sereb N. Yang St.;

WPI: 97-351080/32.

DNA-based human leukocyte antigen class I gene typing method - useful for tissue matching and prevention of graft versus host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 TGGGACCGGGAGACACAGAACTTCAAGGCCCACACACAGACTGACCGAGA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 76.471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: V02693 from: 1 to: 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
ID Q12115 standard; DNA; 1089 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1991.
22-SEP-1989; 247697.
22-SEP-1989; JP-247697.
(OLYU ) OLYMPUS OPTICAL KK.
WPI; 91-182991/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 66.00
Ratio: 4.714
Percent Similarity: 82.353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-1991 (first entry)
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       versus host disease.
Sequence 268 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
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                                                                                                                                              disease
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HIA-C gene, DNA probe and transformant cells - for immunisation of animals and monoclonal antibody development.

Claim 2; Page 1; 13pp; Japanese.

Probes comprising part of the sequence can be used to identify class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HIA-C animals and prodn. of sequence antigen. See also Q1216 (same patent) and J03112486 and J03112487. sequence 1101 BP; 215 A; 335 C; 379 G; 172 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIA-C exon Cb-2. Thuman leukocyte antigen; probe; major histocompatibility complex; MHC; class I; ss. Homo sapiens.
                                                                                                                                                                                                                                  1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                             1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl
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4.062 Gaps: 0
80.000 Percent Identity: 65.000
66.00 Length: 20
3.667 Gaps: 0
90.000 Percent Identity: 65.000
                                                                                                                                                                to: 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: Q12117 from: 1 to: 1101
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1. .1101
/*tag= a
                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q12117 standard; DNA; 1101 BP. 012117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-SEP-1989; 247695.
22-SEP-1989; JP-247695.
(OLYU ) OLYMPUS OPTICAL KK.
WPI; 91-182989/25.
P-PSDB; R12466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-AUG-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              seq_name: N_Geneseq_36:Q12117
                                                                                             alignment_block:
US-08-653-294-32 x Q12115
                                                                                                                                                                Align seg 1/1 to: Q12115
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US-08-653-294-32 x Q12117
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300 GAGCCTGCGG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block
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    Quality:
Ratio:
                                          Percent Similarity:
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! AA227277 zr20h03.rl Stratage
! H23327 ym52e08.rl Soares inf
! AW215398 up03c01.xl NCI_CGAP
                                                                                                                                                                                                                                                                                                                                                     Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz- heidelberg.de;
sequenced by Qiagen within the cDNA sequencing consortium of the
German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block: 175 bp mRNA EST 09-FEB-1996 D8221 375 bp mRNA EST 09-FEB-1996 DEFINITION HUMHD64626 Human pancreatic islet Homo sapiens CDNA similar to HLA-B, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                       No s1 sequence available.

No s1 sequence available at the RZPD in Berlin.

This clone is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 1405

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers

1. 171

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DRFZP56402463"
/clone="DRFZP56402463"
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/loce="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

1. 36 a 53 c 60 g 22 t
                                                                                                AL036690 171 bp mRNA EST 27-SEP-1999
DKFZp564D2463_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone
DKFZp564D2463 5', mRNA sequence.
                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 171)
                                                                                                                                                                                                                                                        Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                     Wiemann, S. 227 (Duesterhoeft, et al.)
Expression 1999)
On Jul 7, 1999 this sequence version replaced g1:5866258.
Contact: Duesterhoeft A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 25
Gaps: 0
Percent Identity: 88.000
 375
479
591
0.0724
0.0972
0.1251
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190.89
188.59
186.62
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                                                                                                                                                          AL036690.3 GI:5927859
65.00
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5.130
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US-08-653-294-32 x AL036690
                                                        seq_name: gb_est38:AL036690
                                                                                   seq_documentation_block:
LOCUS AL036690
                                                                                                                                                                                                    Homo saptens
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Ratio:
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                                                                                                                                           AL036690
                                                                                                                                                                                      human.
              gb_est4:H23327
gb_est44:AW215398
gb_est11:AA227277
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                                                                                                               DEFINITION
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                                                                                                                                                                                   SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                          | Documentation | 1. ALO36690 DNF22564D2463_r1 564 (
| ALO36690 DNF2256 Human pancrea | DB2129 HUMHBC4626 Human pancrea | DB2189 HUMHBC4624 Human pancrea | ALI24815 am56e06.x1 Johnston fr | AAL51891 zoo1f06.x1 Stratagene | AAL51891 zoo1f06.x1 Stratagene | AAL58189 PWC74h11.x1 NCI_CGAP_Pa | AL596864 WC74h11.x1 NCI_CGAP_Pa | AL596864 WC74h11.x1 NCI_CGAP_Pa | AAL58109 zo57h10.s1 Stratagene | AA147151 zoo2406.x1 Stratagene | AA12088 zm22405.x1 Stratagene | AA13068 zm22405.x1 Stratagene | AA112349 zm22405.x1 Stratagene | AA112349 zm27b04.x1 Stratagene | AA166429 vx35b04.x1 Stratagene | C03945 c03945 Human heart cDNA | AA352960 EST51101 Activated T-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A10924 hbc122 Human pancreatic
A1286037 wk14903.x1 NCI_CGAP_Ly
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AA979637 vx38b05.r1 Stratagene
AA361489 EST71032 T-cell lympho
AA43607 zx06h02.r1 Soares_tota
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AA449607 zx06h02.r1 Soares_test
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AA41643 zt67602.r1 Soares_test
C1905 C1905 Human placenta cL
AA381090 EST94155 Activated T-c
W5004 zc92e11.r1 Pancreatic Is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL039796 DKFZP434B1912_r1 434 (AW208428 uo60c03.x1 NCI_CGAP_Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA160317 zo56c07.rl Stratagene
W40489 zc84b01.rl Pancreatic Is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA127128 z187d05.rl Stratagene
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                                                                                                          -MODEL-frame-plan.model -DEV-xlp

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-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000

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-NCPU-6 -ICPU-3 -NO_XLPXY -WAIT -THREADS-1
                                                        software, version 4.5,
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0.0533
0.0568
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                                                        About: Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                 Query: US-08-653-294-32
Query length: 25
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 7600.090000
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                                                                                               Command line parameters:
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gb_est10:AA151891
gb_est10:AA151891
gb_est31:A169664
gb_est31:A169664
gb_est6:A182177
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gb_est10:AA147151
gb_est10:AA13626
gb_est10:AA13626
gb_est11:T52124
gb_est11:T52134
gb_est11:AA310808
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gb_est9:C19056
gb_est13:AA381090
gb_est7:W52004
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gb_est13:AA327128
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gb_est13:AA352534
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gb_est21:AA970332
gb_est10:AA151951
                            Date: Feb 8, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_est38:AL036690
gb_est6:D8221
gb_est6:D82189
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gb_estl:T10924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_est15:A1826037
gb_est17:AA663896
gb_est20:AA879637
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Email: jtakeda@sb.gunma-u.ac.jp
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US-08-653-294-32 x D82189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Human pancreatic islet"
/clone_lib="Human pancreatic islet"
/clone_vector: Lambda ZAPII: Site_1: Eco RI; Site_2: Xho
I: mRNA was prepared from normal adult human islets. CDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. CDNA was size fractionated to remove
sequences <1000 bp in size."
3 others
                                                                                                                                                                                                                                                                                                Human pancreatic islet ESTs
Unpublished (1995)
Unpublished (1995)
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced g1:785255.
Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University 3-39-15 Showa-machi, Maebashi Gunma 371, Japan
Tel: 272-20-8896
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Unpublished (1995)
On April 4, 1993 this sequence version replaced g1:785206.
Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University 3.39-15 Showa-machi, Maebashi Gunma 371, Japan
Tel: 272-20-8856
Fax: 272-20-8896
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                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 375)
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Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: jtakeda@sb.gunma-u.ac.jp.
Location/Qualifiers
1. .375
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Eukaryota; Metazoa; C
Eutheria; Primates; C
1 (bases 1 to 415)
Takeda,J.
                                   GI:1183739
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US-08-653-294-32 x D82221
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D82221
D82221.1
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                                                                                                          human.
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TITLE
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KEYWORDS
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/db_xref="taxon:9606"
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/clone_lib="Human pancreatic islet"
/note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove-
sequences <1000 bp in size."

134 c 133 g 61 t 8 others
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI124815 414 bp mRNA EST 11-SEP-1998 am56e06.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539586 3' similar to gb:MZ4038_cds1 HLA CLASS I HISTOCOMPATIBILITY AMTIGEN, BW-44(B-12) B*4402 (HUMAN); contains MER22.t3 TAR1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
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Gaps: 0
Percent Identity: 76.000
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Location/Qualifiers
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4.348
92.000
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Homo saplens
                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human .
                                                                                                                                                                                                                                                                                                                                                   alignment_scores
                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
/dev_stage="adult"
/lab_lost="50LR (kanamycin resistant)"
/lab_lost="50LR (kanamycin resistant)"
/lab_lost="50LR (kanamycin resistant)"
/lote="0rgan: Drain: Vector: Bluescript SK-; Site_1:
EcoRI: Stanley Neuropathology Consortium
/www.stanleylab.org) brains S-58, S-65, S-67, S-78.
Random + oligo-dT primed into EcoRI site of ZAP II Vector.
Mass excised. Avg insert length 1.9kb. Custom library
privided by Dr. Nancy Johnston [(410) 614-3918,
nli@welchlink.welch.jhu.edul.
140 c 136 g 58 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Butkaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 255)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Hillier,L., Lennon,G., Becker,M., Eowallo,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS AA151891 255 bp mRNA EST 10-DEC-1996
DEFINITION zoO1f06.rl Stratagene colon (#937204) Homo sapiens cDNA clone
IMAGE:566435 5' similar to gb:M15497_cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) A*2401 (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On May 8, 1995 this sequence version replaced gi:800234
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 TGGGACCGGGAGACACAGATCTCCAAGACCAACACACAGACTTACCGAGA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                Length: 25
Gaps: 0
Percent Identity: 76.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 414
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/db_xref="GDB:4590888"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 uAsnLeuArgIleAlaLeuArgTyr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
AA151891
AA151891.1 GI:1720754
                                                                                                                                                                                                                                                                                                                                                                     Ratio: 4.364
Percent Similarity: 88.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AI124815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-653-294-32 x AI124815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_est10:AA151891
                                                                                                                                                                                                                                                                                                                                                   Quality:
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                                                                                                                                                                                                                                                                                                                         alignment_scores:
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KEYWORDS
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ORGANISM
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ORIGIN
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JOURNAL
MEDLINE
COMMENT
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ACCESSION AASSISS 1 Greent Identity: 50 OCCOMENT TO CONTRACT SERVENCE SERVE
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Seq primer: -400r 1118 High quality sequence stop: 4
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 GAACCIGGGATCGCGCTCCGCTAC 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 uAsnLeuArgIleAlaLeuArgTyr 25
                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-32 x AI359260/rev
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                                                                                                                                                                                                                                                                                        4.524
                                                                                                                                                                                                                                                                  95.00
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                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                 128
                                                                                                                                                                                                                                                                                          Ratio
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VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                              BASE COUNT
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TITLE
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ECOR1-Xhol. mRNA was purified from KG1-a cell line, CDNA was synthesized using an Xhol-OligodT linker primer. EcoR1 adaptors were ligated, followed by digestion with Xhol for directional cloning into predigested Lambda Zap Express" 91 c 88 g 40 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Washington University Genome Sequencing Center DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Organ: brain; Vector: p1713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:

LOCUS
A1359260
618 bp mRNA
EST
15-FEB-1999
DEFINITION 9/27b07.x1 NCI_CGAP_Brn23 Homo sapiens CDNA clone IMAGE:2013205
similar to 9b:D32129 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
AW-66(A-10) A*6601 ALPHA (HUMAN);, mRNA sequence.
ACCESSION
A1359260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 618)

NCI/NINDS-CSAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-CSAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index

Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 TGGGACCGGAACACACACAGATCTTCAAGACCAACACACAGACTTACCGAGA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl
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/clone="twage:2013205"
/clone=lib="NcI_CGAP_Brn23"
/tissue_type="0,1oblastoma (pooled)"
/lab_host="0H108"
                                                                                                                                                                                                                Length: 25
Gaps: 0
Percent Identity: 76.000
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                                                                                                                                                                                                                                                                                                                                                                                   to: 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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Seq primer: -(400P from Gibco
High quality sequence stop: 458.
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                                                                                                                                                                                                                                                                                                                                                                                     from: 1
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                                                                                                                                                                                                                95.00
4.130
92.000
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US-08-653-294-32 x AA263158
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Percent Similarity:
                                                                                                                                                                                                                     Quality:
                                                                                               64
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                                                                                               BASE COUNT
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TITLE
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KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 7/48)

2 (bases 1 to 7/48)

3 (bases 1 to 7/48)

4 (bases 1 to 7/48)

5 (bases 1 to 7/48)

5 (bases 1 to 7/48)

6 (bases 1 to 7/48)

7 (bases 1 to 7/48)

7 (bases 1 to 7/48)

7 (bases 1 to 7/48)

8 (bases 1 to 7/48)

9 (bases 1 to 7/48)

10 (bases 1 to 7/48)

11 (bases 1 to 7/48)

12 (bases 1 to 7/48)

13 (bases 1 to 7/48)

14 (bases 1 to 7/48)

15 (bases 1 to 7/48)

16 (bases 1 to 7/48)

17 (bases 1 to 7/48)

18 (bases 1 to 
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
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LOCUS A1696864 748 bp mRNA EST 03-JUN-1999
DEFINITION WC14h11.X1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2324421
Similar to 9b:M28205 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
B-51(B-5) B*5101 ALPHA (HUMAN); mRNA sequence.

ACCESSION A1696864 GI:4984764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364 TGGGACGAGGAGACAGGGAAAGTGAAGGCCCACTCACAGACTGACCGAGA 315
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Gaps: 0
Percent Identity: 76.000
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/clone_11b-"NCI_CGAP_Pan1"
/tissue_type-"adenocarcinoma"
/lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ww-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 t
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
/db_xref="GDB:4623429"
/db_xref="GDB:4623429"
/db_xref="Izaxon:9606"
/clone="Ixaxon:9606"
                                                                                                                                           seq_documentation_block:

LOCUS
AAL58109
495 bp mRNA
DEFINITION 2.057h10.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone
IMAGE:591043 3' similar to gb:U04245 HLA CLASS I HISTOCOMPATIBILITY
ANTIGEN, B-7 B*0702 ALPHA (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 495)
S Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Waterston,R. and Wilson,R. WashU-NCI human EST Project
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1395000.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyT not found
Insert Length: 1581 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham
High quality: sequence stop: 43.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 20
Gaps: 0
Percent Identity: 85.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 g
                                                                                                                                                                                                                                                                                                                                                                             AA158109.1 GI:1732894
311 GAACCTGCGGATCGCGCTC 329
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4.789
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US-08-653-294-32 x AA158109
                                                                                                seq_name: gb_est10:AA158109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 uAsnLeuArg 20
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JOURNAL
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ORIGIN
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dclone_lib="Human pancreatic islet"
/note="vector: Lambda ZAPI; Site_1: Eco RI; Site_2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <1000 bp in size."

49 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human pancreatic islet ESTs
Unpublished (1995)
Unpublished (1995)
Unpublished (1995)
Unpublished (1995)
Con Apr 14, 1993 this sequence version replaced gi:785191.
Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University 3-9-15 Showa-machi, Maebashi Gunma 371, Japan
Tel: 272-20-8856
Fax: 272-20-8896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D82177 330 bp mRNA EST 09-FEB-1996 HUMHBC4504 Human pancreatic islet Homo sapiens cDNA similar to B82177 B82177.1 G1:1183645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 330)
Takeda,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                             1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                 Percent Identity: 76.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps: 0
Percent Identity: 78.261
                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                         to: 748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: jtakeda@sb.gunma-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 uAsnLeuArgileAlaLeuArgTyr 25 | 11 | 11 | 11 | 11 | 11 | 11 | 12 | 142 GAACCTGCGGATCGCGCTCCGCTAC 166
                                                                                                                                                                                                                                                                                                                                            from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: D82177 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.00
4.273
95.652
                                                                                             95.00
4.130
92.000
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                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-32 x AI696864
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US-08-653-294-32 x D82177
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LOCUS D82177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_est6:D82177
                                                                                                                                                                    Percent Similarity:
                                                                                                                                    Ratio:
                                                                alignment_scores:
Quality:
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

TITLE JOURNAL COMMENT REFERENCE AUTHORS

FEATURES

Align seg 1/1

BASE COUNT ORIGIN

12-APR-1995

us-08-653-294-32.rst

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL MEDLINE COMMENT

```
Wilson, R.
The WashUr Marck EST Project

Unpublished (1995)
Contact: Wilson RK
WashIngton University School of Medicine
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1875
High quality sequence stops: 384 Source: IMAGE Consortium, LINL
This clone is available royalty-free through LinL ; contact the
IMAGE Consortium (info@image.linl.gov) for further information.
Insert Length: 1875 Std Error: 0.00
Seq primer: MI3RPl
High quality sequence stop: 384.
                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 459)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Leh,N., Lemnon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                        R13904 459 bp mRNA EST 12-APR-199
YAG2003.r1 Soares infant brain INIB Homo sapiens CDNA clone
YMAGE:26601 5' similar to gb:M64742_cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, A-23(A-9) A*2301 (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="GDB:399148"
/db_xref="taxon:9606"
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/clone_llb="Soares infant brain lNIB"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 0
Percent Identity: 75.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism-"Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: R13904 from: 1
                                                                                                                                                     R13904
R13904.1 GI:766980
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4.400
83.333
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US-08-653-294-32 x R13904
                    seq_documentation_block:
LOCUS R13904
DEFINITION yf62c03.rl Sc
                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                 sequence.
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Ratio:
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ORIGIN
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                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                             2032d06.rl Stratagene colon (#937204) Homo sapiens CDNA clone
IMAGE:588587 5' similar to gb:M64740 HLA CLASS I HISTOCOMPATIBILITY
ANTIGEN, A-24(A-9) A*2402 ALPHA (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 581)

Hillari, Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, M., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rhikin, L., Rohling, T., Schellenberg, K., Soares, M. B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Materston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 272.
                                                                 05-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Sep 12, 1996 this sequence version replaced gi:1393699.
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 others
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Gaps: 0
Percent Identity: 72.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .581
/organism="Homo sapiens"
/db_xref="gdb:462089"
/db_xref="taxon:9606"
/clone="IMAGE:588587"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1 to: 581
                                                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 g
                                                                                                                                                                       AA147151.1 GI:1716526
                                                               581 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.333
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US-08-653-294-32 x AA147151
seq_name: gb_est10:AA147151
                                           seq_documentation_block:
LOCUS AA147151
                                                                                                                                                                                                                                           Homo sapiens
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Ratio:
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                                                                                                                                                        AA147151
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FEATURES

alignment_scores:

COUNT

seq_name: gb_est2:R13904

24

17 uAsnLeuArgIleAlaLeuArg

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Homo saplens
                                                                                                                                                                        286 GGCCTGCGG 295
                                                                                                            17 uAsnLeuArg 20
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VERSION
KEYWORDS
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JOURNAL
COMMENT
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="GDB:3917806"
/db_xref="GDB:3917806"
/db_xref="GDB:3917806"
/db_xref="Inaxon:9606"
/dlone="Inaxon:9606"
/clone="Inaxon:9606"
/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Figure 1: estewatson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should be
kept in mind should you use this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 41)
Hiller,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,N., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rikin,L.,
Rohlfing,T., Schallenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                 Generation and analysis of 280,000 human expressed sequence tags Genome_Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28M13 rev2 from Amersham.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On May 18, 1995 this sequence version replaced gi:811358.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl
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Gaps: 0
Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AA121088 from: 1
291 GAACCTGCGGATCGCGCTCCGC 312
                                                                                                                                                                                                                                                                                                                                                                                                 AA121088
AA121088.1 GI:1678632
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                                                                                                        seq_name: gb_est9:AA121088
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Ratio:
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VERSION
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seq_documentation_block:

LOCUS AA143626 338 bp mRNA EST 08-NOV-1997

DEFINITION 2065h01.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:591793 5' similar to gb:U04245 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN. B-7 B*0702 ALPHA (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.

Eutheria, Primates; Catarrhini, Hominidae, Homo.

I (basea) 1 to 338)

Hillder, L. Allen, M. Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Morte, R., Schellenberg, K., Steptoe, M., Tan, F., Theisiang, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project

On Nov 29, 1993 this sequence version replaced gi:634605.

Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royaity-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1677 Std Error: 0.00
10 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 16
Gaps: 0
Percent Identity: 93.750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 193.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 84.00
Ratio: 5.250
Percent Similarity: 100.000
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US-08-653-294-32 x AA143626
                                                                                                                                                              seq_name: gb_est10:AA143626
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T52124 06-FEB-1995

YD299G6.rl Strattagene fetal spleen (#93725) Homo sapiens cDNA

Clone IMAGE:72634 5' similar to similar to qb:M24032_cds1 HLA CLASS

I HISTOCOMPATIBILITY ANTIGEN, BW-65(B-14) B*1402 (HUMAN), MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High qality sequence stops: 330 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: Mi3RPl sequence stop: 330.

Location/Qualifiers
                                                                                                                                                                                                                    Homo sapiens

Butaryota: Metazoa: Chordata: Craniata; Vertebrata: Mammalla:

Eutheria: Primates; Catarrhini; Hominidae: Homo.

1 (bases 1 to 367)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,

Hillier,L., Lennon,G., DuBuquer,T., Favello,A., Gish,W.,

Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,

Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,

Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thlerry Meg,J.,

Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:72634"
/clone_lib="Stratagene fetal spleen (#937205)"
/tissue_type="fetal spleen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
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4.263 Gaps: 0
95.000 Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. 367
/organism="Homo sapiens"
/db_xref="GDB:494299"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 367
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Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: T52124 from: 1
                                                                                                                                  T52124
T52124.1 GI:653984
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US-08-653-294-32 x T52124
seg_documentation_block:
LOCUS T52124
DEFINITION yb29906.rl S1
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286 GAGCCTGCGG 295
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Ratio:
Percent Similarity:
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AUTHORS
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JOURNAL
MEDLINE
COMMENT
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

February 8, 2000, 04:05:44; Search time 133.56 Seconds (without alignments) 2.660 Million cell updates/sec

US-08-653-294-33 74

1 KAQTDRENLRIALRY 15 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

188963 segs, 23686106 residues Searched:

188963 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

A_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	40.000	mot di toggi	02 CIL m	Peptide B2702.70-8	Peptide fragment o	HLA-B2702 CTL modu	HLA-B2702.60-84. C	Pept1de B2702.60-8	Human HLA-B27-(62-	Peptide fragment o	HLA-B2702 CTL modu	HLA-B2705.60-84. C	Sequence of the hu	Sequence encoded b	Peptide fragment o	늰	84.	Seg	e of		exon.	ě	HLA B27 hypervaria	÷	Human HLA-B27 alph	fragme	Ĕ	hel 13	T-cell modulating	latory	Peptide B2702.75-8	HLA-B2702 CTL modu	CIL	84-72-8		
SUMMAKIES	£	77	R92912	W33795	R41205	R83090	R95416	W33794	R71442	R41221	R83091	R95417	P70590	P70155	R48286	R83093	R95422	X06801	R03142	R03144	R12463	R83071	R50266	R71443	W58992	R41208	R83062	R95413	W07512	W47265	W33784	R92907	R92908	R95428	W33778	W33791
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	or CC	2000	74	74	74	74	74	74	59	29	59	29	29	29	26	26	26	26	26	26	26	53	52	20	20	49	49	49	49	49	49	49	49	49	49	49
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HLA-B7.60-84. Comp HLA-B2702 CTL modu HIA-B2702 CTL modu	HLA-B2702 CTL modu HLA-B2702.75-84(P) HLA-B2702.75-84(F)	T-cell modulating Immunomodulatory p Immunomodulatory p	Peptide B2702.75-8 Peptide B2702.75-8
R95431 R83094 R83095	R83096 R95425 R95426	W07513 W47267 W47269	W33788 W33787
444			
10	2222	223	100
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35	8 8 8 0 8 6 0	<b>4</b> 17	4 4 5

9	R92012 atandard: neptide: 15 AA
N S	R92912;
텀	16-MAY-1996 (first entry)
回回	HLA-B2702 CTL modulating peptide (B2702.70-84).
X	Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KΣ	immunosuppressant; graft versus host disorder; transplantation; therapy;
ΚW	class I MHC; HLA-B2702.
S	Synthetic.
PN PN	W09526979-A1.
Б	12-OCT-1995.
F.	05-APR-1995; U04349.
PR	05-APR-1994; US-222851.
PA	(STRD ) UNIV LELAND STANFORD JUNIOR.
БI	Clayberger C, Krensky AM, Parham P;
DR.	WPI; 95-358582/46.
PŢ	Extension of acceptance period of transplants from MHC unmatched
ΡŢ	donor hosts - using Class I B75-84 MHC antigen of the recipient
Τď	host
S	Example 15; Page 36; 80pp; English.
ပ္ပ	R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
ပ္ပ	class I major histocompatibility complex (MHC) antigens. This sequence
អ	corresponds to residues 70-84 of the alpha-1 domain of the class I MHC
អ	HLA-B2702. These sequences can be used to extend the period of
ប្ដ	acceptance by a recipient of a transplant from an MHC unmatched donor.
ပ္ပ	The peptides are administered to a patient in conjunction with a
ပ္ပ	subtherapeutic amount of an immunosuppressant. This is administered to
ပ္ပ	the patient for a limited period of time (compared to the lifetime
ပ္ပ	administration for current treatments). The peptides particularly
ပ္ပ	modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs)
ပ္ပ	of the patient.
ဝ္ပ	Sequence 15 AA;

Gaps ö Ouery Match
100.0%; Score 74; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels

ô

1 KAQTDRENLRIALRY 15 1 KAQTDRENLRIALRY 15 à g

~

W33795 standard; peptide; 15 AA.
W33795;
19-JUN-1998 (first entry)
Peptide B2702.70-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain; 

rejection. Synthetic. Homo sapiens. W09744351-A1. 27-NOV-1997.

R83090 standard; peptide; 25 AA.

RESULT

1 KAQTDRENLRIALRY 11 KAQTDRENLRIALRY

à g 16-MAY-1996 (first entry)

```
With the sequence in the brackets may optional anique compound of transplants or treating automatical diseases.

For treating activity, including the N-terminal activity diseases.

For the peptide-type compound comprises the formula: A-B, where A, B = C, C example and A-B a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mew peptide(s) based on class I HLA antigen domains - used for modulating cytocoxic T-lymphocyte activity towards targets T-lymphocyte activity towards targets Tolaim 8; Page 53; Glpp; English.

The peptide (or a fragment of at least 10 amino acids, joined at at least one terminus to a sequence other than that of wild type HLA antigen) is used to modulate cytocoxic T-lymphocyte (CTL) activity, and thinbition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAR-1994 (first entry)
Peptide fragment of Class I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia; parasitic disease; cytotoxic T lymphocyte; modulation.
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25-FEB-1993; U01758.
02-MAR-1992; US-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger CA, Krensky AM;
WPI; 93-303134/38.
22-MAY-1997; U08689.
24-MAY-1996; US-553294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Bellow R. Clayberger C, Krensky AM: WPI: 98-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R41205 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Conservative
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Best Local Similarity
Matches 15; Conserv
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R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIA-B2702.60-84.

HIA-B2702.60-84.

HIA, p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; r-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.

Synthetic.

W09513388-A1.
                                                                HIA-B2702 CTL modulating peptide (B2702.60-84).
Cytocoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HIA-B2702.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clayberger C, Krensky AM;
WPI; 95-194027/25.
Compsns. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs.
Example: Page 9; 29pp; English.
R95413, and R95415-R95431 represent palindromes and fragments of
                                                                                                                                                                                                                                                            Clayberger C. Krensky AM, Parham P; WPI; 95-358862446.
Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 74; DB 1; L
100.0%; Pred. No. 3.6e-07;
1ve 0; Mismatches 0;
                                                                                                                                                                                            12-OCT-1995,
05-APR-1995,
05-APR-1994; US-222851,
(STRD ) UNIV LELAND STANFORD JUNIOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-MAY-1995.
10-NOV-1994, U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R95416 standard; peptide; 25 AA.
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Best Local Similarity
Matches 15; Conserv
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RESULT
R95416
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Gaps

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Indels

Length 25;

100.0%; Score 74; DB 1; I 100.0%; Pred. No. 3.6e-07; ative 0; Mismatches 0;

Query Match 100. Best Local Similarity 100. Matches 15; Conservative

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from a T-cell lyst first T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein HSTO. p74 is found in a limited number of cell types, but is particularly expressed on a mamphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-BZ702 palindromic peptide.

Compositions comprising the extracellular fragment of p74 combined with this sequence, induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate composition containing the critisis and antigen presenting cells (APCS), by adding to the mix the extracellular composition containing of the p74 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PERION K, Liapperger C, Mensky AM;

WHI: 98-086530708

New immunomodulating dimer peptide(s) - based on a Class I HIA-B
alpha-1 domain, used for preventing rejection of transplants or
reating autoimmune diseases

Example 1; Page 19; 41pp; English.

PER Example 1; Page 19; 41pp; English.

PER Cativity A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or
C-terminal amidated or esterlified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, Sor N; aa79 = R or G; aa80 = I or N; aad a represents amino acid: aa82 = R or L; aa83 = G or R; and aa represents amino acid: The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets: The compounds comprise at any peptide type bond within the brackets: The compounds comprise or at any peptide type bond within the brackets: The compounds comprise or at any petide type bond within the brackets or of truncated at any petide type bond within the protection of T cells in news or in combination with antigenic peptides or proteins of interest to activate CTLS: They can be used to inhibit the proliferation of T cells in response to anti-CDS. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, response to anti-CDS. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, response to anti-CDS. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, response to an addiagnosis. The products can also be used for detection and diagnosis. The products can also be used for detection and diagnosis. The products can also be used for detection and diagnosis. The products can also be used for detection and diagnosis. The products can also be used for preventing expense t
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  These sequences can be used to isolate the protein p74
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Peptide Ba702.60-84 tested for immunomodulating activity.

Immunomodulating dimer: immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 74; DB 1; Length 25; 100.0%; Pred. No. 3.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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22-MAY-1997; U08689.
24-MAY-1996; US-653294.
(STR ) UNIY LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W33794 standard; peptide; 25 AA.
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nes 15; Conservative
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  HLA-B2702.60-84.
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WO9744351-A1.
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Matches
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The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition.
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Page 45; 103pp; English.

R71439-R71443 are human major histocompatibility complex class 1
(MHC 1) alpha 1 domain and HLA derived peptides and fusion peptides.
They were used to modulate interactions between MHC 1/HLA and cell
surface receptors. Via competitive inhibition the peptides diminish
the receptors response, this feature may be useful for the treatment
of neoplasias, lupus erythematosus and arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                   lupus erythematosus
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Peptide fragment of HLA-B2705 antigen.
Human leukocyte antigen; HLA: peptide: transplantation; neoplasia;
parasitic disease; cytotoxic T lymphocyte; modulation.
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Human HLA-B27-(62-85) antigen derived peptide.
Human HLA-B27-(62-85) antigen derived peptide; cell receptor;
Human HLA-B27-(62-85) antigen derived peptide; lupus erythema
Interaction modulation; arthritis; neoplasias; lupus erythema
                                                                                                                                                                                                                                                                                                                                                                                                       Goldstein A, Goodenow RS, Olsson L;
WPI; 95-089577/13.
Regulating cell surface receptor response - by modulating
Interaction between MHC class I antigen and the cell surface
     Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 59; DB 1; Length 17;
Pred. No. 0.00012;
1; Mismatches 2; Indels
                                      Indels
100.0%; Score 74; DB 1; 1 100.0%; Pred. No. 3.6e-07;
                                    Mismatches
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25-FEB-1993. 001758.
02-MAR-1992; US-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R41221 standard; peptide; 25 AA.
R41221;
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                                                                                                                                                                                         R71442 standard; peptide; 17
R71442;
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WPI; 93-303134/38.
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Best Local Similarity 80.0
Matches 12; Conservative
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                  12-AUG-1994; U09189.
12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA.
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                                                                       1 KAQTDRENLRIALRY 15
                                                                                         11 KAQTDRENLRIALRY 25
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                    Similarity
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WO9505189-A.
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 Query Match
Best Local Simi
Matches 15;
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R71442
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The sequence and the sequence and transments of human-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the than-1205.60-84. These sequences can be used to isolate the protein of from a T-cell lysate. P74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. P74 is cound in a limited number of cell types, but is particularly expressed on amphoteric detergent, and then passed through an affinity column amphoteric detergent, and then passed through an affinity column containing a covalently bound HA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of P74 combined with HA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate Compounds can be screened for their effect on the cytolytic activity of CT-cells, by combining them with the extracellular portion of P74 and determining the amount of binding between the candidate compound and P74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by adding to the CM with P74 for the binding of the P74 ligand.
                                                                                            Compsons. comprising lymphoid surface membrane proteins - which me inhibit cytolytic activity and differentiation of CTLs. Example; Page 9; 29pp; English. R95413, and R95415-R95431 represent palindromes and fragments of
Clayberger C, Krensky AM; WPI; 95-194027/25.
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Best Local Similarity
Matches 12; Conserv
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P70590
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R83061-R83096, R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HIA-B3702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-NOV-1996 (first entry)
HLA-B2705.60-84.
HLA-B2705.60-84.
HLA-P274: alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLA-B2702 CTL modulating peptide (B2702.60-84).
Cytotoxic I lymphocyte, CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                               Gaps
                   This peptide is derived from the HLA-B2705 antigen and corresponds to the amino acid positions 60 \cdot 84 of that antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MHC unmatched
the recipient
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                                                                                                                                                    Score 59; DB 1; Length 25; Pred. No. 0.00019; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 59; DB 1; Length 25;
Pred. No. 0.00019;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Extension of acceptance period of transplants from donor hosts – using Class I B75-84 MHC antigen of
                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Krensky AM, Parham P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-OC1-1995.
05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   R83091 standard; peptide; 25 AA.
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80.0%;
                                                                                                                                                       79.7%;
80.0%;
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                                                                                                                           Ouery Match
Best Local Similarity Bu.v.
Best Local 21 Conservative
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Matches 12; Conservative
                                                                                                                                                                                                                                                            1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                              11 KAQTDREDLRTLLRY 25
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10-NOV-1994; U12985.
10-NOV-1993; US-150493.
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WPI; 95-358582/46.
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Sequence 25
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WO9513288-A1.
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                                                                           Seguence
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R83091
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Length 25;

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                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA coding for antigen HLA B27 - and diagnostic reagents contg.

Such DNA, antigen or antibody
Disclosure: Page 5: 5pp; German.

The DNA may be used as a hybridisation probe for detecting the HLA B27 gene, eg for assessing susceptibility to rheumatic disorders such as ankylosis spondylitis, or may be used to transform cells for prodn. of HLA B27. The HLA B27 may be used to detect HLA B27 antibody in human serum, or to produce mono- or polyclonal HLA B27 sequence 337 AA;
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Pred. No. 0.0033;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                      Sequence of the human histocompatibility antigen HLA B27. Rheumatic disorder; genetic screening; diagnosis; Homo sapiens spondylitis.

Box 22,224.04.A.
                                                    2; Indels
79.7%; Score 59; DB 1; I
80.0%; Pred. No. 0.00019;
iive 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-1985; 542024.
28-NOV-1985; DE-542024.
21-DEC-1985; DE-542576.
(BEHW ) BEHRINGWERKE AG.
Rethmuller G, Meo T, Weiss E, Szots H; WPI; 87-157893/23.
N-PSDB; N70935.
                                                                                                                                                                                                                                                                             P70590 standard; protein; 337 AA.
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80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
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Gaps

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RESULT

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Example 13; Page 32; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HLAB38. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an WHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLAB38 CTL modulating peptide (B38.6084).

Yotocoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLAB38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM:
WPI: 95-194027/25.
Compsns. comprising lymphoid surface membrane proteins - which may inhibit cytolyric activity and differentiation of CTLS.
Example; Page 9; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 25;
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                                                                                      1; Indels
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92.3%; Pred. No. 0.00065;
tive 0; Mismatches 1;
        Score 56; DB 1; Pred. No. 0.00065;
                                                                                      Mismatches
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12-0CT-1995,
05-APR-1995; U04349,
05-APR-1994; US-222851,
(STRD ) UNIV LELAND STANFORD JUNIOR.
(STRD ) Krensky AM, Parham P;
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Synthetic.
W09513288-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                     R83093 standard; peptide; 25
R83093;
        75.7%;
92.3%;
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HLAB38.6084.
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                                                                                      Conservative
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Best Local Similarity
Matches 12; Conserv
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WO9526979-A1.
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Matches 12;
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R95422
AC R95422
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DF CARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Social Weiss E. Dorner C. Lang M. Meo T. Riethmuller G; WPI: 87-171469/25.
WPD B9 171469/25.
NP - PSDB; N70225.
DNA coding for human histocompatibility antigen HLA-B 27 - useful bisclosure: p6: 13pp; German.
Disclosure: p6: 13pp; German.
THE DNA may be used to detect the HLA-B 27 gene (opt. mutated) in human genetic material. The HLA-B 27 may be used to detect anti-HLA-B 27 may be used to detect anti-HLA-B 27 levels in human serum. The antibodies may be used to determine HLA-B 27 levels in human serum, eg for diagnosis of rheumatic disorders, esp. ankylosing spondylitis.
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The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and meoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition. This peptide is derived from the HLA-B38 antigen and corresponds sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAR-1994 (first entry)
Peptide fragment of HLA-B38 antigen.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia; parasitic disease; cytotoxic T lymphocyte; modulation.
                                                                                                                                                                                                                                                                                                                                                               03-APR-1991 (first entry)
Sequence encoded by genomic DNA encoding human histocompatibility
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Pred. No. 0.0036;
.; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     antigen HLA-B 27.
Ankylosing spondylitis; rheumatic disorder; diagnosis.
Homo sapiens.
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25-FEB-1993; U01758.
02-MAR-1992; US-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger CA, Krensky AM;
WPI; 93-303134/38.
                                                                                                                                                                                                                                           P70155 standard; protein; 362 AA
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80.08;
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Best Local Similarity 80.0
Matches 12; Conservative
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01-JAN-1985; DE-542024,
21-DEC-1985; DE-545576,
(BEHW ) BEHRINGWERKE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KAQTDRENLRIALRY 15
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70 KAQTDREDLRTLLRY
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Sequence

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Human-leucocyte-associated antigens. This sequence represents the Highs 6084. These sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein associated at the T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hs70. p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable cell with an ampotent detergent, and then passed through an affinity column comprising a covalently bound HIA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with HIA-B2702.60-84 (see R95416), induces calcium influx, and inhibits compositions can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and centraling the amount of binding between the candidate composition of containing T-cells and antigen presenting cells (APCS), by adding to the mith p74 for the binding of the p74 in an amount sufficient to compete with p74 for the binding of the p74 ligand.
and R95415-R95431 represent palindromes and fragments of
888888888888888888888888888
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Gaps ö Query Match 75.7%; Score 56; DB 1; Length 25; Best Local Similarity 92.3%; Pred. No. 0.00065; Matches 12; Conservative 0; Mismatches 1; Indels

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3 QTDRENLRIALRY .15 || ||||||||||| 13 QTYRENLRIALRY 25

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Search completed: February 8, 2000, 04:05:44 Job time: 9361 sec

us-08-653-294-33.rpr

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

February 7, 2000, 18:04:41; Search time 111.22 Seconds (without alignments) 6.362 Million cell updates/sec

US-08-653-294-33 74 1 KAQTDRENLRIALRY 15 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

142080 segs, 47169319 residues Searched:

142080 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

summaries Post-processing: Minimum Match 0% Listing first 45

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_62:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		59308	180167	JH0541	JH0539	JH0540	180169	180171	_	S03537	HU12	7963	54416	I54493	JHU32	A35997	180174	180168	HLHUB8	162045	I84490	17521	15997	56116	HLHUB2	37485	~	4	38509	4	0
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	Query Match Length	354	354	362	362	362	355	355	363	363	359	365	365	365	274	364	137	354	362	362	362	362	364	338	362	362	362	362	273	274	362
d	Query Match	94.6		94.6				93.2							82.4	82.4	81.1	81.1	81.1	81.1	81.1	81.1	81.1		φ.		٠	•	ď.		
	Score	70	70	70	70	70	69	69	69	69	99	99	99	99	61	61	9	09	9	9	9	9	9	29	59	29	53	59	26	26	26
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362 2 A45834 362 2 184486 362 2 A30345 362 2 159633 362 2 159633 362 2 172808 355 2 137516 362 2 137516 362 2 161861 362 2 161861 365 2 161861 365 2 161861 365 2 161861 367 2 161861 367 2 161861	MHC class I histoc transmembrane glyc	MHC CIASS I DISCOC MHC HLA-B transmem class I histocompa	MHC class I histoc MHC class I HLA-J HLA-B alpha-chain	class I histocompa MHC class I histoc MHC HLA-B44.2 chai	MHC class I histocompa class I histocompa MHC class I heavy class I histocompa
	A45834 I84486	R30345 I59633 S24434	137120 172808 137516	S25415 A45850 I61861	154442 JH0537 167482 S11141
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	556	200		51 51 51	51 47 46
66 675. 75. 75. 75. 75. 75. 75. 75.	31 32	0 E E	3 3 3 8 7 8	39 440 110	4 4 4 4 2 6 4 8

## ALIGNMENTS

-	RESULT 1
_	I59308
	class I histocompatibility antigen – pygmy chimpanzee (fragment)
	C; Species: Pan paniscus (pygmy chimpanzee, bonobo)
	C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 23-Jul-1999
	C; Accession: 159308
	R; McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Wat
	Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
	A; Title: A uniquely high level of recombination at the HLA-B locus.
	A; Reference number: 159308; MUID: 94286544
	A; Accession: 159308
	A;Status: preliminary; translated from GB/EMBL/DDBJ
	A; Molecule type: mRNA
_	A; Residues: 1-354 <res></res>
	A; Cross-references: EMBL: U05575; NID: 9454767; PIDN: AAA50178.1; PID: 9454768
	C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
_	Query Match 94.6%; Score 70; DB 2; Length 354;
	Best Local Similarity 93.3%; Pred. No. 3.5e-05; Matches 14: Conservative 1: Mismatches 0: Indels 0: Gaps 0:
_	Ov 1 KAOTDRENIRIALRY 15

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I80167

Loss I histocompatibility antigen - pygmy chimpanzee (fragment)
C;Species: Pan paniscus (pygmy chimpanzee, bonobo)
C;Species: Pan paniscus (pygmy chimpanzee, bonobo)
C;Accession: 180167
R;McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Wat Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Reference number: 159308; MUID:94286544
A;Accession: 180167
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Cross-references: EMBL:U05578; NID:9454773; PIDN:AAA50181.1; PID:9454774
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

ö 94.6%; Score 70; DB 2; Length 354; 93.3%; Pred. No. 3.5e-05; ive 1; Mismatches 0; Indels Query Match
Best Local Similarity 93.3
Matches 14; Conservative 1 KAQTDRENLRIALRY 15 ò

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class I histocompatibility antigen - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Date: 24-may-1996 #sequence_revision 24-may-1996 #text_change 23-Jul-1999
C;Accession: 18017!
R;McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Wat
                                                                                                                                                                                                                                                                                                                                                                                                                c;Genetics:
A;Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
A;Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Reywords: transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-362/Product: class I histocompatibility antigen heavy chain, Gogo-B0102 #status
F;25-114/Domain: alpha-1 <ALL>
F;25-114/Domain: alpha-1 <ALL>
                                                                                                                                                      A;Reference number: JH0534; MUID:92078860
                              precursor - lowland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               class I histocompatibility antigen - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
                        class I histocompatibility antigen Gogo-B0102 heavy chain precursor – lowla C;Species: Gorilla gorilla gorilla (lowland gorilla)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X60693; NID:g22867; PIDN:CAA43101.1; PID:g22868
A;Experimental source: EBV-transformed B cell
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R; McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A; Title: A uniquely high level of recombination at the HLA-B locus. A; Reference number: 159308; MUID:94286544
A; Accession: 180169
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Pred. No. 5.3e-05;
0; Mismatches 0;
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                                                                                                                     C; Accession: JH0540
Exavlor, D.A.; Warner, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A; Title: Gorilla class I major histocompatibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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93.3%;
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F;207-298/Domain: alpha-3 <AL3>
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Best Local Similarity
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Best Local Simi
Matches 14;
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                                                                                               R;Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A;Title: Gorilla class I major histocompatibility complex alleles: comparison to human A;Reference number: JH0534; MUID:92078860
A;Accession: JH0541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491–1509, 1991
A;Title: Gorilla class I major histocompatibility complex alleles: comparison to human
A;Reference number: JH0534; MUID:92078860
class I histocompatibility antigen Gogo-B0103 heavy chain precursor - lowland gorilla C;Species: Gorilla gorilla gorilla (lowland gorilla) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                class I histocompatibility antigen Gogo-BO101 heavy chain precursor - lowland gorilla C;Species: Gorilla gorilla gorilla (lowland gorilla) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Keywords: transmembrane protein
1-24/Domain: signal sequence #status predicted <SIG>
25-362/Product: class I histocompatibility antigen heavy chain, Gogo-B0103 #status
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Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
Superfamily: class I histocompatibility antigen; immunoglobulin homology; Reywords: transmembrane protein
1-24/Domain: signal sequence #status predicted <SIG>
1-24/Domain: signal sequence #status predicted <SIG>
1-25-362/Product: class I histocompatibility antigen heavy chain, Gogo-B01; 25-114/Domain: alpha-1 <ALL>
                                                                                                                                                                                                                                                                                                                                                                                                                      Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
Superfamily: class I histocompatibility antigen; immunoglobulin homology
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                                                                                                                                                                                                                                                                        A;Molecule type: DNA
X;Residues: 1-36 <LAM>
A;Cross-references: EMBL:X60254; NID:g22869; PIDN:CAA42806.1; PID:g22870
A;Experimental source: EBV-transformed B cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X60255; NID:922865; PIDN:CAA42807.1; PID:922866
A;Experimental source: EBV-transformed B cell
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Pred. No. 3.6e-05;
1; Mismatches 0; Indels
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F.207-298/Domain: alpha-3 (AL3>
F.220-285/Domain: immunoglobulin homology <IMM>
F,299-362/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-114/Pomain: alpha-1 <ALI>
115-206/Domain: alpha-2 <ALI>
200-208/Domain: alpha-3 <ALI>
2200-2085/Domain: intracellular #status predicted <INT>
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Pred. No. 3.6e-05;
l; Mismatches 0;
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Matches 14; Conserv
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Matches 14; Conserv
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C:Species: Homo sapiens (man)
C:Date: 05-Apr.1983 #text_change 22-Jun-1999
C:Accession: A02189
C:Accession: A02189; MUD:82151002
A:Title: Exon/Intron organization and complete nucleotide sequence of an HLA gene.
A:Reference number: A02189; MUD:82151002
A:Molecule type: DNA
A:Residues: 1-359 -KAAL>
C:Superfamily: class I histocompatibility antigen HLA alpha chain #status predicted
C:Reywords: duplication: glyna: 4 -KEXL>
C:Reywords: duplication: signal sequence #status predicted -KEXT>
C:Reywords: duplication: attracellular #status predicted -KEXT>
F:112-203-Moomain: alpha-1 -KEXL>
F:112-203-Moomain: immunoglobulin homology <INM>
F:305-329/Domain: immunoglobulin #status predicted <INM>
F:305-329/Domain: intracellular #status predicted <INM>
F:307-Residues: Residues: #status predicted <INM>
F:307-Residues: 
                                A. Accession: S03337
A. Molecule type: mRNA
A. Recibuse: 1-363 <mxnA
A. Recibuse: 1-363 <mxnA
A. Recibuse: 1-363 <mxnA
A. Resibuse: 1-363 <mxnA
A. Cross-references: EMBL:X13115
C. Superfamily: class I histocompatibility antigen; immunoglobulin homology
C. Reywords: transmembrane protein
F. 1-24 / Domain: signal sequence #status predicted <SIG>F: 25-363/Product: class I histocompatibility antigen alpha chain #status predicted <AN
F: 25-363/Domain: extracellular #status predicted <EXT>F: 220-286/Domain: transmembrane #status predicted <AMM>F: 299-338 / Domain: intracellular #status predicted <IMM>F: 339-363/Domain: intracellular #status predicted <IMM>F: 339-363/Domain: intracellular #status predicted <IMM>F: 339-363/Domain: intracellular #status predicted <INT>F: 330-363/Domain: intracellular #status pre
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S77653
MHC class I histocompatibility antigen HLA-A alpha chain precursor - human (isolate c; Species: Homo sapiens (man)
A; variety: isolate A*2402
C; bate: 13. Jan.1995 #sequence_revision 15-Aug-1997 #text_change 23.Jul-1999
C; Accession: S77963
R; Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MHC class I histocompatibility antigen HLA alpha chain precursor (clone pHLA 12.4)
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86.7%; Pred. No. 0.00019;
ive 2; Mismatches 0; Indels
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100.0%; Pred. No. 5.4e-05;
Live 0; Mismatches 0;
         Reference number: S01171; MUID:89030641
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Best Local Similarity
Matches 14; Conserv
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Matches 13; Conserv
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A; Residues: 1-363 < RES.>
C; Superfamily: class I histocompatibility antigen: immunoglobulin homology
C; Superfamily: class I histocompatibility antigen chain #status predicted
E; Reywords: glycoprotein: membrane protein
F; 1-24 Pomain: signal sequence #status predicted < SIG.>
F; 25-363/Product: class I histocompatibility antigen chain #status predicted
F; 25-363/Pomain: alpha-1 #status predicted < EXI.>
F; 200-285/Domain: alpha-2 #status predicted < EXI.>
F; 307-332/Domain: immunoglobulin homology < INM.>
F; 307-352/Domain: intracellular #status predicted < INT.>
F; 333-363/Domain: intracellular #status predicted < INT.>
F; 110-206/Binding site: carbobydrate (Asi) (covalant) #status predicted
F; 125-188, 227-283/Disulfide bonds: #status predicted
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A;Title: Nucleotide sequences of chimpanzee MHC class I alleles: evidence for trans-sped
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A;Residues: 1-355 CRES>
A;Cross-references: EMBL:U05582; NID:g454781; PIDN:AAA50185.1; PID:g454782
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Reference number: I59308; MUID:94286544
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Pred. No. 5.4e-05;
0; Mismatches 0; Indels
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A; Residues: 1-363 <LADA;
F; Parham, P: Ladvlor, DA; Lomen, C.E.; Ennis, P.D.
J. Immunol: 142, 3937-3950, 1989
A; Tille: Diversity and diversification of HLA-A,B,C alleles.
A; Reference number: 136956; MUID:89235215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 93.2%; Score 69; DB 2; Le Best Local Similarity 100.0%; Pred. No. 5.3e-05; Matches 14; Conservative 0; Mismatches 0;
                                                                                                                                        A.Accession: 180171
A.Status: preliminary; translated from GB/EMBL/DDBJ
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100.0%; Pre
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Best Local Similarity
Matches 14; Conserv
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R;Ennis, P.D.; Zemmour, J.; Salter, R.D.; Parham, P.
Proc. Natl. Acad. Sci. U.S.A. 87, 2833-2837, 1990
A;Title: Rapid cloning of HLA-A,B cDNA by using the polymerase chain reaction: freque A;Reference number: A35997; MUID:90207291
A;Accession: A35997
          R; Krangel, M.S.

J. Exp. Med. 163, 1173-1190, 1986

A; Title: Secretion of HLA-A and -B antigens via an alternative RNA splicing pathway. A; Accession: 155659; MUID:86198522

A; Accession: 155659; MUID:86198522

A; Accession: 155659

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: mRNA

A; Residues: 271-365 <RE2>
A; Cross references: GB:M12377; NID:9187607; PIDN:AAA17889.1; PID:9187608
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A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Seywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen
F;196-261/Domain: immunoglobulin homology <IRM>
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WHC class I histocompatibility antigen HLA-A32 alpha chain - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 13-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Sep-1997
C;Accession: A26088
R;Wan, A.M.; Ennis, P.; Parham, P.; Holmes, N.
J. Immunol. 137, 3671-3674, 1986
A;Title: The primary structure of HLA-A32 suggests a region involved in formation of A;Reference number: A26088; MUID:87058961
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MHC class I histocompatibility antigen HLA-A25 alpha chain precursor - human
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A; Map position: 6p21.3 6p21.3
A; Introns: 25/1; 115/1; 207/1; 299/1; 338/1
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Keywords: glycoprotein
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     A; Cross-references: GB: M64741; NID: 9187615; PIDN: AAA59601.1; PID: 9187616
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Pred. No. 0.00019;
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Pred. No. 0.0011;
2; Mismatches (
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C;Date: 16-Nov-1990 #sequence_revision 16-Nov-1990
C;Accession: A35997
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Best Local Similarity 92.9%;
Matches 13; Conservative
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Best Local Similarity 85.7
Matches 12; Conservative
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F;25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status predi
F;220-285/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                    A:Cross-references: EMBL:M64740; NID:g403142; PIDN:AAA59600.1; PID:g187614
A:Experimental source: cell line KRC 032; isolate A*2402
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1991
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R; Little, A.M.; Madrigal, J.A.; Parham, P.
Immunogenetics 35, 41-45, 1992
A; Title: Molecular definition of an elusive third HLA-A9 molecule: HLA-A9.3.
A; Reference number: IS4493; MUID:92104637
A; Accession: IS4493
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A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: transmembrane protein
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Nature 357, 326-329, 1992
Ayîtike: Unusual HLA-B alleles in two tribes of Brazilian Indians.
A;Reference number: 137120; MUID:92269955
A;Accession: 877963
                                                                                                    not shown
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                                                                                               Status: nucleic acid sequence not shown; translation
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Pred. No. 0.00019;
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A;Molecule type: DNA
A;Residues: 1-365 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.2%;
92.9%;
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Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
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Best Local Similarity
' has 13; Conserve
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                                                                                                            A; Molecule type: mkwa
* Pacidues: 1-365 <BEL>
                                                                                                                                                                                                                                                                           A; Gene: GDB: HLA-A
                                                                                                                                                                                                                                                  C: Genetics:
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A;Residues: 1-364 <ENN>
A;Cross_references: GB:M32321
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology C;Superfamily: class I histocompatibility antigen; immunoglobulin homology C;Reywords: transmembrane protein
F;219-284/Domain: immunoglobulin homology <IMM>

0; Gaps Query Match 82.4%; Score 61; DB 2; Length 364; Best Local Similarity 85.7%; Pred. No. 0.0015; Matches 12; Conservative 2; Mismatches 0; Indels

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Search completed: February 7, 2000, 18:04:41 Job time: 22207 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                         - protein search, using sw model
                                                                                       OM protein
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February 8, 2000, 01:26:01; Search time 68.63 Seconds (without alignments) 6.527 Million cell updates/sec 1 KAQTDRENLRIALRY 15 US-08-653-294-33 Perfect score: Sequence: Run on: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

82229 seqs, 29864866 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

SwissProt_38:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Deartring and	יייייייייייייייייייייייייייייייייייייי		P30379 gorilla gor	P30380 gorilla gor	P30381 gorilla gor	P13750 pan troglod	P01893 homo sapien	^	34	P18462 homo sapien	7		рошо	homo	) homo	homod	homo	homo	homo	homo	homo	homo	homod	P30491 homo sapien	homo	homod	homo	goril	0	oryct	140 oryct	389 homo	63 ношо	180 homo	P30485 homo sapien
	£	3	1B15_HUMAN	1B01_GORGO	1B02_GORGO	1B03_GORGO	1B01_PANTR	HLAH_HUMAN	1A23_HUMAN	1A24_HUMAN	1A25_HUMAN		1B60_HUMAN	1B61_HUMAN	1B62_HUMAN	1B20_HUMAN	1B14_HUMAN	1B16_HUMAN	1B18_HUMAN	ä	-	₹	'n	1B53_HUMAN	1B54_HUMAN	1B05_HUMAN	1B41_HUMAN	1B42_HUMAN	1A04_GORGO	1B40_HUMAN	HA1A_RABIT	HA1B_RABIT	1B02_HUMAN	1B29_HUMAN	33	1B45_HUMAN
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1B55_HUMAN 1B56_HUMAN 1B57_HUMAN 1B58_HUMAN MAUJ_PARVE 1C03_GORGO 1C03_GORGO 1C03_HUMAN 1C04_GORGO 1C03_HUMAN
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## ALIGNMENTS

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40170 MW; 2E33E2B8 CRC32;
                               ch 94.6%;
1 Similarity 93.3%;
14; Conservative
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Best Local Similarity 93.3
Matches 14; Conservative
                                                                                  STANDARD;
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362 AA;
                               Query Match
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Matches 14; Conserv
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DISULFID
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SEQUENCE
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                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 92078860.
LAWLORD D.A., WARREN E., TAYLOR P., PARHAM P.;
LAWLORD D.A., WARREN E., TAYLOR P., PARHAM P.;
GOTILLA class I major histocompatibility complex alleles: comparison
to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                             01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECURSOR.
GOTILLA GOTILLA GOTILLA (Lowland GOTILLA).
ELWARYOTA: Metazoa: Chordata; Cranlata: Vertebrata; Mammalia;
ELWARYOTA: Primates; Catarrhini; Hominidae; Gotilla.
                                                                                                                                                                  Gaps
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALPHA CHAIN. EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIX: JRSP; JRSA.
PROSITE: PS00290; IG_MHC; 1.
PFRM; PF00047; 1.
PFRAM; PF00129; MHC_I; 1.
MHC_I; Transmembrane; Glycoprotein; Signal.
SIGNAL
1 24 BY SMILARITY.
25 362 CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                ö
                                                                                                                                           100.0%; Score 74; DB 1; Length 362; 100.0%; Pred. No. 2.6e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GOGO-BO101 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                  CONNECTING PEPTIDE
                                                                      CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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9798F0BB CRC32;
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SIMILARITY.
SIMILARITY.
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                                                                                                                                                                Conservative
                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                    1 KAQTDRENLRIALRY 15
                                                                                                            362 AA;
                                                                                                                                                      Best_Local Similarity
Matches 15; Conserv
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333
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P30379;
                                                                     DOMAIN
CARBOHYD
DISULFID
DISULFID
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1B01_GORGO
  CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 92078860.
LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
MGOTILLA class I major histocompatibility complex alleles: comparison to human and chimpanzee class I.",
J. Exp. Med. 174:1491-1509(14991).
J. Exp. Med. 174:1491-1509(14991).
INCITION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN PRECURSOR.
GOTILLA GOTILLA (LOWHAND GOTILLA)
BURATYOTA: Metazoa: Chordata; Creniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; roverv; 19; 1. PFAM; PP0047; 19; 1. PFAM; PP0047; MtC_I; 1. MtC_I; Transmembrane; Glycoprotein; Signal.
SIGNAL 1 24 BY SIMILARITORY.
1 24 BY SIMILARITORY.
CHAIN 25 362 CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-BOIO2 ALPHA CHAIN.
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Length 362;
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Pred. No. 1.4e-05;
l; Mismatches 0; Indels
  Score 70; DB 1; Length 362
Pred. No. 1.4e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY.
SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X60693; CAA43101.1; -. PIR; JH0540; JH0540. HSSP; P03989; 1HSA. PROSITE; PS00299; IG_MHC; 1.
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93.38;
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Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Pan.

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Eukaryota; Metazoa;
          Sutheria; Primates;
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                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 92078860.
LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
LO forilla class in major histocompatibility complex alleles: comparison to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
J. Exp. Med. INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last sequence update)
CLASS I HISTOCOMPATIBLITY ANTIGEN, GOGO-B0103 ALPHA CHAIN PRECURSOR.
GOTILLA GOTILLA GOTILLA (Lowland GOTILLA).
ELWATYOTA: Metazca; Chordand GOTILLA; Methazca; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1801_PANTR STANDARD; PRT; 359 AA.
P13750;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                        ANTIGEN
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                                                                                                                                                                                                 THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 70; DB 1; Length 362;
Pred. No. 1.4e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     CLASS I HISTOCOMPATIBILITY
GOG-BOIO3 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONNECTING PEPTIDE
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; FEA6A941 CRC32;
                             362 AA.
                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Signal.
                             PRT;
                                                                                                                                                                                                                                                                                                                      EMBL; X60254; CAA42806.1; -.
PIR; JH0541; JH0541.
HSSP; P03989; JHSA.
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00129; MHC_I; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.6%;
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                            STANDARD;
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332
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SIGNAL 1
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115
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333
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362 AA;
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                 1B03_GORGO
ID 1B03_GORGO
AC P30381;
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                                       MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G., KLEIN J.;
"Nucleotide sequences of chimpanzee MHC class I alleles: evidence for trans-species mode of evolution.";
EMBO J. 7:2765-2774(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN.
B-1 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                  Submitted (FEB-1989) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMONE SYSTEM.
-!- SUBDMIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN H PRECURSOR
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 359;
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; Pred. No. 2.2e-05;
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CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X13115; CAA31507.1; -
PIR; $03537; $03537.
HSSP; P03969; IBSA.
PROSITE; P$050290; IG_MHC; 1.
PFAM; PF00129; MHC_I; 1.
PFAM; PF00129; MHC_I; 1.
NHC I; Transmembrane; Glycoprotein; Signal.
NON_TER 1 20
CHAIN 21 359 CHLA CLASS I HIST
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BY SIMILARITY.
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illarity 100.0%;
Conservative 0
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HLA-H OR HLAH.
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106
359 AA;
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Best Local Similarity
Matches 14; Conserv
SEQUENCE FROM N.A. MEDLINE; 89030641.
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P01893;
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DOMAIN
DOMAIN
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TRANSMEM
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DISULFID
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DISULFID
SEQUENCE
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CARBOHYD
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MEDLINE; 92104637.
LITTLE A.-M., MADRIGAL J.A., PARHAM P.;
MADECULAR definition of an elusive third HLA-A9 molecule: HLA-A9.3.";
Immunogenetics 35:41-45(1992).
-i- FUNCITON: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
-i- SUBGUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
SEQUENCE FROM N.A.
MEDIINE; 82151002.
MALISSEN M., MALISSEN B., JORDAN B.R.;
Exch/intron organization and complete nucleotide sequence of an HLA
gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                          Proc. Natl. Acad. Sci. U.S.A. 79:893-897(1982).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
THE IMMUNE SYSTEM. COULD BE THE PRODUCT OF A PSEUDOGENE.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-23(A-9) ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 7.8e-05;
Mismatches 0; Indels
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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BY SIMILARITY.
5E610F63 CRC32;
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86.7%;
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Best Local Similarity 86.7
Matches 13; Conservative
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110
227
362 AA;
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1115
207
299
309
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P30447;
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DOMAIN
TRANSMEM
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SEQUENCE
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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MEDLINE; 85206128.
N'GUYEN C., SODOYER R., TRUCY J., STRACHAN T., JORDAN B.R.;
N'HE HIA-MA24 qenee; sequence, surroundings and comparison with the HIA-A2 and HIA-A3 genes.";
Immunogenetics 21:479-489(1985).
POLYMORPHISM: THE ONLY ALLELE OF A-23 KNOWN IS A*2301 WHICH IS
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10.24_HUMAN

10. 1A24_HUMAN

10. 1A2
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66; DB 1; Length 365; No. 7.9e-05;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; BIC21094 CRC32;
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PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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Pred. No. 7.9e-
1; Mismatches
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MIM; 142800; -.
PROSITE; PS00290; IG_MHC; 1.
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92.9%;
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Best Local Similarity 92.9
Matches 13; Conservative
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309
110
125
365 AA;
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Conservative
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Best Local Similarity
Matches 13; Conserv
                                                                                           365 AA;
                         206
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                                                                                           SEQUENCE
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SIGNAL
                         VARIANT
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       8544
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
G -> A (IN A*2402, A*2403 AND A*2408).

FTIG-VAR_004354.

FTIG-VAR_004355.
E -> G (IN A*2408).

FTIG-VAR_004356.
G -> R (IN A*2408).

FTIG-VAR_004356.
G -> W (IN A*2408).

FTIG-VAR_004356.
G -> W (IN REF. 6).

FTIG-VAR_04358.
DG -> EW (IN A*2403).
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EXTRACELULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MICROGLOBULIN).
-!- POLYMORPHISM: THE FOLLOWING ALLELES OF A-24 ARE KNOWN: A*2401, A*2401, A*2401 A*2401.
                                                                                                                                                                                                                                                                                                                                                                                 KASHIWASE K., TOKUNAGA K., ISHIKAWA Y., QIU L., FURUYA M., SAWANAKA K., AKAZA T., TADOKORO K., JUJI T.; A new A9 sequence HiA-A9HH from Japanese."; MHC 3:9-14(1996).

-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.

-i- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
SEQUENCE FROM N.A. (A*2402).
MEDLINE; 92269955.
BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
"Unusual HLA-B alleles in two tribes of Brazilian Indians.";
Nature 357:326-329(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM: PF00047; 1g; 1.
PFAM: PF00129; MFC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
SIGNAL
                                                                                                                                [5]
SEQUENCE FROM N.A. (A*2402).
LAFORET M., TONGTO M.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                        GAO X., MCCLUSKEY J.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M64740; AAA59600.1; -.
M64741; AAA59601.1; -.
U19733; AAB60651.1; -.
U18987; AAB60651.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z72422; CAA96532.1; -. EMBL; D83516; BAA11936.1; -. HSSP; P01892; IAQD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 142800; -.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                 SEQUENCE OF 26-206 FROM N.A.
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (A*2408).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (A*2501).
MEDLINE; 90207291.
ENNIS P.D., ZEMOUR J., SALTER R.D., PARHAM P.;
ENDIS CONTING Of HLA-A,B CDNA by using the polymerase chain reaction: frequency and nature of errors produced in amplification.";
Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-25(A-10) ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
/FIId=VAR_004359.

A -> T (IN A*2402, A*2403, A*2408 AND REF. 5).

/FIId=VAR_004360.

DE23D06E_CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MICROGLOBULIN).
-!- POLYMORPHISM: THE FOLLOWING ALLELES OF A-25 ARE KNOWN: A*2501
AND A*2502. THE SEQUENCE SHOWN IS THAT OF A*2501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID 1A25_HUMAN STANDARD; PRT; 365 AA.

AC P18465_2 093562, 203562

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-DEC-1999 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                       Score 66; DB 1; Length 365;
Pred. No. 7.9e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM: PF00047; 1g; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
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EMBL; X97802; CAA6589.1; -.
PIR; A35997, A35997.
HSSP; P01891; 2HLA.
MIM; 142800; -.
PROSITE; PS00299; IG_MHC; 1.
                                                            40644 MW;
                                                                                                       89.2%;
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298
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                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1A32_HUMAN STANDARD; PRT; 365 AA.
P10314, 029838;
01-MAR-1999 (Rel. 10, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
115-UUL-1999 (Rel. 38, Last annotation update)
HLA CLEASS I HISTOCOMPATIBILITY ANTIGEN, A-32(AW-19) ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 87058961.
WAN A.M., ENNIS P., PARHAM P., HOLMES N.;
"The primary structure of HLA-A32 suggests a region involved in formation of the Bw4Bw6 epitopes.";
J. Immunol. 137:3671-3674(1986).
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Immunogenetics 45:76-77(1996).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                     Length 365;
                                                                                                                                                                                                                                                                                     Score 61; DB 1; Length 36:
Pred. No. 0.00066;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-BLOOD;
MEDLINE; 97045038.
ZINO E., SEVERINI G.M., MAZZI B., BORDIGNON C., BENAZZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMENA J.D.;
Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                  H -> Q (IN A*2502).
/FIId=VAR_004361.
131A8F20 CRC32;
                                                  CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
H -> Q (IN A*2502)
     CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 25-298 FROM N.A. (A*3201).
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                                                                                                                                                                                                                                                                                     82.4%;
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                                                                                                                                                                                                             41218
                                                                                                                                                                                                                                                                                Query Match 82.4
Best Local Similarity 85.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                95 SQTDRESLRIALRY 108
                                                                                                                                                                                                                                                                                                                                                                                     2 AQTDRENLRIALRY 15
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                                                                                                                                                                                                           365 AA;
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DOMAIN
CARBOHYD
DISULFID
DISULFID
                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 90207291.

ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;

"Rapid cloning of HLA-A,B cDNA by using the polymerase chain
reaction: frequency and nature of errors produced in amplification.";

Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                       HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-32(AW-19) ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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MEDLINE; 91067476.

INCLEDIC ROLLESTONE J., MILSTEIN C.;

"Nucleotide sequence of an HLA-BW57 gene.";

Nucleic Acids Res. 18:6702-6702(1990).

-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMONE SYSTEM.

-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPAIDELITY ANTIGEN, B-57(B-17) B*5701 ALPHA
CHAIN PRECURSOR (BW57.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 365;
                                                           Glycoprotein; Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.4%; Score 61; DB 1; Length 365
85.7%; Pred. No. 0.00066;
.ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
R -> H (IN A*3202).
/FTId=VAR_004373.
L -> Q (IN A*3202).
/FTId=VAR_004374.
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PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_I; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AQTDRENLRIALRY 15
                                                               MHC I; Transmembrane; SIGNAL 1 24 CHAIN 25 365
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Best Local Similarity
Matches 12; Conserv
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1110
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175
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AC P18466,
DT 1860_HUMAN
AC 01-NOV-1990
DT 01-NOV-1990
CC EUKATYOTA; M
CC NAEDLINE; 902
RA ENNIS P.D.,
RA ISAMAT M., (
RY MEDLINE; 91R
CC -1- FUNCTIO
CC -1- FUNCTIO
CC -1- SUBUNIT
CC This SWISS-
CC TH
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CARBOHYD
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TRANSMEM
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01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5702 ALPHA CHAIN
PRECURSOR (BW57.2)
                                                                               HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MADDLINE, 9305560B.
MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
LITTLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
MARYELL R.W., DU TOIT E.D., PARHAM P.;
"Distinctive HLA-A.B antigens of black populations formed by
interallelic conversion.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Immunol. 149:3411-3415(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INMUNE SYSTEM.
-!- SUBDATT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                     B-57(B-17) B*5701 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                     Score 60; DB 1; Length 362;
Pred. No. 0.001;
0; Mismatches 1; Indels
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BY SIMILARITY.
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                                                           Glycoprotein; Signal.
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       HSSP; P30491; IAIM.
MIM; 142830; -.
PROSITE: PS00290; IG_MHC; 1.
PFAM; PF00047; ig; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; GlycoprosiGNAL
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92.9%;
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PFAM; PF00129; MHC_I; 1.
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PIR; D35997; D35997
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                                         HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5702 ALPHA CHAIN. EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3. CONNECTING PEPTIDE.
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Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-1997) to the PRESENTATION OF FOREIGN ANTIGENS TO
I-FUNCTINE SYSTEM.
-1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
115-JUJ-1998 (Rel. 36, Last annotation update)
115-JUJ-1998 (Rel. 36, Last annotation update)
114 CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-58(B-17) B*5801 ALPHA HLA-B OR HLAB.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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WAYS J.P., COPPIN H.L., PARHAM P.;
"The complete primary structure of HLA-Bw58.";
J. Biol. Chem. 260:11924-11933(1985).
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EMBL, AB008102; BAA22916.1; -.
PIR; A23895; HLHUBB.
HSSP: P30491; IAIM.
MIM; 142830; -.
PROSTE; P500290; IG_MHC; 1.
PFAM; PF00129; MHC_1; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
SIGNAL
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Pred. No. 0.001;
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MHC 1; Transmembrane; Glycoprotein; Signal.
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MEDLINE; 91268545.
CHOO Y.S., FAN L.A., HANSEN J.A.;
"A novel HLA-B27 allele maps B27 allospecificity to the region around position 70 in the alpha 1 domain.";
J. Immunol. 147:174-180(1991).
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-i- SUBDINI: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                      01-ARR-1993 (Rel. 25, Created)
01-ARR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2707 ALPHA CHAIN (B27-HS).
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
BW-58(B-17) B*5801 ALPHA CHAIN.
EXTRACELLUIAR ALPHA-1.
EXTRACELLUIAR ALPHA-2.
EXTRACELLUIAR ALPHA-3.
CONNECTING PEPTIDE.
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0.001;
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CONNECTING PEPTIDE.
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                                                                              CYTOPLASMIC TAIL.
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Pred. No. 0.001
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Best Local Similarity 92.9
Matches 13; Conservative
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PFAM; PF00129; MHC_I; 1.
MHC_I; Transmembrane; Gl
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13-AGG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SZOETS H., RIETHMUELLER G., WEISS E., MEO T.; "Complete sequence of HLA-B27 cDNA identified through the characterization of structural markers unique to the HLA-A, -B, and
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MADDEN D.R., GORGA J.C., STROMINGER J.L., WILEY D.C.;

MADDEN D.R., GORGA J.C., STROMINGER J.L., WILEY D.C.;

The structure of HIA-B27 reveals nonamer self-peptides bound in a extended conformation.

Nature 353:321-325(1991).

-I. FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMONE SYSTEM.

-I. SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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EQUERRA A., BRAGADO R., VEGA M.A., STROMINGER J.L., WOODY J.,
LOPEZ DE CASTRO J.A.;
"Primary structure of papain-solubilized human histocompatibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 92405152.
MADDEN D.R., GORGA J.C., STROMINGER J.L., WILEY D.C.;
"The three-dimensional structure of HLA-B27 at 2.1-A resolution suggests a general mechanism for tight peptide binding to MHC."; Cell 70:1035-1048(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Score 59; DB 1; Ler
Pred. No. 0.0014;
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Biochemistry 24:1733-1741(1985).
                       79.7%;
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Query Match 79.7%; Score 59; DB 1; Length 361; Best Local Similarity 80.0%; Pred. No. 0.0015; Matches 12; Conservative 1; Mismatches 2; Indels

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11: Sp_vodent: *
13: Sp_varus: *
14: Sp_unclassified: *
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74
1 KAQTDRENLRIALRY 15
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2: sp_bacteria:*
3: sp_fungi:*
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Listing first 45
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DB seq length: 1000000
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## ALIGNMEN

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"Molecular cloning of orangutan and gibbon MHC class I cDNA. The HLA-A and -B loci diverged over 30 million years ago."; J. Immunol. 148:2547-2554(1992).
                                                                                                                                                                                                                    STRAIN=BOSONDJO;
MEDLINE; 94.286544.
MEDLINE; 94.286544.
MACADAM S., 19.2801 J.E., LIU X., GARBER T.L., HUGHES A.L.,
BONTROP R.E., WATKINS D.I.;
"A uniquely high level. of recombination at the HLA-B locus.";
Proc. Natl. Acad. Sci. U.S.A. 91:5893-5897(1994).
EMBL; U05578; AAA50181.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 095412 PRELIMINARY; PRT; 354 AA.
095412;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I (FRACMENT).
Hylobates lar (Common gibbon).
Bukaryota: Metacos; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
                                                                             Pan paniscus (Pygmy chimpanzee) (Bonobo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
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MEDILINE; 9218857.
CHEN Z.W., MCADAM S.N., HUGHES A.L., DOGON A.L., LETVIN N.L.,
WATKINS D.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 70; DB 7; Length 354; Pred. No. 9.6e-05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.2%; Score 69; DB 7; Length 354; 100.0%; Pred. No. 0.00014; Ive 0; Mismatches 0; Indels
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CHEN 2.W., MCADAM S.N., HUGHES A.L., WATKINS D.I.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, U50091: AAB08074.1;
HSSP: P30491; 1A1M.
01-NOV-1999 (TrEMBLrel. 12, Last annotation update) CLASS I HISTOCOMPATIBILITY ANTIGEN (FRAGMENT).
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354 AA; 39401 MW; 6E38CFFE CRC32;
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354 AA; 39748 MW; 43EDEC6F CRC32;
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93.3%;
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PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
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Best Local Similarity 93.3
Matches 14; Conservative
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Best Local Similarity 100.
Matches 14; Conservative
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PFAM; PF00129; MHC_I; 1.
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                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                    MEDLINE; 96408732.
CEREB N., KONG Y., LEE S., MAYE P., YANG S.Y.;
"Nucleotide sequences of MHC class I introns 1, 2, and 3 in humans and intron 2 in nonhuman primates.";
Tissue Antigens 47:498-511(1996).
EMBL; U37323; AAB49915.1;
EMBL; U37323; AAB49915.1;
EMBL; U37323; AAB49915.1;
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MEDLINE; 94286544.
MCADAM S.N., BOYSON J.E., LIU X., GARBER T.L., HUGHES A.L.,
BONTROP R.E., WATKINS D.I.;
A uniquely high level of recombination at the HLA-B locus.";
Proc. Natl. Acad. Sci. U.S.A. 91:5893-5897(1994).
BEMEL, U05575; AAA50178.1; -.
HSSP; P30491; lalm.
FROSITE; PS00290; IC_MHC; 1.
FRAM; PF00129; MHC_I: 1.
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pan paniscus (Pygmy chimpanzee) (Bonobo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 94.6%; Score 70; DB 7; Length 181; Best Local Similarity 93.3%; Pred. No. 4.7e-05; Matches 14; Conservative 1; Mismatches 0; Indels
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Pred. No. 9.6e-05;
1; Mismatches 0; Indels
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN (FRAGMENT).
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(TrEMBLrel. 02, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                    181 181 181 181 181 AM; FFB51D78 CRC32;
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354 AA; 39227 MW; 5D75939D CRC32;
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  Gorilla gorilla gorilla (Lowland gorilla).
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Best Local Similarity 93.3%;
Matches 14; Conservative
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                                                                                                             SEQUENCE FROM N.A.
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01-FEB-1997 (
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CHANDANAYINGYONG D., SIRKONG M., LUANGTRAKOOL K., SRINAK D., RUGROUNG E., BEJCHANDRA S.;
RUMRICHONG E., BEJCHANDRA S.;
Submitted (OCT.1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF030922; AAB87057.1;
EMBL; AF030921; AAB87057.1;
HSSP; P01891; 11MC.
PFAM; PF00129; MHC_I; 1.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
RUNGROUNG E., BEJCHANDRA S.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF030920; AAB87056.1;
EMBL, AF030919; AAB87056.1;
HSSP; P01891; ITMC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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90.5%; Score 67; DB 7; Length 180;
Best Local Similarity 86.7%; Pred. No. 0.00016;
Matches 13; Conservative 2; Mismatches 0; Indels
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I HLA-A (FRAGMENT).
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I HLA-A (FRAGMENT).
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180 AA; 20811 MW; CECC3537 CRC32;
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20811 MW; CECC3537 CRC32;
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Matches 14; Conservative
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PFAM; PF00129; MHC_I; 1.
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MEDLINE: 94286544.
MCADAM S.N., BOYSON J.E., LIU X., GARBER T.L., HUGHES A.L.,
BONTROP R.E., WARKINS D.I.;
"A uniquely high level of recombination at the HLA-B locus.";
Proc. Natl. Acad. Sci. U.S.A. 91:5893-5897(1994).
EMBL; U05580; AAA50183.1; -.
PROSTE; PS00209; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                              Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.2%; Score 69; DB 7; Length 363; 100.0%; Pred. No. 0.00015;
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Submitted (APR-1990) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 23-363 FROM N.A.
MEDLINE: 89235215.
PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
"Diversity and diversification of HLA-A,B,C alleles.";
J. Immunol. 142:3937-3950(1989).
BMBL, M24045; AA35424-1;
HSSP; P30491: 1A1M.
PROSITE: PS00290; IG_MHC; 1.
                                                                                                                                           095529 PRELIMINARY; PRT; 355 AA. 095529. 01-529; (TrEMBLrel. 02, Created) 01-FEB-1997 (TrEMBLrel. 02, Last sequence update) 01-FEB-1999 (TrEMBLrel. 12, Last annotation update) CLASS I'HISTOCOMPATIBILITY ANTIGEN (FRAGMENT).
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Q30988;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CHIMPANZEE MHC CLASS I CHLA CHAIN.
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PFAM; PF00129; MHC_I; 1.
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PFAM; PF00129; MHC_I; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Best Local Similarity
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SEQUENCE
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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86.7%; Pred. No. 0.00034;
11ve 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; UZ5971; AAA73518.1;
HSSP: P01802; 1HHH.
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; 1g; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
CHOPEK M., NIELSEN J., ZHANG H.;
SUDMITTED (SEP-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, U36914; AAA80238.1; -.
HSSP, P01891; ITMC.
PFRM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TIEMBLREL 01, Created)
01-NOV-1996 (TIEMBLREL 01, Last sequence update)
01-NOV-1999 (TIEMBLREL 12, Last annotation update)
MHC CLASS I ANTIGEN HLA-A (FRAGMENT).
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01.NOV-1996 (TrEMBLrel. 01, Last sequence update)
01.NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I ANTIGEN HIA-A2407
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Best Local Similarity 86.7%; Pred. No. 0.00016;
Matches 13; Conservative 2; Mismatches 0;
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NON_TER 181 181

SEQUENCE 181 AA; 20912 MW; D475FCD7 CRC32;
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                                                                                                                                                                                                                                     181 AA
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Best Local Similarity 86.7
Matches 13; Conservative
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94 QSQTDRENLRIALRY 108
                                                                                                                                                                                                                                     PRELIMINARY;
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1 KAQTDRENLRIALRY 15
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029689
DC 029689
DC 029689
DT 01-NOV-
DT 01-NOV-
DD 01-NOV-
DD HIA-A-
OC EUKATYO
CC EUKAT
                                                                                                                                                  RESULT 12
029724
AC 029724
AC 029724
DT 01-NOV
DT 01-NOV
DT 01-NOV
DC NHLA-A.
OC EURALY
CC EURAL
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CHANDANATINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGROUNG E., BEJCHANDRA S.;
Submitted (OCT.1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF030924; AAB87425.1; -
EMBL; AF030923; AAB87425.1; -
HSSP; P01891; 1TMC.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CHANDRAYINGVONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGROUNG E., BEZTHANDRA S.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF030926; AAB87058.1; -.
EMBL, AF030925; AAB87058.1; JOINED.
PFRM; PF00129; MHC_I; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.00016;
2; Mismatches 0; Indels
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I HLA-A (FRAGMENT).
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I HLA-A (FRAGMENT).
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Best Local Similarity 86.7%;
Matches 13; Conservative
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Best Local Similarity 86.7%;
Matches 13; Conservative ;
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                                               1 KAQTDRENLRIALRY 15
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SEQUENCE
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Tissue Antiques 50:340-346(1997).
EMBL: Z72423; CAA96533.1;
PFAM: PF00129; MHC_I: 1.
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MEDLINE; 98007772.
LAFORET M., FROELICH N., PARISSIADIS A., BAUSINGER H., PPEIFFER
TONGIO M.M.;
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                                                                                                             Gorilla gorilla gorilla (Lowland gorilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.00018;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                          Score 66; DB 7; Length 90;
Pred. No. 0.00011;
2; Mismatches 0; Indels
                                                                                                                                                                                               GRIMSLEY C., WATHER K.A., OBER C.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: AFO22173; AAC99794.1; -.
PFAM: PFO0129; MHC_I; 1.
                         046697;
01-JUN-1998 (TEMBLrel. 06, Created)
01-JUN-1998 (TEMBLrel. 06, Last sequence update)
01-JUNY-1999 (TEMBLrel. 10, Last annotation update)
MHC CLASS I ANTIGEN HLA-H ORTHOLOG (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               078209 PRELIMINARY; PRT; 138 AA. 078209; 01-NOV-1998 (TrEMBLrel. 08, Created) 01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-MAY-1999 (TrEMBLrel. 10, Last annotation update) HUMAN LEUKOCYTE ANTIGEN PRECURSOR (FRAGMENT).
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138 138
138 AA; 15610 MW; B8417FAO CRC32;
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NON_TER 90 90
SEQUENCE 90 AA; 10689 MW; 5E5F2495 CRC32;
              90 AA.
                PRT;
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Best Local Similarity 92.9%;
Matches 13; Conservative
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Best Local Similarity 86.7%;
Matches 13; Conservative
                PRELIMINARY;
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                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=SHAMBA;
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SEQUENCE
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Search completed: February 8, 2000, 19:16:17 Job time: 21504 sec

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AF030929 Homo sapiens MHC cl
AF030915 Homo sapiens MHC cl
U59699 Human MHC class I (HL
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/translation="APWIEDEGEPEYWDRETQICKAKAQTDRENLRIALRYYNQSEAGS
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RVAEQLRAYLEGECVEWLRRYLENGKETLQR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (14-DEC-1994) Effie Petersdorf, Human Immunogenetics,
Fred Hutchinson Cancer Research Center, 1124 Columbia, Seattle,
                                                                                                                                                                               seq_documentation_block:
LOCUS HSU18659 399 bp mRNA PRI 30-APR-1995
DEFINITION Human MHC class I HLA-B mRNA (HLA-B-27KSH allele) exons 2 and ACCESSION U18659
VERSION U18659.1 GI:790214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Journal Submission reports an HLA-B-2702 variant (HLA-B-2785H) that differs from the published B-2702 sequence, GenBank Accession Number X03664"
/phenotype="HLA-B-27"
/ 119 c 145 g 48 t
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Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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      gb_pr3:HS639HLA1
gb_pr3:HS8151HLA1
gb_pr4:HSKM315S1
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1025971 Human MHC class I antige
1026971 Human MHC class I antige
1006692 H.sapiens HLA-B gene, ex
1006693 H.sapiens HLA-B gene, ex
AF022159 Homo sapiens isolate C
114590 Sequence 67 from patent
114591 Sequence 68 from patent
114592 Sequence 69 from patent
114593 Sequence 70 from patent
114593 Sequence 70 from patent
114594 Sequence 70 from patent
114593 Sequence 70 from patent
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AF030921 Homo sapiens MHC class
AF030919 Homo sapiens MHC class
AF140723 Homo sapiens MHC class
AF140723 Homo sapiens MHC class
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U37112 Human HLA-A24 gene, alle
U37112 Human HLA-A24 gene, alle
U18987 Human MHC class I antige
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                                                                                                                                                                                                                                   -MODEL-frame-p20.model -DEV-x1p
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-DB-GenEmb1 -OFMT-fasta.9 -SUFFIX-r=ge -GAPDF-4.000 -GAPDFXT-4.000
-GAPDFXT-0.100 -LOOPCL-0.000 -LOOPEXT-0.000 -FGAPOP-4.500
-GAPDFXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -ALIGN-15 -MODE-LOCAL
-UST-45 -DOCALIGN-200 -THR_SCORE-pct -ALIGN-15 -MODE-LOCAL
-OUTFWT-pfs -NORW-ext -MINLEN-0 -MAXIEXEN-1000000 -USER-US08653294
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AF067436 H
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                                                                                                                        About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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      GenEmbl:*
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Query: US-08-653-294-33
Query length: 15
Database: GenEmbl:*
Database sequences: 821193
Database length: -1518192014
Search time (sec): 10176.920000
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                                                                PM
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                                                                Date: Feb 8, 2000 10:25
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gb_pr3:нA1109нLA1
gb_pr3:нS507нLA1
gb_pr3:нS522HLA1
gb_pr3:нS5342HLA1
gb_pr4:нS2301HL1
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gb_pr2:HSHL24SA01
gb_pr2:HSHL24YM01
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gb_pr3:HS1109HLA1
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9b_pr2:GGU37323
9b_pr1:PPU05575
9b_pr1:CGB0101
9b_pr1:GGB0103
9b_pr1:GGB0103
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gb_pr2:HSU25971
gb_pr1:HSHLABHBA
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gb_pr4:AF115460
gb_pr2:PTCHLAB1
gb_pr1:CHPMHCAA
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gb_pr2:HSA011699
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gb_pr1:PTU05580
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gb_pat:114591
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gb_pat:114593
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US-08-653-294-33 x HUMHLABC
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                                                                                                                                                                                                                                                                                       human.
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                                Align seg 1/1
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ORIGIN
                                                                                                                                                                                                                                                                                                      ORGANISM
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AUTHORS
TITLE
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FEATURES
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                                                                                                                                                                                                                                     VERSION
                                                                                                                                                                                                                                                                                   SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RFITYGYVDDTLEVREDSDAASPREEPRAPHTEOEGFEYWDBEDTLEKAKAQTDRENL
RIALRYYNQSEAGSHTLQNMYGCDVGPDGRLLRGYHQDAYDGKDY IALNEDLSSWTAA
PAGOITORKWEAARVAEOLRAYLEGECVEWLRRYLENGKETLGRAPPRITYTHHPI
SDHEATLRCWALGFYPAEITTWQROEDGYDDTELVETRPAGDRTFQKWAVVVPSG
EEDRYYTCHQHEGLERPLITRREPSSGSTVPIVGIVAGLAVLAVVYIGAVVAAVWCRR
KSSGGKGGSYSQAACSDSAGGSDVSLTA"
                                                                                                 HUMHLABC 1089 bp mRNA. PRI 11-JUL-1995
Homo sapiens (clones 18.1, 18.2, 19.2) MHC class I HLA-B*2702 mRNA,
complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'translation="MRVTAPRTLLLLLWGAVALTETWAGSHSMRYFHTSVSRPGRGEP
                                                                                                                                                                               L38504.1 GI:896270

cell surface antigen; cell surface glycoprotein; class I gene;
Integratal membrane protein; major histocompatibility complex.

Homo sapiens (clone: B18.1) cDNA to mRNA; Homo sapiens (clone: 18.2) cDNA to mRNA; demo sapiens (clone: 18.2) cDNA to mRNA.

Homo sapiens
                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1089)
Parham, P., Arnett, K.L. and Adams, E.J.
On the nucleotide sequences of B*2702 and B*2705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="major histocompatibility complex"
/protein_id="AAA69724.1"
 Length: 15
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_line="NV"
/cell_type="EBV-transformed B-cell"
/haplotype="HLA A2/3; B7; Cw2,7"
/clone="18,2"
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                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1.1089
/organism="Homo saplens"
/db_xref="taxon:9606"
/clone="B18.1"
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/gene="HLA-B*2702"
1055. .>1089
/gene="HLA-B*2702"
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/gene="HLA-B*2702"
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/gene="HLA-B*2702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="19.2"
/map="6p21.3"
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Percent Similarity: 100.000
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                                                                seq_name: gb_pr2:HUMHLABC
                                                                                                  seq_documentation_block:
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Quality:
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1. .1241
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/cell_line="BRUG"
join(<79. .151,280. .549,793. .1068.X03667.1:6. .281,
X03667.1:1299. .>1639)
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X03667.1:373. .489,X03667.1:930. .962,X03667.1:1069. .1112)
/gene="HLA-B27K"
join(79. .151,280. .549,793. .1068,X03667.1:6. .281,
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RIALRYYNQSEAGSHTLQNNYGCDVGPDGRLLRGYHQDAYDGKDYIALNEDLSSWTAA
DTAAQITQRKWEAARVAEQLRAYLEGECVEWLRRYLENGKETLQRADPPKTHVTHHPI
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| Dackein_id="Carstrain" | Carstrain | Ca
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EEQRYTCHVQHEGLPKPLTLRWEPSSQSTVPIVGIVAGLAVLAVVVIGAVVAAVMCRR
KSSGGKGGSYSQAACSDSAQGSDVSLTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human
                                                                                                                                                                                                                                                                                                                                                                                                        HSHLAKI 1241 bp DNA PRI 28-JAN-1997
Human class I MHC gene HLA-B27K exons 1-3 (BRUG cell line).
X03664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases I to 1241)

Seemann, G.H., Rein, R.S., Brown, C.S. and Ploegh, H.L.

Gene conversion-like mechanisms may generate polymorphism in
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                                                                                                                                                1 LysalaGlnThraspargGluAsnLeuArgIleAlaLeuArgTyr 15
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Gaps: 0
Percent Identity: 100.000
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to: 1089
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EMBO J. 5 (3), 547-552 (1986)
86220133
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/qene="HLA-B27K"</pre>
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/label=HLA CDS
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793. .1068
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Ratio: 4.933
Percent Similarity: 100.000
     to: HUMHLABC
                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
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                                                                                                                                                                                                                                                                                                      seq_name: gb_prl:HSHLAK1
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RKWEARVABOLRALLGGLOYEWLRYLENGKETLORADPRYTHVFHHPISDHEATLE
CWALGFYPAEITLTWRDGEDOTQDTELVETRRAGDRTFOKWAAVVPSGQEORYTCH
VQHEGLPEPLILRWEPSSQSTIPIVGIVAGLAVLAVVTGAVVAAVWCRKRKSSGGRGG
                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (25-JAN-1994) Jonathan E. Boyson, Watkins Unit, Wisconsin
Regional Primate Research Center, 1220 Capitol Court, Madison, WI
53715, USA
                             PPU05575 1065 bp mRNA PRI 08-OCT-1994
Pan paniscus class I histocompatibility antigen Papa-B (Papa-B-03 ullele) mRNA, partial cds.
U05575 U05575 GI:454767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS PPUG5578 1065 bp mRNA PRI 08-OCT-1994
DEFINITION Pan paniscus class I histocompatibility antigen Papa-B (Papa-B-02 allale) mRNA, partial cds.
ACCESSION U05578.1 GI:454773
                                                                                                                                                               pygmy chimpanzee.
Pan paniscus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Euthoria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 1065)
McAdam,S.N., Boyson,J.E., Liuu,X., Garber,T.L., Hughes,A.L.,
Bontrop,R.E. and Watkins,D.I.
A uniquely high level of recombination at the HLA-B locus
Proc. Natl. Acad. Sci. U.S.A. 91 (13), 5893-5897 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="class I histocompatibility antigen"
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Gaps: 0
Percent Identity: 93.333
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1. 1065
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Boyson, J.E.
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US-08-653-294-33 x PPU05575
seq_name: gb_pr1:PPU05575
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LOCUS PPU05575
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GPDGRLLRGYSQSARDCKDYIALNEDLSSWTAADTAAQITQRKWEAAREAEQLRAYLE
GTCVEWLRRYLENGRETLQRA"
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New York, NY
                                                                                                                                                                                                                                                                                                                                  Gorilla gorilla
Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalla;
Butheria; Primates; Catarrhini; Hominidae; Gorilla.
1 (bases 1 to 792)
Cereb.N., Kong.Y., Lee,S., Maye,P. and Yang,S.Y.
Nucleotide sequences of MHC class I introns 1, 2, and 3 in humans
and intron 2 in nonhuman primates
                                                                                                                                                                                                                     GGU37323 792 bp DNA PRI 21-MAR-1997 Gorilla gorilla MHC class I B antigen gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 792)
Yang, S.Y. and Cereb, N.
Direct Submission
Submitted (29-SEP-1995) Soo Yang, Immunology Program,
Sloan-Ketlering Cancer Center, 1275 York Ave, Box 41,
10021, USA
                                                                                         Gaps: 0
Percent Identity: 93.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 t
                                                        to: 1241
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271. .516
/number=2
517. .792
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Percent Similarity: 100.000
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US-08-653-294-33 x GGU37323
                                                      Align seg 1/1 to: HSHLAK1
alignment_block:
US-08-653-294-33 x HSHLAK1
                                                                                                                                                                 seq_name: gb_pr2:GGU37323
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us-08-653-294-33.rge

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RFIIVGYVDDIQEVRFDSDAASPRMEPRAPWIEQEGPEYWDREIQISKAQAQIDRENL
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                                                                 alleles
Medicine, Dept of Cell Biology, Stanford CA 94305, USA 2 (bases 1 to 1089)
Lawlor, D.A., Warren, E., Taylor, P. and Parham, P. Gorilla class I major histocompatibility complex allely comparison to human and chimpanzee class I
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1. .1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chain"
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Gaps: 0
Percent Identity: 93.333
                                                                                                  J. Exp. Med. 174 (6), 1491-1509 (1991) 92078860 See X60248-59 & X60692-3. Location/Qualifiers 1. 1270 / Organism="Gorilla gorilla"
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73. .1086
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/number=7
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Ratio: 4.667
Percent Similarity: 100.000
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FEATURES
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Direct Submission
Submitted (25-JAN-1994) Jonathan E. Boyson, Watkins Unit, Wisconsin Submitted (25-JAN-1994) Jonathan E. Boyson, Watkins Unit, Wisconsin Sagional Primate Research Center, 1220 Capitol Court, Madison, WI 53715, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation-"VLLLLSAALALTETWAGSHSMRYFYTSVSRPGAGEPRFISVGYV
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VYGRGLPEPLTLRWEPSSQSTTPIVGTVAGLAVVTGAVVAAVMCRRKSSGGKGG
SYSGASSSSSSSSTRIY
1 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B locus allele; Class I major histocompatibility gene; heavy chain; major histocompatibility gene; peptide binding protein; transplantation antigen.
                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 1065)
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1 (bases 1 to 1270)
Lawlor, D.A.

Direct Submission
Submitted (25-JUN-1991) D.A. Lawlor, Stanford Univ School of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1992
                                                                                                      McAdam, S.N., Boyson, J.E., Liu, X., Garber, T.L., Hughes, A.L., Bortrop, R.E. and Warkins, D.I.
A uniquely high level of recombination at the HLA-B locus Proc. Proc. Natl. Acad. Sci. U.S.A. 91 (13), 5893-5897 (1994)
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G.gorilla MhcGogo-B0101 gene for Mhc class I heavy chaln.
X60255 X60255.1 GI:22865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"class I histocompatibility antigen"
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    1065
    /organism="Pan paniscus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="HLA-B-02 allele"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="HLA-B" <1. .1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="HLA-B"
                                                                                                                                                                                                       (bases 1 to 1065)
        pygmy chimpanzee.
Pan paniscus
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Ratio: 4.667
Percent Similarity: 100.000
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US-08-653-294-33 x PPU05578
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US GGB0101
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alignment_scores:
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RIALRYYNOSEAGSHTFORNEGCDVGPDGRLLKGYSGSAYDGKDYIALNEDLSSWTAA
PAAOITORKWEAARREAEOLRAYLEGTCVEWLRRYLENGRETLGRADTPKTHVTHPI
SDHEATLRCWALGFYPEITLIWORDGEDGTODTELVETRPAGDGTFOKWAAVVVPSG
EEERYTCHVOHEGLPKPLILRWEPSSGSTIPIVGIVAGIAVLAVVIGAVVTAVICRR
                                                                                                                                                                                                                                                                                    x60693.1 GI:22867
B locus allele: Class I major histocompatibility gene; heavy chain; major histocompatibility gene; peptide binding protein; transplantation antigen.
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                                                                                                                                                                                                             seq_documentation_block:
LoCUS GGB0102 1270 bp mRNA PRI 07-FEB-1992
DEFINITION G.gorilla MhcGogo-B0102 gene for Mhc class I heavy chain.
ACCESSION X60693
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhin; Hominidae; Gorilla.
1 (bases 1 to 1270)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (25-JUN-1991) D.A. Lawlor, Stanford Univ School of
Medicine, Dept of Cell Biology, Stanford CA 94305, USA
2 (bases I to 1089)
Lawlor, D.A., Warren, E., Taylor, P. and Parham, P.
Gorilla class I major histocompatibility complex alleles:
comparison to human and chimpanzee class I
J. Exp. Med. 174 (6), 1491-1509 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /isolate="calabar"
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/db_l_type="lymphoblast"
/cell_line="calabar B lymphoblastoid cell line"
//clone_lib="CAB181"
                                                                                                                   280 CAGGCACAGACTGACCGAGAGAACCTGCGGGATCGCGCTCCGCTAC 324
                                                                                               1 LysAlaGlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
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Location/Qualifiers
1 1270
/organism="corilla gorilla"
                                                          from: 1 to: 1270
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/codon_start=1
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/note="alpha 1"
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/gene="MhcGogo-B0102"
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                                                        to: GGB0101
alignment_block:
US-08-653-294-33 x GGB0101
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DEFINITION
ACCESSION
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B locus allele; Class I major histocompatibility gene; heavy chain; major histocompatibility gene; peptide binding protein; transplantation antigen.
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Primates; Catarrhini; Hominidae; Gorilla.
1 (bases 1 to 1270)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (25-JUN-1991) D.A. Lawlor, Stanford Univ School of
Medicine, Dept of Cell Biology, Stanford CA 94305, USA
2 (bases 1 to 1089)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lawlor,D.A., Warren,E., Taylor,P. and Parham,P.
Gorilla class I major histocompatibility complex alleles:
comparison to human and chimpanzee class I
J. Exp. Med. 174 (6), 1491-1509 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
LOCUS GG80103 1270 bp mRNA PRI 07-FEB-
DEFINITION G.gozilla MhcGogo-B0103 gene for Mhc class I heavy chain.
VERSION x60254
VERSION x60254.1 GI:22869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 CAGGCACAGACTGACCGAGAGAACCTGCGGATCGCGCTCCGCTAC 324
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Gaps: 0
Percent Identity: 93.333
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Location/Qualifiers
1.1270
/organism-"Gorilla gorilla"
                                                                                                                                                                                                                                                                                                                                                                                                              217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 1270
/gene="MhcGogo-B0102"
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                                                                                                                                                                                                                       1013. .1045
/gene="MhcGogo-B0102"
                                                                                                                                                                                                                                                                                /number=6
1046. .1089
/gene="MhcGogo-B0102"
                                                                                                                                                                                                                                                                                                                                                /note="cytoplasmic 2"
                                                               620. .895
/gene="MhcGogo-B0102"
                                                                                                                                            896. .1012
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                                                                                                                                                                                     /note="transmembrane
                                                                                                                                                                                                                                                                  /note-"cytoplasmic 1'
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                                                                                                    /note="alpha 3"
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388 c
                                          /number=3
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                                                                                                                                                                                                        'number=
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Ratio: 4.667
Percent Similarity: 100.000
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US-08-653-294-33 x GGB0102
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CDS

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/codon_start=1
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OptofyrepsobaasprageprawigspeptwymogrolistrnogTrebrityry
QSEDGSHTLOTMYGCJUGPOGALROYRQYAYDGKDYIALNDLSSWTAADTAAQITO
RKWEAAHEAEQMRAYLEGRCLEWLRRYLENGKETLQREPFETHVTHHPISDHEAALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CWALGFYPAEÏTLTWQRDGEDQTQDTELVETRPAGĎRTFQKWVAVVPSGEEGRYTCH
VQHEGLPEPLTLRWEPSSQSTIPIVGIVAGLAVLAVVVTGAVVAAVMWRRKSLGGKGG
                                                                                             1 (bases 1 to 1065)
Chen, Z.W., McAdam, S.N., Hughes, A.L., Dogon, A.L., Letvin, N.L. and
Watkins, D.I.
                                                                                                                                                   Molecular cloning of orangutan and gibbon MHC class I cDNA. The HLA-A and -B loci diverged over 30 million years ago J. Immunol. 148 (8), 2547-2554 (1992)
                                                                                                                                                                                                                                     Chen.Z.W., McAdam,S.N., Hughes,A.L. and Watkins,D.I.
Chen.Z.W., McAdam,S.N., Hughes,A.L. and Watkins,D.I.
Direct Submission
Submitted (27-FEB-1996) Pathology, Wisconsin Regional Primate
Research Center, 1220 Capitol Court, Madison, WI 53703, USA
Location/Qualifiers
                                     Hylobatés lar
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
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Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 1068)
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Aunquely high level of recombination at the HLA-B locus Proc. Natl. Acad. Sci. U.S.A. 91 (13), 5893-5897 (1994) 94286544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pan troglodytes class I histocompatibility antigen Patr-B (Patr-B-09 allele) mRNA, partial cds.
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Gaps: 0
Percent Identity: 100.000
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    10.5065
    /organism="Hylobates lar"
    /db_xref="taxon:9580"
    1065

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LOCUS PTU05580 1068 bp
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Boyson, J.E.
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Ratio: 4.929
Percent Similarity: 100.000
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US-08-653-294-33 x HLU50091
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Pan troglodytes
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                          TITLE
                                                                                                                                                                                                                                         RFITVGYVDDTQEVRFDSDAASPRMEPRAPWIEQEGPEYWDRETQTSKAQAQTDRENL
RIALRYYNQSEAGSHTIQWMYGCDMGPDGRLLRGYSQSAYDGKDYIALNEDLSSWTAA
                                                                                                                                                                                                                                                                            DTAAQITQRKWEAAREAĒQLRAYLEGTCVEWLRRYLĒNGRETLQRADTPKTHVTHHPI
SERPATLKVAALGYYPAEITLITWQROGEDQYQDTELVETRPAGDGTFQKWAAVVVPSG
EERYTCHYQHEGLPKPLILEWEPSSQSTIPIVGIVAGLAVLAVVVIGAVVTAVICRR
KSSGGKGGSYSQAASDSAQGSDVSITA.
                                                                                                                                                                                                                    'translation="MRVTAPRTLLLLSAALALTETWAGSHSMRYFDTAVSRPGRGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA PRI 14-SEP-1996
I (Hyla B*01) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280 CAGGCACAGACTGACCGAGAGAACCTGCGGATCGCGCTCCGCTAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LysalaGlnThraspargGluasnLeuargIlealaLeuargTyr 15
                                                                                                                                   /product="Mhc_class I heavy chain"
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                                                                                                                                                                                                                                                                                                                                                                                                 73. 1086
/gene="MhcGogo-B0103"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lenyth: 15
Gaps: 0
Percent Identity: 93.333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: GGB0103 from: 1 to: 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                             74. .343
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/note="alpha 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144. .619
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/gene="MhcGogo-B0103"
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'gene="MhcGogo-B0103"
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/gene="MhcGogo-B0103"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1046. .1089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note-"alpha 2"
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Hylobates lar MHC class
U50091 GI:1545833
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                                                            number-1
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Percent Similarity: 100.000
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US-08-653-294-33 x GGB0103
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LOCUS HLU50091
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
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ORIGIN

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LOCUS AF115460 1089 bp mRNA PRI 16-OCT-1999
DEFINITION Pan troglodytes isolate 35B-1 MHC class I antigen (HLA-B) mRNA, complete cds.
ACCESSION AF115460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 1089).
Matsul,M., Machida,S., Feinstone,S.M. and Akatsuka,T.
Molecular analyses of five new chimpanzee MHC class I alleles:
Implications for differences between evolutional mechanisms of
HIA-A, -B, and -C loci
Blochem. Blophys. Res. Commun. 261 (1), 46-52 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matsui,M., Machida,S., Feinstone,S.M. and Akatsuka,T.
Direct Submission
Submitted (18-DE-1998) Microbiology, Saitama Medical School,
Moroyama-Cho, Iruma-Gun, Saitama 350-0495, Japan
Location/Qualifiers
1. 1089
/organism="Pan troglodytes"
/isolate="358-1"
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                              /note-"HLA-B-10 allele"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              356 g
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1 .1068
/gene="HLA-B"
<1. .1060
                                                                                                /gene-"HLA-B"
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                                                                  .1068
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Ratio: 4.929
Percent Similarity: 100.000
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US-08-653-294-33 x PTU05582
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="class I histocompatibility antigen"
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OUGGLEPRFTILKMESSOSSIIPIVGIVAGLAAVLVTVAVAVVAAVVAAVLARKSSGGRG
         Direct Submission
Submitted (25-JAN-1994) Jonathan E. Boyson, Watkins Unit, Wisconsin
Regional Primate Research Center, 1220 Capitol Court, Madison, WI
53715, USA
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Direct Submission
Submitted (25-JAN-1994) Jonathan E. Boyson, Watkins Unit, Wisconsin
Regional Primate Research Center, 1220 Capitol Court, Madison, WI
53715, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1 (bases 1 to 1068)

McAdam,S.N., Boyson,J.E., Liu,X., Garber,T.L., Hughes,A.L.,
Bontrop,R.E. and Watkins,D.I.

A uniquely high level of recombination at the HLA-B locus
Proc. Natl. Acad. Sci. U.S.A. 91 (13), 5893-5897 (1994)
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Gaps: 0
Percent Identity: 100.000
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1. 1068
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/isolate="Teppie"
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/gene="HLA-B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSYSQAASSDSAQGSDVSLTA"
327 c 354 q 1
                                                                                                                           Location/Qualifiers
1. .1068
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Ratio: 4.929
Percent Similarity: 100.000
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94286544
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RIALRYINQSEAGSHTWOTMYGCDVGPDGRLLRGYGOFAYDGKDYIALNQDLSSWTAA
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EEGRYTCHVQHEGLFRPLTLTMEPSSQSTIPIVGIVAGLAVLAVVVIGAVVAAVWCRR
KSSGGKGSYSQASSDSAQGSDYSLTA"
338 c 173 t
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/translation="APRTVLLLLSAALALTETWAGSHSMRYFYTSVSRPGRGEPRFIT
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rfitvgyvddtofvrfdsdaasprmeprapwieoegpeywdretrnvkasaotdrenl
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Submitted (03-0CT-1988) W.E. Mayer, Stanford University, Dept. of
Bloogical Sciences, Stanford, CA 94305-5020, USA
2 (bases 1 to 1507)
Mayer, W.E., Jonker, M., Klein, D., Ivanyi, P., van Seventer, G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequences of chimpanzee MHC class I alleles: evidence for trans-species mode of evolution EMBO J. 7 (9), 2765-2774 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chimpanzee.
Pan troglodytes
Eukaryota: Metazoa: Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 1507)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submission
Submitted (17-FEB-1989) to the EMBL/GenBank/DDBJ databases
Position 607 is c in [1], [3] and u in [2].
Location/Qualifiers
1. 1507
/organism-*Pan troglodytes*
/db_aref="taxon:3598"
/chromosome="5."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTCHLABI 1507 bp mRNA PRI 27-MAR-19 Chimpanzee mRNA for class I antigen ChLA-B1. X13115 X12781 X13115.1 G1:38205 antigen; cell surface glycoprotein; class I antigen; major histocompatibility complex; surface antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="lymphocyte"
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<1. .62
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                                                                                                                                                                                                                                          Length: 14
Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                          Quality: 69.00
Ratio: 4.929
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AF115460
                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-33 x AF115460
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LOCUS
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KEYWORDS
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JOURNAL
COMMENT
FEATURES
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QITQRKWEAAREAEQRRAYLEGTCVEWLRRYLENGKETLORADPPKTHYTHHPISDHE
TALCWALGEYPAEITLIYWQROGEDOYODIELVEIRPEGDRIPOKWAAVVVPSGEEQR
YTCHVOHEGLFRPLILEWEPSSOSTIPIVGIVAGLAVLVYTVAVVAVWAAVMCRRKSS
GGRGGSYSQAASSDSAQGSDVSLIA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Draft entry and computer-readable sequence for [2] kindly submitted
RYYNQSEAGSHTWQTMYGCDMGPDGRLLRGYGQYAYDGKDYIALNEDLSSWTAADTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHEMICAA 1537 bp mRNA chain mRNA, complete cds, clone 39.
Chimpanzee MHC class I ChlA chain mRNA, complete cds, clone 39.
M24045 M24025 M24020
cell surface antigen; cell surface glycoprotein; class I gene; integratal membrane protein; major histocompatibility complex.
Chimpanzee (Tank) EBV-transformed B lymphoblastoid cell, cDNA mRNA, clone 39.
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Eutherla; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 87; 1180 to 1537)
                                                                                              /product="ChLA-B1 mature protein (AA 1-339)"
63. .332
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Parhan, P., Lawlor, D.A., Lomen, C.E. and Ennis, P.D.
Diversity and diversification of HLA class I alleles
J. Immunol. 142, 3937-3950 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 14
Gaps: 0
Percent Identity: 100.000
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885. .1001
/hote="transmembrane domain"
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                                                                                                                                     63. .332
/note="alpha-1 domain"
333. .608
/note="alpha-2 domain"
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20. .1111
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1507
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Location/Qualifiers
1. .1537
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435 c 452 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 69.00
Ratio: 4.929
Percent Similarity: 100.000
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US-08-653-294-33 x PTCHLAB1
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LOCUS CHPMHCAA
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ERQRYTCHYWDFGLERPLILWWEPSSSSTIPIVGIVAGLAVLVVTVAVVAVVAVCR
RKSSGGRGGSYSQAASSAQGSDVSLTA"
324 a 445 c 459 9 330 t
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Align seg 1/1 to: CHPMHCAA from: 1 to: 1537

alignment_block: US-08-653-294-33 x CHPMHCAA THIS PAGE BLANK (USPTO)

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Sequence encoding cephalosp S.aureus topoisomerase IV g S.aureus mutant grlA coding Enterococcus faecalis genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA coding for antigen HLA B27 - and diagnostic reagents contg. such DNA, antigen or antibody.

Claim 2: Page 4: 5pp; German.

Claim 2: Page 4: 5pp; German.

B27 gene, e.g. for assessing susceptibility to rheumatic disorders such as ankylosis spondylitis, or may be used to transform cells for prodn. of HLA B27. The HLA B27 may be used to detect HLA B27 antibody in human serum, or to produce mono- or polyclonal HLA B27 antibodies for use in immunoassay.

Sequence 1026 BP; 213 A; 307 C; 344 G; 162 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-3-1991 (first entry)
Sequence of genomic DNA encoding human histocompatibility antigen
HIA-B 27.
                                                                                                                                                                                                                                                                                                                              10-APR-1991 (first entry)
Sequence encoding the human histocompatibility antigen HLA B27.
Rheumatic disorder; genetic screening; diagnosis;
ankylosing spondylitis; ss.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nLA-B 27.
Ankylosing spondylitis; rheumatic disorder; diagnosis; Homo sapiens.
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Gaps: 0
Percent Identity: 80.000
   2325
2403
2403
5330
410.23
426.62
426.62
1.1e+03
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DE3542024-A.
DE3542024-A.
28-NOV-1985; 542024.
28-NOV-1985; DE-542024.
21-DEC-1985; DE-545576.
(BEHW ) BEHRINGWERKE AG.
Richtmuller G, Meo T, Welss E, Szots H; WPI; 87-157893/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .1026
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102.58
102.28
102.28
94.91
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N70935;
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/*tag= b

1090. .1506

/*tag= c

/*tag= d

2450. .2566
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36.00
36.00
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Ratio: 4.538
Percent Similarity: 86.667
                                                                                                                                                                  seq_name: N_Geneseq_36:N70935
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US-08-653-294-33 x N70935
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N_Geneseq_36:N60607
N_Geneseq_36:T12562
N_Geneseq_36:T12573
N_Geneseq_36:X13261
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1 Sequence encoding the human hi

24 | Sequence of genomic DNA encoding

153 | HLA B27 consensus sequence. De

0 | HLA-Bw 52 exon 2 alpha-1 domain

86 | Sequence encoding HLA-B51 anti

86 | Sequence encoding HLA-Bw52 anti

89 | HLA-Bw52 gene for production of

89 | HLA-Bw53 exon. HLA-Bw53 gene,

1 Oligonucleotide probe with phote
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24 Carcinoembryonic antigen CEA-1
25 Carcinoembryonic antigen CEA-1
26 Carcinoembryonic antigen CEA-1
27 CEA protein encoding cDNA. Clc
28 Carcinoembryonic antigen general encoding contigen general encoding contigen general encoding cannot contigen a continuation (4 of 6) of 1
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                                                                                                                                                                                                                                                             About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Database sequences: 311585
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Search time (sec): 873.190000
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Query: US-08-653-294-33
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N_Geneseq_36:070152
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N_Geneseq_36:V52155
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N_Geneseq_36:075973
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                                                                 Date: Feb 8, 2000
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claim 1; p6; 13pp; German.
THE DNA may be used to detect the HLA-B 27 gene (opt. mutated) in human genetic material. The HLA-B 27 may be used to detect anti-HLA-B 27 antibodies in human serum. The antibodies may be used to determine HLA-B 27 levels in human serum, e.g. for diagnosis of rheumatic disorders, esp. ankylosing spondylitis.
Sequence 3874 BP; 751 A; 1094 C; 1171 G; 858 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "HLA-B27 3' flanking region, downstream of 3' untranslated region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "3' flanking region diagnostic for genetic predisposition to SNSA" 4270. .4556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note- "3' flanking region diagnostic for genetic predisposition to SNSA"
                                                                                                                                                                                                                                                                                                       - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-1997 (first entry)
HIA B27 consensus sequence.
HIA B27; seronegative spondylarthropathy; ankylosing spondylitis;
Reiter's syndrome; arthritis; acute anterior uveitis; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= d
/note= "absence of cytosine at this site is
indicative of a predisposition to SNSA"
                                                                                                                                                                                                                                                                                                    DNA coding for human histocompatibility antigen HLA-B 27 for diagnosis and antigen and antibody prodn.
                                                                                                                                                          01-JAN-1985; DE-542024.
21-DEC-1985; DE-545576.
(BEHW ) BEHRINGWERKE AG.
S21: 4 Weiss E, Dorner C, Lang M, Meo T, Riethmuller WPI: 87-171469/25.
P-PSDB; P70155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LysAlaGlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
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Gaps: 0
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(CEDA-) CEDARS SINAI MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID T61639 standard; DNA; 6553 BP.
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US-08-653-294-33 x N70225
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16-AUG-1996; U13256.
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Ratio:
Percent Similarity:
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                                                                                                                                            21-NOV-1986;
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                                                                                             EP-226069-A
                                                                                                                       24 - JUN - 1987
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         intron
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Detecting pre-disposition to seronegative spondylarthropathies - Trom the absence of a C residue at a specific position in the 3'-flanking region of the HLA B27 allele
Claim 1; Page 52-56; 68pp; Bng1sh.
C Genetic predisposition to seronegative spondyloarthropathies (SNSA) is detecrining the absence of a cytosine nucleotide in the 3' flanking region (see also T61647-48) of an HLA-B3 gene at a position corresponding to nucleotide 4495 of the HLA-B37 consensus c sequence given in T61689. Probes and primers (see also T61640-46) based on this region can be used in diagnostic assays to detect the genetic predisposition to SNSA, and permit the distinction of B27+ individuals who are resistant to SNSA from B27+ normal individuals who are resistant to SNSA from B27+ normal individuals who are resistant to SNSA from B27+ normal individuals Sequence 6553 BP; 1443 A; 1619 C; 2017 G; 1474 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analysis of expression of gene structure, and prodn. of mouse model of human disease

Disclosure: Fig 1; 8pp; Japanese.
The sequence shows the exon 2 alpha-1-domain of the human leukocyte antigen-Bw 52 gene. The complete gene may be introduced into non-human mammals, pref. rat or mouse, or their ancestors at the primary developmental biological step via transplantation into the zygote or embryo to generate transgenic non-human mammals incorporating the HiA-Bw 52 gene in both their germ cells and somatic cells. Transgenic non-human mammals contg. HA-Bw 52 are useful for the analysis of expression of the gene, its structure, and prodn. of mouse models of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAR-1993 (first entry)
HLA-Bw 52 exon 2 alpha-1 domain.
Human leukocyte antigen; transgenic; germ cells; somatic cells;
expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic non-human mammalian HLA-Bw 52 gene - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1087 AAGGCACAGACTGACCGAGAGGACCTGCGGACCCTGCTCCGCTAC 1131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 59.00 Length: 15
Ratio: 4.538 Gaps: 0
Percent Similarity: 86.667 Percent Identity: 80.000
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Gaps: 0
Percent Identity: 92.308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      See also 029166-72
9 A; 88 C; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: 029167 from: 1 to: 270
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25-MAR-1992.
03-AUG-1990; 207329.
03-AUG-1990; JP-207329.
(OLYU ) OLYMPUS OPTICAL CO.
WPI; 92-342893/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID 029167 standard; DNA; 270 BP.
AC 029167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: N_Geneseq_36:Q29167
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92.308
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US-08-653-294-33 x T61639
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US-08-653-294-33 x Q29167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
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14-FEB-1990.

10-AUG-1989

alignment_scores:

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Allotype specific monoclonal anti- HLA antibodies prodn. - using hybridomas derived from transgenic animals carrying HLA gene and immunised with HLA antigen of different allotype Disclosure; Fig 1 A-G; Z0pp; Engilsh.

The human HLA-B51 gene was injected into fertilised mouse eggs and then these introduced into the uterus of a pseudo pregnant mouse. The young were tested to ensure incorporation of the gene into the produces is young, seven of which carried the HLA-B51 gene. The transgeneic offspring were immunised with HLA-B51 gene. The transgeneic offspring were immunised with HLA-B51 gene. The spleen lymphocytes were fused with myeloma cells. Hybridomas
                                                                                                                                                                                                                                                                                                                                                                  QUOSON-1991 (first entry)
03-JAN-1991 (first entry)
HLA-B51 gene for production of monoclonal antibodies.
Alloptype specific monoclonal anti-HLA antibodies; hybridomas;
transgenic animals; HLA-B51 gene; ss.
Key
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Gaps: 0
Percent Identity: 92.308
  Percent Identity: 92.308
                                                                                                                                                                                            285 CAGACTTACCGAGAGACCTGCGGATCGCGCTCCGCTAC 323
                                                                                                                                                                 3 GlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                                                  to: 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        335 C;
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96. .1012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               producing antibodies were selected.
                                                                                                                  from: 1
                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID Q05693 standard; DNA; 1089 BP.
AC Q05693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 A;
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1043. .1089
/*tag= g
/number=7
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/*tag= f
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07-FEB-1990; 102424.
08-FEB-1989; JP-029313.
(OLYU ) OLYMPUS OPTICAL KK.
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/number=5
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/number=2
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4.667
92.308
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  Percent Similarity: 92.308
                                                                                                                                                                                                                                                           seq_name: N_Geneseq_36:Q05693
                                                                                                                  Align seg 1/1 to: Q01822
                                           alignment_block:
US-08-653-294-33 x Q01822
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WPI; 90-255479/34.
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Quality:
Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA for class 1 human leucocyte antigens and derived probes and transformed cells, useful for DNA typing, as immunogens etc. Claim 1; Page 11; 23pp; English.

The HLA class I DNA can be used a source of probes for use in DNA typing. Transformed cells, which are useful as immunogens, can be obtained by introducing these DNAs into eucaryotic cells. Sequence 1086 BP; 224 A; 334 C; 356 G; 172 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New DNA for class 1 human leucocyte antigens and derived probes and transformed cells, useful for DNA typing, as immunogens etc.
Claim 2: ppil-12; 23pp; English.

The HLA class I DNA can be used a source of probes for use in DNA typing. Transformed cells, which are useful as immunogens, can be obtained by introducing these DNAs into eucaryotic cells.
Sequence 1086 BP; 23 A; 335 C; 356 G; 170 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 13
Gaps: 0
Percent Identity: 92.308
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213 CAGACTTACCGAGAGCACCTGCGGATCGCGCTCCGCTAC 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
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Gaps:
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                                                                                                                                                                                    Sequence encoding HLA-B51 antigen.
Probe; HLA class I DNA; immunogen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAY-1991 (first entry)
Sequence encoding HLA-Bw52 antigen.
Probe; HLA class I DNA; immunogen; ss.
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1. .1086
/*tag= a
                                                                                                                                                                                                                                                                                                                             11-AUG-1988; JP-200758.
(OLYU) Olympus Optical Co., Ltd.
Kano K, Takiguchi:
WPI: 90-046289/07.
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(OLYU) Olympus Optical Co., Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
ID 001822 standard; DNA; 1086 BP.
                                                                                     seq_documentation_block:
ID Q01834 standard; DNA; 1086
                                                                                                                                                            19-MAR-1991 (first entry)
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4.667
92.308
                                           seq_name: N_Geneseq_36:Q01834
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US-08-653-294-33 x Q01834
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WPI; 90-046289/07.
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Ratio:
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Ratio:
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                                                                                                                                                                                                                                     Homo sapiens.
EP354580-A.
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Ë 173

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357

alignment_scores:

EP-354580-A.

10-AUG-1989

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286 CAGACITACCGAGAGAACCTGCGGATCGCGCTCCGCTAC 324
                                                                                                Q12114 standard; DNA; 1089
Q12114;
                                                                                                                                  29-AUG-1991 (first entry)
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US-08-653-294-33 x Q12114
                                                                                    seq_documentation_block:
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Percent Similarity:
                                                                                                                                                   HLA-Bw53 exon.
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WO9322680-A.
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                                                                                                                                                                                                                                                                  J03112487-A.
                                                                                                   The spleen lymphocytes were fused with myeloma cells (P3x63-Ag8.653). Hybridomas producing antibodies were selected. Sequence 1089 BP; 223 A; 336 C; 359 G; 171 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Allotype specific monoclonal anti- HLA antibodies prodn. - using hybridomas derived from transgenic animals carrying HLA gene and immunised with HLA antigen of different allotype Disclosure; Fig 1 A-G; 20pp; English. The human HLA-BW52 gene was introduced into mouse L cells and then these cells used to immunise one of the transgenic mice (see Q05693).
                                                                                                                                                                                                                               03-JAN-1991 (first entry)
HLA-Bw52 gene for production of monoclonal antibodies.
Alloptype specific monoclonal anti-HLA antibodies; hybridomas;
transgenic animals; HLA-Bw52 gene; ss.
Location/Qualifiers
exon
1. 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 13
Gaps: 0
Percent Identity: 92.308
                                                                                                  286 CAGACTTACCGAGAGAACCTGCGGATCGCGCTCCGCTAC 324
                                                                                  3 GlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
                                                   to: 1089
                                                                                                                                                                                                                                                                                                                                                                                                               /note="alpha 1-domain"
344. .619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="alpha 2-domain"
520. .895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note-"alpha 3-domain"
196. .1012
                                                 Align seg 1/1 to: Q05693 from: 1
                                                                                                                                                                                  seq_documentation_block:
ID Q05701 standard; DNA; 1089 BP.
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/*tag= f
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07-FEB-1990; 102424.
08-FEB-1989; JP-029313.
(OLYU ) OLYMPUS OPTICAL KK.
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/number=1
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/*tag= b
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/number=5
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/number-7
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4.667
92.308
                                                                                                                                                  seq_name: N_Geneseq_36:Q05701
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alignment_block:
US-08-653-294-33 x Q05693
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US-08-653-294-33 x Q05701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 90-255479/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rakiguchi M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP-383183-A
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intron

exon

exon

exon

exon

exon

3 GlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15

from: 1 to: 1089

Align seg 1/1 to: Q05701

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The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAY-1994 (first entry)
oligonucleotide probe with photoremovable protecting group.
Probe: hybridisation; screening; target sequence; protecting group;
photoactivation; photochemical deprotection; ss.
                                                                       Human leukocyte antigen; probe; major histocompatibility complex; MHC; class I; ss.
Homo saplens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     predetermined region formation on support reactive with biological polymer - by attaching thiol cpd. and photochemical deprocection, for immobilising oligo-nucleotide probe array on polyvinylidene fluoride support, mol. electronic devices and sepn. stationary phases
Example 7; Page 27; 34pp; English.
This oligonucleotide probe was immobilised on a solid support. probe carries a thiol group which is covalently coupled to a photochemically removable protecting group. Many probes can be
                                                                                                                                                                                                                                                                                                                                                                                        HIA-BW53 game, DNA probe and transformant cells - used for immunisation, identifying specificity of antiserum etc. Claim 1; Page 1; 11pp; Japanese.

Claim 1; Page 2; 11pp; Japanese.

Probes comprising part of the sequence can be used to identify class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HIA-BW53 antigen. See also J03112485 and J03112486.

Sequence 1089 BP; 222 A; 337 C; 356 G; 174 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 13
4.667 Gaps: 0
92.308 Percent Identity: 92.308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 CAGACTTACCGAGAGCACCTGCGGATCGCGCTCCGCTAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 1089
                                                                                                                                                      Location/Qualifiers
1. .1089
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-1993; U03767.
24-APR-1992; US-874849.
AFPY-) AFFYMAX TECHNOLOGIES NV.
FOGOT SP, MCGALL GH, Sheldon EL;
WPI: 93-368991/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: Q12114 from: 1
BP.
                                                                                                                                                                                                                                                      14-MAY-1991.
22-SEP-1889; 247697.
22-SEP-1989; JP-247697.
(OLYU ) OLYMPUS OPTICAL KK.
WPI: 91-182991/25.
P-PSDB; R12463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID Q51474 standard; DNA; 30 BP.
AC Q51474;
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重して

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PHIA-B7 expression vector.

expression vector; pHLA-B7; heavy human HLA-B7; bicistronic mRNA; light beta-2 microglobulin; class I major histocompatibility complex; MHC; human leukocyte antigen; HLA; covalently closed circular DNA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "kanamycin resistance gene open reading frame;
the gene is taken from the transposable element
Tn903"
immobilised on the solid support at one time and irradiation will remove the protecting group and allow the probe to hybridise with a complementary sequence. Selective irradiation in defined regions will activate only those probes required/chosen to be used in a given screening of a sample solution. The invention allows simultaneous screenings for many different sequences in a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3' LTR promoter region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .354
7.*tag=
//otg= "pBR322 backbone contg. bacterial origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New vectors for gene therapy, partic for tumours - comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag= e
'note= "3' untranslated region of HLA-B7
                                                                                                                                                                                                                                                                                         Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "SV40 polyA signal sequence" complement (1412, .1560)
                                                                                                                                                                                       10 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= f
/note= "HLA-B7 open reading frame"
complement (2886. 3415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "SV40 small t intron"
complement (1561. .1794)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= g
/note= "Rous sarcoma virus
                                                                                                                                                                                       9
G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (1795, .2880)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nabel GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "pBR322 backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (1410.
/*tag= c
                                                                                                                                                                                       0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heavy chain mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to reverse of: 051474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AlaGlnThrAspArgGluAsnLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lew D, Marquet M, Nabel EG, WPI; 95-036494/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID Q75974 standard; cDNA; 4059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .4059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355. .1170
                                                                                                                                                                                       2 A;
                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-33 x Q51474/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seg_name: N_Geneseg_36:Q75974
                                                                                                                                                                                                                                                                                              Quality: 45.00
Ratio: 5.000
Percent Similarity: 100.000
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(VICA-) VICAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-1994.
27-MAY-1994; U06069.
07-JUN-1993; US-0743
                                                                                                                                                                                       30 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polya_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                        alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9429469-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         075974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3' utr
                                                                                                                                                                 step.
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     888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONTRACTOR OF STATE O
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genetic material encoding one or more cistron(s) which express immunogenic or therapeutic peptide(s)

(laim 9; Page 42-43; Sopp; English.

This HLA-B7 antigen encoding plasmid was developed to incorporate many advantageous features, eg. the kanamycin resisitance gene. The eradication of two open reading frames encoding portions of SV40 viral proteins lowers the risk of tumourigenicity. The vector may also operate as a cassette into which distrons may be inserted and removed at will for the transcription and subsequent translation of peptides of interest. The vector is used partic. for the treatment of neoplastic disease, eg. melanoma, and provides enhanced gene delivery and expression in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain, derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG'1995 (first entry)
pHLA-B7/Deta-2 microglobulin expression vector.
expression vector; pHLA-B7/Deta-2 microglobulin; heavy human HLA-B7;
light beta-2 microglobulin; class I major histocompatibility complex;
MHC; bicistronic mRNA; human leukocyte antigen; HLA;
covalently closed circular DNA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heavy chain mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          region of a synthetic oligonucleotide which modifies this requiatory sequence to effect a higher level of expression of downstream sequences. The oligonucleotide removes a polyadenylation signal sequence originally found in the RSV DNA sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "tag= :
note= "3' untranslated sequence of HLA-B7 heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "rtag" C
note= "HLA-B7 heavy chain open reading frame"
35. .606
                                                                                                                                                                                                                                                                                                                                                          1000 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/note= "Rous sarcoma virus LTR promoter don
for the Schmidt-Rupin strain nucleotides
8673-9146. This region also includes a 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= consensus_Kozak_signal_sequence
535. .1620
/*tag= c
                                                                                                                                                                                                                                                                                                                                                          1033 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 10
Gaps: 0
Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag* d
note= "encodes putative signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        putative HLA-B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :
ლ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1
                                                                                                                                                                                                                                                                                                                                                          1051 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLA-B7 heavy chain" 607 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LysAlaGlnThrAspArgGluAsnLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to reverse of: Q75974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e
"encodes I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
ID Q75973 standard; cDNA; 4965 BP.
                                                                                                                                                                                                                                                                                                                                                          975 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1621. .1853
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chain mRNA"
1854. .1888
/*tag- g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-653-294-33 x Q75974/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouality: 41.00
Ratio: 4.100
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: N_Geneseq_36:Q75973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note-
                                                                                                                                                                                                                                                                                                                                                          4059 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3'utr
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                 HARRES CARRES CONTRACTOR CONTRACT
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1338 G;

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1293

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1171 A;
                                                                                                                                                                                                                                                                                             T05843 standard; DNA; 934 BP. T05843;
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ID N92449 standard; DNA; 534 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.00
3.545
73.333
                                                                 Quality: 41.00
Ratio: 4.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                      seq_name: N_Geneseq_36:T05843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: N_Geneseq_36:N92449
                                                                                                                          alignment_block:
US-08-653-294-33 x Q75973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-653-294-33 x T05843
              4965 BP;
                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                             WO9531548-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block
                                                                                                                                                                    Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1
 in vivo.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXECAC
  ပ္ပင္တ
                                                                                                                                                                                                                                                                                                /*tag= 1 ...3111 /note= "bovine growth hormone 3'UTR and transcriptional terminator; it starts at a blunt-ended BglI site within the 3'UTR of the mRNA coding sequence" /*tag= m /*tag= m 3112...3157
                                                                 /note- "murine encephalomyocarditis CAP-independent translational enhancer (EMCV-CITE); taken from nucleotides 255-843 of cloned EMCV genomic DNA. It is a non-coding regulatory sequence functioning as an internal entry point for the eukaryotic ribosomal subunits when located within a mRNA mol. It enables the translational start codon of the beta-2 microglobulin, downstream of the HLA-B7 stop codon on this biscistronic mRNA to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= o
/note= "kanamycin resistance gene open reading frame;
/note= samenistance gene is taken from the transposable element
rn903"
                                                                                                                                                                                                   2480. .2839
/*tag= "encodes beta-2 microglobulin; this cDNA is deriv. from chimpanzee (differs to the human cDNA by only 4 bases)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4014. .4965
//rtag- p
//note- pBR322 backbone contg. bacterial origin of
replication, it represents nucleotides 2244-3193"
/note- "multiple cloning site, forms a junction between the HIA-B7 sequence and the EMCV-CITE sequence, and is used to facilitate subcloning" 1889. . 2479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         //tag- n
//fag- nsynthetic linker to facilitate cloning"
complement (3151. .3967)
                                                                                                                                                                                                                                                                                               /*tag= j
/ote= "3' untranslated region of the beta-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lew D, Marquet M, Nabel EG, Nabel GJ; WPI; 95-036494/05.
                                                                                                                                                                                                                                                                                                                microglobulin mRNA"
2847. .2870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-DEC-1994.
27-MAY-1994; U06069.
07-JUN-1993; US-074344.
(UNM.) UNIV MICHIGAN.
(VICA-) VICAL INC.
                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                        misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      polya_signal
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16-MAY-1995; U06119.

16-MAY-1995; U06119.

16-MAY-1995; U06119.

16-MAY-1995; U06119.

17-MAY-1995; U06119.

18-MAY-1995; U06119.

18-MAY-1995; U06119.

19-MAY-1995; U06119.

10-MAY-1995; U08-243546.

10-MAY-1995; U08-243546.

10-MAY-1995; U08-243546.

10-MAY-1995; U08-24546.

10-MAY-1995; U08-2464.

10-MAY-1995; U08-2466.

10-MAY-1996; U08-2466.

10-MAY-1996; U08-2466.

10-MAY-1996; U08-2466.

10-MAY-1996; U08-2466.

10-MAY-1996; U08-2466.

10-MAY-1996; U08-2466.

10-MAY-1996.

10-MAY-1996; U08-2466.

10-MAY-1996; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.APR-1996 (first entry)
Repeat sequence of cps gene locus operon of S.pneumoniae.
Capsular polysaccharide; cps; peptide; flanking region; detect serotype; diagnosis; prevention; Streptococcus pneumoniae; ss. Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAY-1990 (first entry)
Sequence of carcinoembryonic antigen domain III.
Carcinoembryonic antigen; domain III; domain A; domain B.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 15
Gaps: 0
Percent Identity: 46.667
Length: 10
Gaps: 0
Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                        to: Q75973 from: 1 to: 4965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: T05843 from: 1 to: 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        814 CAGGCACAGACTGACCGAGAGAGCCTGCGG 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LysAlaGlnThrAspArgGluAsnLeuArg 10
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to: 2031

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Carcinoembryonic antigen fragments - used in assays to determine the presence and amt. of the antigen in samples also contg. related antigens. Disclosure; page 4; 15pp; English.

CEA fragments can be used in assays to determine the presence and amt. of CEA in samples which also may contain related antigens including its normal cross-reacting antigen or the 128 kD antigen.

Sequence 534 BP; 137 A; 172 C; 110 G; 115 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carcinoembryonic antigen (CEA) derivs - useful as reagents in immunoassay for diagnosis of neoplastic diseases claim 4; Page 18; 30pp; English.

Claim 4; Page 18; 30pp; English.

Q71567 is the DNA sequence which encodes carcinoembryonic antigen (CEA) R60619. CEA is free from cross-reactive CEA-like antigens, it is antigenically indistinguishable from the solution form of CEA shed from tumour cells, and it is devoid of ethanolamine. R60619 can be used in a reagent composition for detecting neoplastic diseases in biological samples, or in an immunoassay process where it can specifically detect the presence of tumour cells in a biological sample e.g. blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-MAY-1995 (first entry)
Carcinoembryonic antigen DNA.
Carcinoembryonic antigen; CEA; neoplastic diseases; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 0
Percent Identity: 63.636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to reverse of: N92449 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 AspargGluAsnLeuArglleAlaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-OCT-1994.
15-MAR-1994; 103986.
25-MAR-1993; EP-810214.
(HOFF ) HOFFMANN LA ROCHE & CO AG F.
MACh J, Pelegrin A, Terskikh A;
WPI; 94-304461/38.
P-PSDB; R60619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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ID Q71567 standard; DNA; 2031 BP.
AC Q71567;
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4.222
81.818
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29-NOV-1989.
24-MAY-1989; 305232.
25-MAY-1988; US-198289.
(CITY) City of Hope.
Shively JE;
WPI: 89-349991/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: N_Geneseq_36:Q71567
                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
Quality:
Ratio:
Percent Similarity:
                               misc_feature
                                                                             misc_feature
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alignment_scores:

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Percent Identity: 63.636
                     Gaps:
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US-08-653-294-33 x Q71567/rev
38.00
4.222
81.818
Quality:
Ratio:
Percent Similarity:
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T24384 crs1519 lambdaZAPST R
D74882 CELK089FYF Yuj1 Kohar
AV202520 AV202550 Yuj1 Kohar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)

E Genome Res. 6 (9), 807-828 (1996)

E 9704478

On May 8, 1995 this sequence version replaced gi:800234.

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1810

Fax: 314 286 
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

( pases 1 to 255)
Hiller,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Rucaba,T., Lacy,M., Le,N., Le,N.,
Mardis,E., Moore,B., Moortis,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Treveskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -3' adaptor sequence: 5'
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Oligo dT. T-84 colonic epithelial cell line. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTT 3'"
                                                                                                                               seq_documentation_block: 255 bp mRNA EST 10-DEC-1996 LOCUS AA151891 255 bp mRNA STATON 2001G0.r1 Stratagene colon (#937204) Homo sapiens cDNA clone DEFINITION 2001G6435 5' similar to 9b:M15497_cds1 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) A*2401 (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           others
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Gaps: 0
Percent Identity: 92.857
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AA151891.1 GI:1720754
  40.00
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Percent Similarity: 100.000
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US-08-653-294-33 x AA151891
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                                                                                            seq_name: gb_est10:AA151891
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                                                                                                                                                                                                                                                      sednence.
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                human.
gb_est1:T24384
gb_est5:D74882
gb_est36:AV202520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                   KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
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ORIGIN
                                                                                                                                                                                                                                                                         ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R20529 4906c01.r1 Source infant
A1007865 EST20216 Normalized r
A2003523 HS_2229_A2_D07_MR CIT
D82177 HUMHBC4504 Human pancree
AA633983 ac33f01.s1 Stratagene
AA633983 ac33f01.s1 Stratagene
AA633983 ac33f01.s1 Stratagene
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A0056225 CIT-HSP-233953.TR CIT-
B21407 T10C5-Sp6 TAMU Arabidops
AQ53331 HS_238_B2_EC0_SP6E RF
AA817822 UI-R-A0-ae-d-07-0-UI.s
AA819533 EST21772 Adrenal gland
AA319533 EST21772 Adrenal gland
AV058574 AV058574 Mus musculus
AV065386 AV064196 Mus musculus
AU070735 Rice FOOL OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Documentation ...

AA15191 zo01f06.r.1 Stratagene
A1359260 qy27b07.x1 NCI_CGAP_Br
AA147121 zo534606.r.1 Stratagene
AL03690 DKF2p564D2463.r.1 564 (
R13904 yf62c03.r.1 Soares infant
c03945 zo3945 Human heart cDNA
AA263158 PMYC034 KG1-a Lambda Z
D82221 HUMHBC4626 Human pencrea
A1696864 wc74h11.x1 NCI_CGAP_P4
A1696864 wc74h11.x1 NCI_CGAP_P4
A1124815 am56e06.x1 Johnston fr
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AQ328864 nbxb0043P20r CUGI 1
AQ579309 nbxb0084M23r CUGI 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      out_format : pfs
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                                               6:23
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gb_est28:AL036690
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gb_gss9:AQ164696
gb_est32:AI731234
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gb_est26:AI008245
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gb_est24:C99613
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human

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

AUTHORS TITLE

REFERENCE

JOURNAL COMMENT

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AA147151 S81 bp mRNA EST 05-DEC-1996
2032d06.rl Stratagene colon (#937204) Homo sapiens cDNA clone
IMAGE:588587 5' similar to gb:M64740 HLA CLASS I HISTOCOMPATIBILITY
ANTIGEN, A-24(A-9) A*2402 ALPHA (HUMAN);, mRNA sequence.
AA147151. GI:1716526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Sep 12, 1996 this sequence version replaced gi:1393699.
On Sep 12, 1996 this sequence version replaced gi:1393699.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 272.
High quality sequence stop: 272.
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

11 (bases 1 to SB1)

11 (lasse; Lo SB1)

11 (lasse, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Markins, M., Hulkman, M., Kucaba, T., Lacy, M., Le, N., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rikin, L., Rohlfing, T., Schallenberg, K., Soares, M.B., Tan, F., Thierry Meg, J., Trevassis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Marra.M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
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LOCUS AL036690 171 bp mRNA EST 27-SEP-1999
DEFINITION DKF2p564D2463_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone
DKF2p564D2463_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 14
Gaps: 0
Percent Identity: 85.714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AlaGlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RATIO: 4.429
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.00
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US-08-653-294-33 x AA147151
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           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
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                                                                                                                                                                                                                                                                                                       human.
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                                                                                                                                                                                                                                                          KEYWORDS
SOURCE
ORGANISM
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                                             LOCUS
DEFINITION
                                                                                                                                                                                     ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
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JOURNAL
MEDLINE
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. 618
/organism="Homo sapiens"
/db_Arsf="texon:9606"
/clone="InAGE:201305"
/clone=lib="NCI_CGAP_Brn23"
/clone=lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab.host="glioblastoma (pooled)"
/lab.ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                       seq_documentation_block:

LOCUS A1359260 618 bp mRNA EST 15-FEB-1999

DEFINITION qy27b07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013205 3 similar to 95:D32129 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,

AW-66(A-10) A*6601 ALPHA (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases: Primates; Catarrhini; Hominidae; Homo.

1 (bases: Prof18)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index (GAP/BTGAP), Tumor Gene Index (GAP/BTGAP), Tumor Gene Index Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 14
Gaps: 0
Percent Identity: 92.857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soares and M.Fatima Bonaldo."
171 c 182 g 137 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert Length: 691 Std Error: 0.00 Seq primer: -400P from Gibco High quality sequence stop: 458. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: AI359260
                                                                                                                                                                                                                                                          AI359260
AI359260.1 GI:4110881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-33 x AI359260/rev
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Percent Similarity: 100.000
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seq_name: gb_est26:AI359260
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                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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Ratio:
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source

FEATURES

alignment_scores:

BASE COUNT

ORIGIN

d

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Wilson, R.
The WashU-Marck EST Project
In Unpublished (1995)
Contact: Wilson RK
WashIngton University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Construction of a normalized directionally cloned cDNA library from adult heart and analysis of 3040 clones by partial sequencing Genomics 35 (1), 231-235 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS
LOCUS
C03945
DEFINITION C03945 Human heart cDNA (YNakamura) Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 232)
1 (bases 1 to 232)
1 Annaka,T., Ogiwara,A., Uchiyama,I., Takagi,T., Yazaki,Y. and Nakamura,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:26801"
/clone_llb="Soares infant brain lNIB"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 13
Gaps: 0
Percent Identity: 92.308
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/organism="Homo sapiens"
/db_xref="GDB:399148"
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C03945.1 GI:1467196
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Percent Similarity: 100.000
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US-08-653-294-33 x R13904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
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ORGANISM
                                                    TITLE
JOURNAL
COMMENT
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                                                                 EST (Duesterhoeft, et al.)
Unpublished (1999)
Un Jul 7, 1999 this sequence version replaced gi:5866258.
Contact: Duesterhoeft A MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    German Genome Project.

No sl sequence available.

This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS
LOCUS
R13904
DEFINITION yf62c03.r1 Soares infant brain INIB Home sapiens cDNA clone
IMAGE:26801 5' similar to gb:M64742_cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, A-23(A-9) A*2301 (HUMAN);, mRNA
                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 17)
Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 459)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI" 53 c 60 g 22 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LysAlaGlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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/clone=lib="564 (synonym: hfbr2)"
/tissue_type="brain"
/dev_stage="fetal"
/lab_host="X1-2blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps: 0
Percent Identity: 80.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1
AL036690
AL036690.3 GI:5927859
EST.
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R13904
R13904.1 GI:766980
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4.538
86.667
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                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                          Wiemann, S.
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                                                                                                            human.
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Tel: 272-20-8856
Fax: 272-20-8896
Email: jtakeda@sb.gunma-u.ac.jp.
Location/Qualifiers
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US-08-653-294-33 x AA263158
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US-08-653-294-33 x D82221
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LOCUS D82221
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PMY0534 KG1-a Lambda Zap Express CDNA library Homo sapiens CDNA 5',
mRNA sequence.
AA263158
                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="3NHC2454"
/clone=lib="Human heart cDNA (YNakamura)"
/dev_stage="adult"
/note="Organ: heart; normalized directionally cloned cDNA
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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 283)
Claudio,J.O., Liew,C.C., Dempsey, A.A., Cukerman, E., Stewart, A.K.,
Na, E., Atkins, H.I., Iscove, N.N. and Hawley, R.G.
Identification of sequence-tagged transcripts differentially
expressed within the human hematopoietic hierarchy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Toronto Hospital
CRCS-424, 67 College St., Toronto, Ontario M5G 2M1, Canada
Tel: 416 3403834
Fax: 416 3403453
Email: r.hawley@utoronto.ca
Similar to M58636 MHC class I HLA-Bw gene. Clone was randomly
picked from KGla primary library.
Seq primer: 5, GAATMARCCTCACTACTAAAGGG 3'
High quality sequence stop: 283.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone_lib="KGl-a lambda Zap Express CDNA library"
/cell_type="promyeloblast"
On Oct 24, 1995 this sequence version replaced gi:1040105.
Contact: Yusuke Nakamura
Institute of Medical Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           One May 5, 1995 this sequence version replaced gi:797810. Contact: Hawley RG Oncology Research Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                        Length: 13
Gaps: 0
Percent Identity: 92.308
                                                   University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108,
Tel: 81-3-5449-5372
Exx: 81-3-5449-5433
Email: yusuke@ims.u-tokyo.ac.jp.
Location/Qualifiers
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77 c 68 o
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US-08-653-294-33 x C03945
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LOCUS AA263158
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   COMMENT
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_llb="Human pancreatic islet"
/clone_llb="Human pancreatic islet"
/note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <1000 bp in size."
3 others
/note="Vector: Lambda Zap Express (Stratagene); Site_1:
ECORI; Site_2: XhoI; Unidirectional cloning sites:
ECORI.*XhoI. mRNA was purified from KGI-a cell line, cDNA.
was synthesized using an XhoI-oligodT linker primer. EcoRI
adaptors were ligated, followed by digestion with XhoI for
directional cloning into predigested Lambda Zap Express.
91 c 88 g 40 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Institute for Molecular and Cellular Regulation, Gunma University 3-39-15 Showa-machi, Maebashi Gunma 371, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D82221 375 bp mRNA EST 09-FEB-1996
HUMHBC4626 Human pancreatic islet Homo sapiens cDNA similar to
HLA-B, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 375)
Takeda,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human pancreatic islet ESTs
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:785255.
Contact: Jun Takeda
                                                                                                                                                                                                                                                                                                                                         Length: 13
Gaps: 0
Percent Identity: 92.308
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Gaps: 0
Percent Identity: 92.308
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE

JOURNAL COMMENT

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1. .414
/organism="know sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1539586"
/clone="IMAGE:153968"

                                                                                                                                                                                    Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

Eutheria: Primates; Catarrhin; Hominidae; Homo.

Eutheria: Primates; Catarrhin; Hominidae; Homo.

El (bases I to 414)

Stiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R. Washingth Liss Project

Unpublished (1997)

Unpublished (1997)

Unpublished (1997)

Londact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40ml3 fwd. Er from Amersham.

Location/Qualifiers

Location/Qualifiers
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LOCUS
D82189
DEFINITION HUMHEC4524 Human pancreatic islet Homo sapiens cDNA similar to
ACCESSION
D82189
D82189.1 GI:1183662
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 415)
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Gaps: 0
Percent Identity: 84.615
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    AI124815
AI124815.1 GI:3593329
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84.615
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US-08-653-294-33 x AI124815
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Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Contact: Robert Straubberg, Ph.D.
Tel: (301) 496-1558.
Email: Robert_Strausberg(@ih.gov
Email: Robert_Strausberg(@ih.gov)
Email: Robert_Strausbe
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                                                                                                                                                                                                                                             seq_documentation_block:

LOCUS A1696864 748 bp mRNA EST 03-JUN-1999

DEFINITION WC74hil.x1 NCI_CGAP_Panl Homo sapiens CDNA clone IMAGE:2324421 3'

Similar to gb:N28205 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,

B-51(B-5) B*5101 ALPHA (HUMAN);, mRNA sequence.

ACCESSION A1696864

VERSION A1696864.1 GI:4984764
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LOCUS A1124815 414 bp mRNA EST 11-SEP-1998
DEFINITION am56606.xJ Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539586 3' similar to gb:M24018_cds1 HLA CLASS HISTOCOMPATIBILITY ANTIGEN, BW-44(B-12) B*4402 (HUMAN); contains MER22.t3 TARI repetitive element ;, mRNA sequence.
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Percent Identity: 92.308
                                                297 CAGACTTACCGAGAGAACCTGCGGATCGCGCTCCGNTAC 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: -40UP from Gibco
High quality sequence stop: 424.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11548-013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.667
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US-08-653-294-33 x AI696864
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                                                                                                                                                                  seq_name: gb_est31:AI696864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
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FEATURES

BASE COUNT ORIGIN

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double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatina Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIO07865 325 bp mRNA EST 25-JAN-1999
EST202316 Normalized rat brain, Bento Soares Rattus sp. cDNA clone
REMAY89 3' end, mRNA sequence.
AIO07865.1 GI:3221697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases I to 325)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1998)
On Jan 17, 1998 this sequence version replaced gi:1900396.
Contact: Lee, NH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Normalized rat brain, Bento Soares"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, Tel: (301)-838-3529 Fax: (301)-838-0208 Email: nhlee@tigr.org
                                                                                                 /organism="Momo sapiens"
/db_xref="GDB:403812"
/db_xref="taxon:9606"
/clone="IXAAGE:31465"
/clone_llb="Soares infant brain INIB"
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Gaps: 0
Percent Identity: 83.333
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/db_xref="ATCC (inhost):2016137"
/db_xref="taxon:10118"
/clone="RBRAV89"
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   High quality sequence stop: 345.
Location/Qualifiers
1..567
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                                                                                                                                                                                                                                                           /sex="female"
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4.455
91.667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_est22:AI007865
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US-08-653-294-33 x R20954
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LOCUS AI007865
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Rattus sp.
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VERSION
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                                          FEATURES
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                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_llb="Human pancreatic islet"
/note="Vector: Lambda ZAPI; Site_1: Eco RI; Site_2: Xho
I; mRNA was prepared from normal adult human islets. CDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. CDNA was size fractionated to remove
sequences <1000 bp in size."

a 134 c 133 g 61 t 8 others
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Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Fax: 314 286 181
                             Human pancreatic islet ESTs
Unpublished (1995)
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced g1:785206.
Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University 3-39-15 Showa-machi, Maebashi Gunma 371, Japan
Tel: 272-20-8856
Fax: 272-20-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 567)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yg06c01.rl Soares infant brain lNIB Homo saplens cDNA clone
IMAGE:31465 5' similar to gb:M15497_cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) A*2401 (HUMAN);, mRNA
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4.545 Gaps: 0
84.615 Percent Identity: 84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 415
                                                                                                                                                                                                                                                                                     Email: jtakeda@sb.gunma-u.ac.jp.
Location/Qualifiers
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Ratio:
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AUTHORS
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AUTHORS
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 410)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:

LOCUS AQ033523 410 bp DNA GSS 02-JUL-1998

DEFINITION HS_2229_A2_D07_MR CIT Approved Human Genomic Sperm Library D Homo Sapiens genomic clone Plate=2229 Col=14 Row-G, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="texon:9606"
/clone="Plate=2229 Col=14 Row=G"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Ouean Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2229 row: G column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 others
                                                                                                                       Length: 11
Gaps: 0
Percent Identity: 72.727
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3.214 Gaps: 0
93.333 Percent Identity: 53.333
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                                                                                                                                                                                                                                                                                                     204 GACAGGAAGAATGTACGGTTGGCATTGAGATAC 236
                                                                                                                                                                                                                                                 to: 325
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Location/Qualifiers
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US-08-653-294-33 x AQ033523/rev
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Percent Similarity: 100.000
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Class: BAC ends
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KEYWORDS
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MEDLINE
COMMENT
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AUTHORS
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/clone_lib="Manah pancreatic islet"
/note="Vector: Lambda ZAPII; Site=]: ECO RI; Site_2: Xho
I; MRNA was prepared from normal adult human islets. CDNA
was directionally synthesized from the Xho I in the vector
to the ECORI site. CDNA was size fractionated to remove
sequences c1000 bp in size.
4 to there
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Institute for Molecular and Cellular Regulation, Gunma University 339-15 Showa-machi, Maebashi Gunma 371, Japan Tel: 272-20-8856 Fax: 272-20-8856
                                                                                                                                                                      D82177 330 bp mRNA EST 09-FEB-1996
HUMHBC4504 Human pancreatic islet Homo sapiens cDNA similar to
D82177
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 330)
Takeda,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human pancreatic islet ESTs
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:785191.
Contact: Jun Takeda
                                            1 LysalaGlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15 || || || :::|||::::|||||||||| 218 AAGAAGAAGAACAAGAATCTTAAAATAGTTTTGAGGTAT 174
Align seg 1/1 to reverse of: AQ033523 from: 1 to: 410
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Gaps: 0
Percent Identity: 90.909
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/db_xref="taxon:9606"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: D82177 from: 1
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4.400
90.909
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US-08-653-294-33 x D82177
                                                                                                                                                                                     seq_documentation_block:
Locus D82177
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 8, 2000, 04:05:44; Search time 133.56 Seconds (without alignments) 1.773 Million cell updates/sec Run on:

US-08-653-294-34 51 1 RESLRNLRGY 10

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

A_Geneseq_36:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

Description	e fra	LA-B7	T-cell modulating	Peptide B7.75-84 t	Peptide B7.75-84 t	HLA-B7 CTL modulat	34-	Peptide B7.84-75/7	Peptide B7.84-75/7	Peptide fragment o	HEALT SONG THE	G	٠.	Dentide fragment	HLA-BW46 CTL modul	HLA-Bw46.60-84. Co	HLA-C exon Cb-1. H		Breast cancer asso	Consensus sednence	T-cell modulating		HLA-alpha-1. Use o	nenc	SABP encoded by pC	Tobacco salicylic	Avenacinase-like p	. thermophil	ō	<u>ა</u>	HΙΛ	ப	Glucoamylase from
SUMMARIES	R41209	R83061	W07515	W33786	W33796	R92913	R95415	W33790	W33797	R41207	NO.07.3	1040H	R32413	R41204	R83072	R95418	R12465	R12466	Y07033	P80911	W07518	R44112	R71629	R47268	R74305	W04316	R85199	W57445	W05178	W90345	R42577	R11329	R77674
th DB	:							20 1					3 0	1 1			99	99	99	74				68	80	68	8	20	ဓ္က	10	م		24 1
% Query e Match Length	100.0	100.0	100.0	100.0	100.0	100.0	100.0	51 100.0	100.0	100.0	0.00		100.0		86.3	86.3	86.3 3	86.3 3	86.3 3	80.4	72.5	9.89	9.89	68.6	68.6	68.6	64.7 7	64.7 8	64.7 11	64.7 12	62.7	62.7 4	62.7 6
Result No. Score								8							* *	4	4	4	4	4	m	m	m	m .	m	m	m	m	m	m	m	m	m

Mouse frizzled-8 p Type I interferon	Varicella-zoster v Lipoxygenase, Prod	Rice lipoxygenase. Varicella-zoster v	Peptide fragment o T-cell modulating	ZAP-70 N-terminal	Cdil polypeptide. Banana bunchy top
W31274 R04907	P70347 R20670	R23797 R22615	R41211 W07521	W30133	R54922 W54071
пп	<del></del>	~ ~		۳,	<b>⊣</b>
685	854 865	865 868	22	93	212
62.7	62.7 62.7	62.7	60.8 60.8	8.09	8.09 80.8
32	32 32	3 32	31	31	31
3 3 3 3	37 38	4 0 0	41	43	4 4 5

## ALIGNMENTS

RESULT 1 R41209 standard; peptide; 10 AA.  AC R41209  ID R41209  ID R41209,  AC R41209,  DE Peptide fragment of Class I HLA peptide.  Peptide fragment of Class I HLA peptide.  Be prassitic disease; cytotoxic T lymphocyte; modulation, neoplasia; W parasitic disease; cytotoxic T lymphocyte; modulation.  Synthetic.  W09317699-A.  PD 16-SEP-1993; UG-844716.  PR 02-MAR-1992; UG-844716.  PR 03-MAR-1992; UG-844716.  PR 04-MAR-1992; UG-844716.  PR 04-MAR-1992; UG-844716.  PR 04-MAR-1992; UG-844716.  PR 05-MAR-1992; UG-844716.  PR 06-MAR-1992; UG-844716.  PR 07-MAR-1992; UG-844716.  PR 07-MAR-1992; UG-844716.  PR 07-MAR-1992; UG-844716.  PR 07-MAR-1992; UG-847716.  PR 07-MAR-1992; UG-97-MAR-198716.  PR 07-MAR	Juery Match dest Local Sim datches 10; datches 10; l RESLRN l RESLRN R83061 stan R83061; I-MAY-1996 HLA-B7 CTL Cytotoxic T Immunosuppr class I MHC Synthetic. Synthet
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rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treatment of auto-immune disease by admin. of peptide(s) corresp. to major histocompatibility complex antigens - esp. for delaying onset of clinical symptoms of insulin dependent diabetes by modulating T cell madiated attack on target cells

Claim 7: Page 20; 24pp; English.

W07512-W07518 represent T-cell modulating peptides that can be used in the method of the invention. These sequences are based on a portion of the major histocompatability complex (MHC) class I antigen (see for the major histocompatability complex (MHC) class I antigen (see involving T-cell mediated destruction of tissue in mammals. These involving T-cell mediated destruction of tissue in mammals. These peptides are used especially to treat insulin-dependent diabetes mellitus, preferably being administered during the pre-clinical stage to delay onset of the disease. Other diseases that can be treated are multiple sclerosis, rheumatoid arthritis, psoriasis, pemphigus vulgaris, sjourist, etc. The peptides modulate T-cell mediated attack on autologous target cells, and may also reduce inflammation, swelling, and release of
                                              Claim 13; Page 66; 80pp; English.

This sequence represents a fragment of a class I major histocompatibility complex (MHC) antigen. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HLA-B7. This sequence, and the peptide fragments represented by R83062-R83085, R83090-R83096 and P82907-R82913 can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of period of time (compared to the lifetime administration for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
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T-cell modulating peptide #4.
T-cell modulator; autoimmune disease; tissue destruction; alphal-domain;
T-cell modulator; autoimmune disease; tissue destruction; alphal-domain;
mammal; major histocompatability complex; MHC class I; antigen; perforin;
insulin-dependent diabetes mellitus; multiple sclerosis; inflammation;
rheumatoid arthritis; psoriasis; pemphigus vulgaris; Sjogren's disease;
thyroid disease; Hashimoto's thyroiditis; myasthenia gravis; granzyme;
autologous target cell; cytokine release; T cell activation; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          target cells, and may also reduce inflammation, swelling, and release of cytokines, perforins, granzymes etc. associated with T cell activation. Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
- using Class I B75-84 MHC antigen of the recipient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 51; DB 1; Length 10; 100.0%; Pred. No. 0.00074; ive 0; Mismatches 0; Indels
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05-ART-1996; U04710.
12-MAY-1995; US-440504.
(SANG-) SANGSTAT MEDICAL CORP.
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Best Local Similarity 100.
Matches 10; Conservative
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donor hosts
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Gaps
                                                                                     19-JUN-1998 (first entry)
Peptide Br.75-84 tested for immunomodulating activity.
Immunomodulating dimer: immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUN-1998 (first entry)
Peptide B7.75-84 tested for immunomodulating activity.
Immunomodulating dimer; immusouppressant drug; CTL activation; transplantation; autochmune disease; Class I HIA-B alpha-1 domain;
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                                                                                                                                                                                                                24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-653294.
LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                         Beulow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
                                                               W33786 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W33796 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
                                                                                                                                                                                      27-NOV-1997.
22-MAY-1997; U08689
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1 RESLRNLRGY 10
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WO9744351-Al.
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22-MAY-1997; U
24-MAY-1996; U
(STRD ) UNIV I
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WO9744351-A1.
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Gaps

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1 RESLRNLRGY 10

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Beulow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.

New immunomodulating dimer peptide(s) - based on a class I HLA-B man immunomodulating dimer peptide(s) - based on a class I HLA-B relating autoimmune diseases
Example 1; Page 19; 41pp; English.

Example 2; 41pp; English.

Example 1; Page 19; 41pp; English.

Example 2; 41pp; English.

Example 3; 41pp; English.

Example 2; 41pp; English.

Example 2; 41pp; English.

Example 3; 41pp; English.

Example 3; 41pp; English.

Example 4; 41pp; English.

Example 4; 41pp; English.

Example 5; 41pp; English.

Example 6; 41pp; 41pp;
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R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B7. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (comparate to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CLLs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAY 1996 (first entry)
HLA-B7 CTL modulating peptide (B7.84-75/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B7.
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12-OCT 1995.
05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R92913 standard; peptide; 20 AA.
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HIA-B7.84-75-84 Palindrome.
HIA-B7.84-75-84 Palindrome.
HIA-B7.84-75-84 Palindrome.
HIA-P74: alphal-hellx; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
                                                    Gaps
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Peptide B7.84-75/75-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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                                                Indels
Pred. No. 0.0015; Mismatches 0;
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(STRD ) UNIV LELAND STANFORD JUNIOR.
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R95415;
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Conservative 0
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       Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserv
                                                                                                                    1 RESLRNLRGY 10
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WPI; 95-194027/25.
                                                                                                                                                             11 RESLRNLRGY
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WO9744351-Al
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12-OCT-1995.
05-APR-1995; U04349.
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16-MAY-1996
                                                                                                                                                            Sequence
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WHI: 98'08030JUGE.

PUT Immunomodulating dimer peptide(s) - based on a Class I HIA-B
alpha-1 domain, used for preventing rejection of transplants or
treating autoimmune diseases.

Frample 1: Page 19: 41pp: English.

Example 1: Page 19: 41pp: English.

Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
activity. A peptide-type compound or variant is claimed which has
climmunomodulating activity, including the N-terminal acjated and/or
immunomodulating activity, including the N-terminal acjated and/or
c-terminal amidated or esterified forms of up to 60 amino acids, where
the peptide-type compound comprises the formula; A-B, where A, B =

C-terminal amidated or esterified forms of up to 60 amino acids, where
the peptide-type compound comprises the formula; A-B, where A, B =

C-terminal amidated or esterified forms of up a81-a hydrophobic or
and any peptide type bond within the brackets. The compounds comprise
acid. The sequences related to a Class I HiA-B alphal domain (positions)
acid. They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
undesirably attacking cells in a host or in vitro. They can also be
used in combination with antigenic peptides or proteins of interest to
activate CTLs. They can also inhibit the proliferation of T cells in
response to anti-CD3. The peptide can be used for preventing rejection
of transplants or for treating autoimmune diseases, e.g. diabetes,
cused for detection and diagnosis. The products can also be
conserved.
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New immunomodulating dimer peptide(s) - based on a class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases

Example 1; Page 19; 41pp; English.

Example 1; Page 19; 41pp; English.

Peptides W33784-98 and W33778-9 were assayed for their immunomodulating activity, including the N-terminal acylated and/or C-terminal acylated and/or C-terminal acylated and/or C-terminal anidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B - (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 - E or V; aa77 - D, S or N; aa79 - R or G, aa80 - I or N; aa81- a hydrophobic or small amino acid; aa82 - R or L; aa83 - G or R; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W33797;
9-JUN-1998 (first entry)
Peptide B7.84-75/75-84 fested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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            22-MX-1997; U08689.
24-MX-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Bellow R. Clayberger C. Krensky AM:
WPI; 98-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 NOV-1997.
22-MAY-1997. U08689.
42-MAY-1995. US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beulow R, Clayberger C, Krensky AM; WPI; 98-086530/08.
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Matches 10; Conservative
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WO9744351-A1.
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Cytocoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immnosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-Bw62.
    (positions
amino acid sequences related to a class I HLA-B alphal domain (position 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of I cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autolimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. The products can also be
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Peptide fragment of Class I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic T lymphocyte; modulation.
Synthetic.
W09317699-A.
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                                                                                                                                                                                                                                                                                                                                                                                     used for detection and diagnosis.
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity
Matches 10; Conservat
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                                                                                  Similarity
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WPI; 95-194027/25
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                                                                                  Best Local Sin
Matches 10;
                                             Query Match
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                                                                                                                                                                                                                                                                  Example 13; Page 32; 80pp; English.
R83061-R83085, R83090-R83096 and R92207-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HIA-BW62. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched domor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLA-B7.60-64.
HL
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                                                                                                                                                       Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                             Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R95431 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R95431;
12-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clayberger C, Krensky AM;
WPI; 95-194027/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-NOV-1994; U12985
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16 RESLRNLRGY 25
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Matches
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R95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigans. This sequence represents the human-leucocyte-associated antigans. This sequence represents the HLA-Bw62.60-84. These sequences can be used to isolate the protein p74 cross reactive with the heat shock protein p74 is associated with T-cell activation in mammalian T-cells, and is also membrane protein exclusion associated with T-cell activation in mammalian T-cells, and is also membrane protein exclusion associated with T-cells p74 can be isolated by lysis of a suitable cell with an amphoreric detergent, and then passed through an affinity column containing a compressing the extracellular fragment of p74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits compounds can be screened for their effect on the cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of compounds the amount of binding between the candidate composition containing the amount of binding between the candidate composition containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, induce containing the p74 indand composition of with p74 for the binding of the p74 ligand.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         his base, co.co.
The p74: p74: p74: p74: p74: heal below protein; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Compsns. comprising lymphoid surface membrane proteins - which may hiblbit cytolytic activity and differentiation of CTLs. Example: Page 9: 29pp; English. R95413, and R95415-R95431 represent palindromes and fragments of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human leukocyte antigen; probe; major histocompatibility complex; MHC; class I.
Homo sapiens.
J03112486-A.
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100.0%; Score 51; DB 1; Length 25;
.larity 100.0%; Pred. No. 0.0019;
Conservative 0; Mismatches 0; Indels
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10-000-1994; U12985.
10-000-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytolysis; antigen presenting cell. Synthetic.
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R95419;
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Best Local Similarity 100.
Matches 10; Conservative
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us-08-653-294-34.rag

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mew peptide(s) based on class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets claim 9; Rage 53; 61pp; Engilsh.

Claim 9; Rage 53; 61pp; Engilsh.

The peptide (or a fragment of at least 10 amino acids, joined at at least one terminus to a sequence other than that of wild type HLA antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which beind to it and removing subsets of CTLs from a T-cell composition.
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                           W-PSDB; 012115.

HLA-B35 gene - used in DNA probe and transformant cells for immunising animals, for developing monoclonal antibody.

Claim 1; Page 1; Hpp; Japanesse.

Probes comprising part of the sequence encoding this sequence can be used to identify class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HLA-B35 antigen. See also J03112485 and J03112487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-1994 (first entry)
Peptide fragment of Class I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
parassitic disease; cytotoxic T lymphocyte; modulation.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-1993; U01758.
02-MAR-1992; US-844716.
(STRD) UNIV LELAND STANFORD JUNIOR.
Clayberger CA, Krensky AM;
WPI; 93-303134/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R41206 standard; peptide; 25 AA
                                     22-SEP-1989; JP-247697.
(OLYU ) OLYMPUS OPTICAL KK.
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Best Local Similarity 90.0
Matches 9; Conservative
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22-SEP-1989; JP-247
                                                                               WPI; 91-182991/25.
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R41206
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Search completed: February 8, 2000, 04:05:44 Job time: 9361 sec

1 RESLRNLRGY 10 

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Gaps

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Wed Feb

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 7, 2000, 18:04:41; Search time 111.22 Seconds (without alignments) 4.241 Million cell updates/sec Run on:

US-08-653-294-34 51 1 RESLRNLRGY 10 score: Title: Perfect so Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

142080 segs, 47169319 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

PIR_62:* Database :

pir1:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	class I	н	н	H	cell sur	MHC class I histoc	•	<b>D</b>	cell surface antig	O	MHC class I lympho	MHC HLA B71 - huma	н	Н	н	•	I his	ist	MHC class I histoc	н	class I	lass I	ss I hist	class	н	н	MHC class I histoc	MHC HLA-B8 chain -		lymphocyte antigen
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HLA-B*5501 - human HLA-B*5602 - human HLA-B*5601 - human MHC class I histoc HLA-B alpha chain lymphocyte antigen HLA-B*401 - human MHC class I protei HLA-B*401 - human MHC class I protei HLA-B*401 - human MHC HLA-B*401 - human MHC HLA-B*401 - HLA
172752 172753 172754 138437 138437 154505 156130 156149 159655 159655 161865 161865
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000000000000000000000000000000000000000

## ALIGNMENTS

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Grossion: 138875
R:Garber, T.L.: Butler, L.M.: Trachtenberg, E.A.: Erlich, H.A.: Rickards, O.; De Stef
R:Garber, T.L.: Butler, L.M.: Trachtenberg, E.A.: Erlich, H.A.: Rickards, O.; De Stef
Immunogenetics 42, 19-27, 1995
A:Title: H.A.B alleles of the Cayapa of Ecuador: new B39 and B15 alleles.
A:Reference number: 138860; MUID:95317819
A:Reference number: 138876
A:Return: preliminary; translated from GB/EMBL/DDBJ
A:Return: preliminary;
A:Molecule type: DNA
A:Resolutes: L-137 < RES
A:Resolutes: Resolutes: Resolutes: L-137 < RES
A:Resolutes: Resolutes: Re
MHC class I antigen - human (fragment)
C;Species: Homo saplens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
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ö Gaps ö 100.0%; Score 51; DB 2; Length 13 100.0%; Pred. No. 0.0045; ive 0; Mismatches 0; Indels Query Match Best Local Similarity 100.0 Matches 10; Conservative

1 RESLRNLRGY 10 40 RESLRNLRGY 49 ò 셤

MHC class I antigen - human (fragment)

C; Species: Homo sapiens (man) (1590m.)
C; Species: Homo sapiens (man) (1590m.)
C; Date: (07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999 C; Date: (07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999 C; Accession: I3886 Esquence_revision 07-Jun-1996 #text_change 23-Jul-1999 C; Accession: I38876 Esquence number: 13886; MUID:95317819 A; Reference number: 138876 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Molecule

Gaps ö Query Match 100.0%; Score 51; DB 2; Length 137; Best Local Similarity 100.0%; Pred. No. 0.0045; Matches 10; Conservative 0; Mismatches 0; Indels

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1 RESLRNLRGY 10 40 RESLRNLRGY 49 ò a

The state of the state of the state of

Gaps

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Length 181;

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Cipate: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change properties 30, 200-207, 1989
A;Mucller, C.A.; Engler-Blum, G.; Gekeler, V.; Stelert, I.; Weiss, E.; Schmidt, H.
A;Recence number: 154463; MuID: 89379286
A;Accession: 168774
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-274 <RES
A;Cross-references: GB:M29865; NID:q187676; PIDN:AAA36223.1; PID:q187677
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein A; Residues: 1.270 < LCD> C; Comment: Comparison of a number of class I allelic sequences (-B40 vs. -B7 and -A2 C; Comment: Comparison of a number of class I allelic sequences (-B40 vs. -B7 and -A2 y restricted to the alpha-1 and alpha-2 domains. The most conspicuous clustering of vossible alloantigenic determinants of these antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GDB:120048; OMIM:142830
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: duplication: glycoprotein; heterodimer; membrane protein; transplantation
F;1-90/Domain: alpha-1 <EXI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIC class I histocompatibility antigen HLA-B40 alpha chain - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 28 Aug-1985: #sequence_revision 28-Aug-1985 #text_change 02-Sep-1997
C;Accession: A01186: Rsequence_revision 28-Aug-1985 #text_change 02-Sep-1997
C;Accession: A01186: Rsioper de Castro, J.A.; Bragado, R.; Strong, D.M.; Strominger, J.L.
Biochemistry 22, 3961-3969, 1983
A;Tille: Primary structure of papain-solubilized human histocompatibility antigen HLA
A;Tille: Primary Structure of papain-solubilized human histocompatibility antigen HLA
A;Reference number: A02186; MOID:84000412
A;Map position: 6p21.3-6p21.3
A;Introns: 90/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: glycoprotein
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F:86/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:101-163,202-258/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                Query Match 100.0%; Score 51; DB 2; Length 18
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 10; Conservative 0; Mismatches 0; Indels
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Pred. No. 0.0095;
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100.0%;
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Best Local Similarity
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74 RESLRNLRGY
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                                                                                                                        MHC class I antigen - human (fragment)
C;Species: Homo sapiens (man)
C;Species: T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stefanc R;Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stefanc A;Title: HLA-B alleles of the Cayapa of Ecuador: new B39 and B15 alleles.
A;Reference number: I38860: MUID:95317819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stefand Immunogenetics 42, 19-27, 1995
Tritle: HIA-B alleles of the Cayapa of Ecuador: new B39 and B15 alleles.
A;Reference number: I38860; MUID:95317819
A;Accession: I38874
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C; Species: Homo sapiens (man)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C; Accession: 159189
R; Bronson, S; K.; Pel, J.; Taillon-Miller, P.; Chorney, M.J.; Geraghty, D.E.; Chaplin, D. Proc. Natl. Acad. Sci. U.S.A. 88, 1676-1680, 1991
Proc. Natl. Acad. Sci. U.S.A. 88, 1676-1680, 1991
A; Title: Isolation and characterization of yeast artificial chromosome clones linking the A; Reference number: 159188; MUD:91156671
A; Reference number: IS9188; MUD:91156671
A; A; Resion: IS9188
A; Resion: IS9188
A; Resions: Preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-181 <RES>
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;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
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A;Status: prelininary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Mosidues: 1-137 < RES.
A;Essidues: 1-137 < RES.
A;Cross-references: EMBL:U14756; NID:9930328; PIDN:AAC50171.1; PID:9930329
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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A; Molecule type: DNA
A; Molecule type: DNA
A; Mosidues: 1-137 < RES.
A; Cross-references: EMBL:U15638; NID:9930330; PIDN:AAA74045.1; PID:9930331
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
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C;Genetics:
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A;Gross_references: GDB:120048; OMIM:142830
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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C;Date: 07-Jun-1996
C;Accession: I38874
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Length 274;

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C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C;Accession: 168747
R;Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.
Immunogenetics 29, 297-307, 1989
A;Title: Allelic variation in HiA-B and HiA-C sequences and the evolution of the HiA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 02-7ul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C;Accession: 154308
R;Rodriguez, S.G.; Johnson, A.H.; Hurley, C.K.
Hum. Immunol. 37, 192-194, 1993
A;Title: Molecular characterization of HLA-B71 from an African American individual.
A;Reference number: 154308; MUID:94064392
  02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                 A;Residues: 1.308 <RES>
A;Cross-references: GB:M24044; NID:g176812; PIDN:AAA35423.1; PID:g176813
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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100.0%; Pred. No. 0.012;
Mismatches 0; Indels
                       C; Accession: 136956
R; Parhlam, P., Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
J. Immunol. 142, 3937-3950, 1989
A; Title: Diversity and diversification of HLA-A,B,C alleles. A; Reference number: 136956; MUID:89235215
A; Accession: 136956; Augusted from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
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A;Accession: 168747
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-350 < RES>
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168747
MHC class I lymphocyte antigen - human (fragment)
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MHC HLA B71 - human (fragment)
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserv
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R;Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garbe Nature 357, 329-333, 1992
Nature 357, 329-333, 1992
Nature 357, Number HLA-B alleles in a tribe of South American Amerindians indicate A;Reference number: S24027; MUID:92269956
A;Accession: S24439
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R; Annor, D.; Lillie, J.W.; Auffray, C.; Kappes, D.; Strominger, J.L.
Immunogenetics 20, 237-252, 1984

A; Title: Inter-locus and intra-allelic polymorphisms of HLA class I antigen gene mRNA.

A; Reference number: 154412; MUID:84287690

A; Recession: 168701

A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                           class I histocompatibility antigen HLA-B-3901 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 07-Nov-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
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A:Rosidues: 1-300 <RES>
A:Rosidues: 1-300 <RES>
A:Cross-references: GB:M27540; NID:g187733; PIDN:AAA59638.1; PID:g386890
A:Cross-references: GB:M27540; NID:g187733; PIDN:AAA59638.1; PID:g386890
A:Cross-references: GB:M27540; NID:g187733; PIDN:AAA59638.1; PID:g386890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Superfamily: Class I histocompatibility antigen; immunoglobulin homology C.Sepwords: glycoprotein F:1-74/Product: class I histocompatibility antigen HIA-B-3901 #status precipity: 1-90/Domain: alpha-1 #status predicted <EXI>F:1-90/Domain: alpha-2 #status predicted <EXI>F:91-182/Domain: alpha-2 #status predicted <EXI>F:96-261/Domain: alpha-2 #status predicted <EXI>F:96-561/Domain: immunoglobulin homology <IMM>F:96/Psinding site: carbohydrate (Asn) (covalent) #status predicted F:101-164,203-259/Disulfide bonds: #status predicted
  Gaps
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100.0%; Pred. No. 0.0095;
ive 0; Mismatches 0;
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C;Species: Pan troglodytes (chimpanzee)
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 10; Conservative
  Conservative
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                                                                                    FESTRNINGY 84
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A; Residues: 1-274 <WAT>
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                                                    1 RESLRNLRGY
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10;
Matches
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class I histocompatibility antigen HLA-B-4801 precursor - human (fragment)
C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Species: 22-NOv-1993 #sequence_revision 18-Jul-1997 #text_change 07-Nov-1997
C;Accession: S24438
R;Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Ga Nature 357, 329-333, 1992
A;Title: New recombinant HLA-B alleles in a tribe of South American Amerindians indic A;Reference number: S24027; MUID:92269956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene: HLA-B-4801
Superfamily: class I histocompatibility antigen; immunoglobulin homology
Keywords: glycoprotein; transmembrane protein
1.17/Domain: signal sequence #status predicted <SIG>
1.17/Domain: signal sequence #status predicted <SIG>
1.7-354/Product: class I histocompatibility antigen HLA-B-4801 #status predicted <WA
1.107-199/Domain: alpha-2 #status predicted <EXI>
1.107-198/Domain: alpha-2 #status predicted <EXI>
1.212-277/Domain: immunoglobulin homology <IMM>
                                                                                          Gaps
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7:324-354/Domain: intracellular #status predicted <INNT>
F;102/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;117-180,219-275/Disulfide bonds: #status predicted
                       Score 51; DB 2; Length 354;
Pred. No. 0.012;
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Pred. No. 0.012;
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Job time: 22207 sec
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Matches 10; Conserv
                                                                                                                                                      1 RESLRNLRGY 10
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Residues: 1-354 <WAT>
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Best Local Similarity
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R;Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garbe
Rswatkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garbe
Rsture 357, 329-333, 1992
A;Title: Sow recombinant HLA-B alleles in a tribe of South American Amerindians indicate
A;Reference number: S24027; MUID:92269956
A;Accession: S24436
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C. Keywords: glycoprotein; transmembrane protein
C. Keywords: glycoprotein; transmembrane protein
F.1-17/Domain: slyani sequence #status predicted <SIG>
F.17-299/Domain: slyani sequence #status predicted <EXT>
F.17-299/Domain: alpha-2 #status predicted <EXT>
F.107-198/Domain: alpha-2 #status predicted <EXT>
F.207-277/Domain: alpha-2 #status predicted <IMM>
F.307-353/Domain: immunoglobulin homology <IMM>
F.307-353/Domain: intransmembrane #status predicted <IMM>
F.307-354/Domain: intracellular #status predicted <INT>
F.102/Binding site: carbohydrate (Asn) (covalent) #status predicted
F.117-180,219-275/Disulfide bonds: #status predicted
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R;Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garbe Mature 357, 329-333, 1992
A;Title: New recombinant HLA-B alleles in a tribe of South American Amerindians indicate A;Reference number: S24027; MUID:92269956
A;Accession: S24437
A;Accession: S24443
A;Molcule type: mRNA
A;Residues: 1-354 <WAIP>
C;Genetics:
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C. Keywords: glycoprotein; transmembrane protein
C. Keywords: glycoprotein; transmembrane protein
F.1-17/Domain: signal sequence #status predicted <SIG>
F.17-294/Product: class I histocompatibility antigen HIA-B-4802 #status predicted
F.17-299/Domain: extracellular #status predicted <EXI>
F.107-199/Domain: alpha-2 #status predicted <EXI>
F.212-277/Domain: alpha-2 #status predicted <IMM>
F.300-323/Domain: immunoglobulin homology <IMM>
F.300-323/Domain: intransmembrane #status predicted <IMM>
F.301-247/Domain: intransmembrane #status predicted <INM>
F.301-25/Domain: status predicted <INM>
F.302-35/Domain: status predicted
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C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 18-Jul-1997 #text_change 07-Nov-1997
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C;Date: 22-Nov-1993 #sequence_revision 18-Jul-1997 #text_change 07-Nov-1997
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                                                            Indels
. 0.012;
                          Pred. No. 0.0
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A; Residues: 1-354 <WAT>
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STANDARD;
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182
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202
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270 AA;
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Best Local Similarity
Matches 10; Conserv
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1B24_HUMAN
1D 1B24_HUMAN
AC P30470;
DT 01-APR-1993 (CD 01-APR-1999 (CD 07 15-201-999) (CD 07 15-201-999) (CD 07 15-201-1999) (CD 07 15-20
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SEQUENCE
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P30470 homo sapien
P16210 pan troglod
P01889 homo sapien
P30460 homo sapien
P30463 homo sapien
P30464 homo sapien
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4.352 Million cell updates/sec
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                                                                                        ; Search time 68.63 Seconds
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P30483
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             4.5
Compugen Ltd
                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                  82229 seqs, 29864866 residues
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            GenCore version
Copyright (c) 1993 - 2000
                                                                                      February 8, 2000, 01:26:01
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1810_HUMAN
1811_HUMAN
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1B02_HUMAN
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1B21_HUMAN
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1B32_HUMAN
1B34_HUMAN
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1846_HUMAN
1848_HUMAN
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1B24_HUMAN
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1B04_HUMAN
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1856_HUMAN
1857_HUMAN
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Listing first 45 summaries
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1B26_HUMAN
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    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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51
1 RESLRNLRGY 10
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Maximum DB seq length: 1000000
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Perfect score:
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Created) Last sequence update) Last annotation update)

354 AA

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            LAWLOR D.A., WARREN E., WARD F.E., PARHAM P.; "Comparison of class I MHC alleles in humans and apes."; Immunol. Rev. 113:147-188(1991).
-I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                              THE IMMUNE SYSTEM.
-1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_1; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                             EMBL; M30679; AAA87971.1; -.
                                                                                                                                                                                                                                     PS00290; IG_MHC; 1.
 MEDLINE; 90201944
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PROSITE; PS002
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P01889;
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B-35 B*3504 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-5 ALPHA CHAIN PRECURSOR.
Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                    -:- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-:- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3504 ALPHA CHAIN
PRECURSOR (FRAGMENT).
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                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                     SEQUENCE FROM N.A.
MEDLINE; 92269956.
WATKINS D.I., MCADAM S.N., LIU X., STANG C.R., MILFORD E.L.,
LEVINE C.G., GARBER T.L., DOGON A.L., LORD C.I., GHIM S.H.,
TROUP G.M., HUGHES A.L., LETVIN N.L.;
"New recombinant HLA-B alleles in a tribe of South American
                                                                                                                                                            Amerindians indicate rapid evolution of MHC class I loci."; Nature 357:329-333(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 354;
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EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 6564795A CRC32;
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                                        Homo sapiens (Human)
                                                                                                                                                                                                                          MICROGLOBULIN).
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354 AA;
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Best Local Similarity
Matches 10; Conserv
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                           HLA-B OR HLAB.
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P16210;
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CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,

A-5 ALPHA CHAIN. EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3. CONNECTING PEPTIDE

CYTOPLASMIC TAIL.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
"Rapid cloning of HLA-A,B cDNb by using the polymerase chain
reaction: frequency and nature of errors produced in amplification.";
Proc. Natl. Acad. Sci. 0.5.A. 87:2833-2837(1990).
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARHAM P., BENJAMIN R.J., CHEN B.P., CLAYBERGER C., ENNIS P.D., KRENSKY A.M., LAWLOR D.A., LITTMAN D.R., NORMENT A.M., ORR H.T., SALTER R.D., ZEMMOUR J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-02-1996 (Rel. 34, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-7 B*0702 ALPHA CHAIN
PRECURSOR (B7.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                            Query Match 100.0%; Score 51; DB 1; Length 362; Best Local Similarity 100.0%; Pred. No. 0.0066; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                97E6CE8A CRC32;
BY SIMILARITY.
BY SIMILARITY.
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362 AA.

PRT;

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                                                                                                                                                                                                                                                                                         "Nucleotide sequences of chimpanzee MHC class I alleles: evidence for trans-species mode of evolution.";
EMBO J. 7:2765-2774(1988).
                                                                                            01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-2 ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                             Submitted (FEB-1989) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                              Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                              MEDLINE; 89030641.
MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G.,
                                                                                                                                                                                                                                                                                                                                                                                                                              THE IMMUNE SYSTEM.
-1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I: 1.
MHC I; Transmembrane; Glycoprotein; Signal.
SIGNAL
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HSSP; P30685; 1A1N.
PROSITE; PS00290; IG_MHC; 1.
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Best Local Similarity 100.
Matches 10; Conservative
                                                                  STANDARD;
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362 AA;
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                                                                1802_PANTR
P13751;
01-JAN-1990 (
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                                                                              MEDLINE; 85287366.
SOOD A.K., PAN J., BIRO P.A., PEREIRA D., SRIVASTAVA R., REDDY V.B.,
DUCEMAN B.W., WEISSMAN S.M.;
"Structure and polymorphism of class I MHC antigen mRNA.";
Immunogenetics 22:101-121(1985).
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B-7 B*0702 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                        ORR H.T., LOPEZ DE CASTRO J.A., LANCET D., STROMINGER J.L.;
"Complete amino acid sequence of a papain-solubilized human
histocompatibility antigen, HLA-B7. 2. Sequence determination and
search for homologies."
Biochemistry 18:5711-5720(1979).
"Diversity of class I HLA molecules: functional and evolutionary interactions with T cells."; Cold Spring Harb. Symp. Quant. Biol. 54:529-543(1989).
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                                                                                                                                                                                                                                                                                                                                                                         THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 100.0%; Score 51; DB 1; Length 362; I Similarity 100.0%; Pred. No. 0.0066; 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                             SEQUENCE FROM N.A. ELLEXSON M.E., ZHANG L., HILDEBRAND W.H.; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AALA -> GPW (IN REF. 3).

Q -> E (IN REF. 5).

W -> S (IN REF. 3).

R -> G (IN REF. 3).

GL -> RP (IN REF. 3).
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EMBL; M16102; AAA59622.1; ALT_SEQ.
EMBL; U29057; AAA91229.1; -.
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PIR; B35997; B35997.
HSSP; P30460; 1AGB.
MIM; 142830; --
PROSITE; PS00290; IG_MHC; 1.
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Best Local Similarity
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MEDLINE; 80088278.
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                            Gaps
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         Length 362;
100.0%; Score 51; DB 1; Length 36
100.0%; Pred. No. 0.0066;
Vienatches 0; Indels
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                                                                                                                PRT;
                                                                                                                STANDARD;
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P30460;
                                                                                             RESULT 6
1B04_HUMAN
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1 RESLRNLRGY 10

CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-2 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.

BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 4BF65A6C CRC32; CYTOPLASMIC TAIL.

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01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-65(B-14) B*1402 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-14 B*1401 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                       MEDLINE; 89235215.
PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
Diptersity and diversification of HLA-A,B,C alleles.";
J. Immunol. 142:3937-3950(1989).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                               01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-14 B*1401 ALPHA CHAIN
                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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1. SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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362 AA.
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PFAM; PF00047; 19: 1.
PFAM; PF00129; MHC_I: 1.
MHC I; Transmembrane; Glycoprotein; Signal.
SIGNAL
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AC 930463;
DT 01-APR-1993
DT 01-APR-1993
DE HLA CLASS I
DE PRECURSOR.
GN HLA-B OR HLA
OC EUKAIYOLA; M
1B07_HUMAN
P30462;
01-APR-1993 (
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-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO FIE IMMUNE SYSTEM.
-!- SUBBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-8 B*0801 ALPHA CHAIN
PRECURSOR.
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                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE; 89235215.
PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
"Diversity and diversification of HLA-A,B,C alleles.";
J. Immunol. 142:3937-3950(1989).
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B-8 B*0801 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
CXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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PDB; 1AGB; 16-JUN-97.
PDB; 1AGC; 16-JUN-97.
PDB; 1AGC; 16-JUN-97.
PDB; 1AGE; 16-JUN-97.
PDB; 1AGE; 16-JUN-97.
PDB; 1AGE; 16-JUN-97.
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PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-75(B-15) B*1502 ALPHA CHAIN
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"The HLA-BACK subtype of B15: molecular characterization and comparison with crossreating antigens.";
Tissue Antigens 38:186-190(1991).
                                                                                                                                                                                                                                                                                                                              DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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                                                                                                                                          PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.; "Diversity and diversification of HLA-A,B,C alleles."; J. Immunol. 142:3937-3950(1989).
Sutheria; Primates; Catarrhini; Hominidae; Homo.
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MIM: 142830; -
PROSTTE; PS00290; 1G_MHC; 1.
PFAM: PF00047; 1g; 1.
PFAM; PF00129; MHC_I; 1.
MHC I: Transmembrane; Glycoprotein; Signal.
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ID 1B10_HUMAN STANDARD;
AC P30464;
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MEDLINE; 89235215.
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MEDLINE; 93056508.
MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
LITLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
MARTELL R.W., DU TOIT E.D., PARHAM P.;
"Distinctive HiA-A,B antigens of black populations formed by
interallelic conversion.";
MEDLINE, 96369309.

LIN L., TOKUNAGA K., TANAKA H., NAKAJIMA F., IMANISHI T.,

LIN L., TOKUNAGA K., TANAKA H., NAKAJIMA F., IMANISHI T.,

LIN L., TOKUNAGA K.,

SHIBATA Y., JUJI T.,

"Further molecular diversity in the HLA-B15 group.";

"Further molecular diversity in the HLA-B15 group.";

"Issue Antigens 47:265-274(1996).

-I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMONE SYSTEM.

THE IMMONE SYSTEM.

-I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-72(BW-70) B*1503 ALPHA
HLA-B OR HLAB.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
i) 8CF9BCDO CRC32;
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EMBL; D50293; BAA08824.1; -.
HSSP; P30685; IAIN.
MIM; 142830; -.
PROSITE; P500290; IG_MRC; 1.
PFAM; PF00147; 14; 1.
MRC I; Transmembrane; Glycoprotein; Signal.
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125
227
362 AA;
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Best Local Similarity
Matches 10; Conserv
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FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
                   THE IMMUNE SYSTEM
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P30466;
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TRANSMEM
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1B13_HUMAN
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                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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   J. Immunol. 149:3411-3415(1992).
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-62 B*1504 ALPHA CHAIN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDILINE; 92569956.
WATKINS D.I., MCADAM S.N., LIU X., STANG C.R., MILFORD E.L.,
LEVINE C.G., GAREBER T.L., DOGON A.L., LORD C.I., GHIM S.H.,
TROUP G.M., HUGHES A.L., LETVIN N.L.;
"New recombinant HIA-B alleles in a tribe of South American
Amerindians indicate rapid evolution of MHC class I loci.";
Nature 357:329-333(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 51; DB 1; Length 362; Best Local Similarity 100.0%; Pred. No. 0.0066; Matches 10; Conservative 0; Mismatches 0; Indels
                                                          -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAMOS M., BARBER D.F., LAYRISSE 2., DE CASTRO J.A.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99D70546 CRC32;
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BY SIMILARITY.
BY SIMILARITY.
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                                       THE IMMUNE SYSTEM
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334
110
125
227
362 AA;
                                                                              MICROGLOBULIN).
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HLA-B OR HLAB.
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ID 1812_HUMAN
AC P30513;
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TRANSMEM
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CARBOHYD
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                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Jubersity and diversification of HLA-A,B,C alleles.";
J. Immunol. 142.3937-3950(1989).
i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA CHAIN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
-! - SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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BY SIMILARITY.
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EMBL; U70528; AAB16918.1; --
PIR; S24433; S24433.
HSSP; P30685; IAIN.
MIM; 142830; --
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_1; 1.
MHC_1; Transmembrane; Glycoprotein; Signal.
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362 AA;
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                         MICROGLOBULIN).
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Best Local Similarity
Matches 10; Conserv
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362 AA
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Best Local Similarity 100.
Matches 10; Conservative
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2298
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332
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362 AA;
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P30468;
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CARBOHYD
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DISULFID
SEQUENCE
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1B22_HUMAN
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                                                                                                                                      HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
B-18 B*1801 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 89339610.
OOBA T., HAYASHI H., KARAKI S., TANABE M., KANO K., TAKIGUCHI M.;
"The structure of HLA-B35 suggests that it is derived from HLA-B45B
by two genetic mechanisms.";
Immunogenetics 30:76-80(1989).
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P30683.
01-ARR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
115-DEC-1998 (Rel. 37, Last annotation update)
11A-CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3501 ALPHA CHAIN
PRECURSOR.
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MEDLINE; 96209671.
SMITH K.J., REID S.W., STUART D.I., MCMICHAEL A.J., JONES E.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS).
MENSESR R., ORTH P., ZIEGLER A., SAENGER W.;
Submitted (APR-1998) to the PDB data bank.
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                       100.0%; Score 51; DB 1; Length 362; 100.0%; Pred. No. 0.0066;
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-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
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BY SIMILARITY.
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038EC3FC CRC32;
                                                                     HNM: 142830; -...
PROSITE; PS00290; IG_MHC; 1.
PPAM; PF00047; 19; 1.
PPAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                        40275 MW;
                                                      EMBL; M24039; AAA59662.1;
HSSP; P30460; 1AGB.
                                                                                                                                                                                                                                                                                                            Conservative
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Matches 10; Conserv
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CARBOHYD
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1B21_HUMAN
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SEQUENCE FROM N.A.

SEQUENCE F. P. P. PERRERA M., FAINBOIM L., SATZ M.L.;

CHERTKOFF L.P., HERRERA M., FAINBOIM L., SATZ M.L.;

"Complete nucleotide sequence of a genomic clone encoding HLA-B35

JSOIAted from a Caucasian individual of Hispanic origin.

Identification of a new variant of HLA-B35.";

Hum. Immunol. 31:153-158(1991).

- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO

THE IMMUNE SYSTEM.

THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3502 ALPHA CHAIN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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R EMBL; M28109; AAA59617.1; -.
R EMBL; M28109; AAA59617.1; JOINED.
R EMBL; M28111; AAA59617.1; JOINED.
R EMBL; M28112; AAA59617.1; JOINED.
R EMBL; M28112; AAA59617.1; JOINED.
R EMBL; M38114; AAA59617.1; JOINED.
R PIR; A45880; A45880.
R PDB; IAA18: 08-APR-98.
R PDB; IAA18: 08-APR-98.
R PDB; IAA95; I8-NOV-98.
R MIM; 142830; -.
R PRAM; PFO0047; 19: 1.
R PFAM; PFO0129; MHC_1; 1.
R PFAM; PFO129; MHC_1; 1.
R MG_1; Transmembrane; Glycoprotein; Signal; 3D-structure.
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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BY SIMILARITY.
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SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

MICROGLOBULIN)

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BECK Y., SATZ L., TAKAMIYA Y., NAKAYAMA S., LING L., ISHIKAWA Y., NAGAO T., UCHIDA H., TOKUNAGA K., MULLER C., JULI T., TAKIGUCHI M.; POLYMOTPHISM Of human minor histocompatibility antigens: T cell recognition of human minor histocompatibility peptides presented by HIA-BS subtype molecules."

J. Exp. Med. 181:2037-2048(1995).

-:- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
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MEDLINE; 92176661.
ZEMMOUR J., LITILE A.M., SCHENDEL D.J., PARHAM P.;
"The HLA-A,B 'negative' mutant cell line C1R expresses a novel
HLA-B35 allele, which also has a point mutation in the translation
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3503 ALPHA CHAIN
PRECURSOR.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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                                                                                                                                                         HSSP; P30685; 1A1N.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                       EMBL; M63454; AAA59682.1; -. HSSP; P30685; 1A1N.
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B-35 B*3503 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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EMBL; D5029; BAA08828.1; -.
HSSP, P30685; 1AlN.
MIN; 142830; -.
PROSITE; PS00290; IG_MHC; 1.
PRAM: PF0047; 149; 1.
PFAM: PF00129; MHC_I; 1.
MHC_I; Transmembrane; Glycoprotein; Signal.
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CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGKOUNG E., BECCHANDRA S.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF014769; AAB67807.1; -.
PENBL; PF00129; MHC_I; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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019525,
01-JAN-1998 (TYEMBLrel. 05, Created)
01-JAN-1998 (TYEMBLrel. 05, Last sequence update)
01-NOV-1998 (TYEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENI).
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    protein search, using sw model

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CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D., RUNGROUNG E., BEJCHANDRA S.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AF014775; ABG/813.1; -- PFAM; PF00129; MHC_I: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGROUNG E., BEJCHANDRA S.;
SUBmitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
SWBL; AFO14777; ABB67815.1; -.
PFAM; PF00129; MHC_I; 1.
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                                                                                                                                                                                                                         Length 81;
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 08, Last annotation update)
MIC CLASS I ANTIGEN HLA-B (FRAGMENT).
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
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81 81
81. AA; 9405 MW; 073087CE CRC32;
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81 81
81 AA; 9405 MW; 073087CE CRC32;
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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SEQUENCE FROM N.A.
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                            SEQUENCE FROM N.A.
CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGKOUNG E., BEJCHANDRA S.;
SUNDHITLED (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF014771; AAB67809.1; -.
PFAM; PF00129; MHC_I: 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGKOUNG E., BEJCHANDRA S.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF014773; AAB67811.1;
PFAM: PF00129; MHC_I: 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.013;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
HLA-B.
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81 81
81 AA; 9405 MW; 073087CE CRC32;
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81 AA; 9405 MW;
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Best Local Similarity 100.
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Best Local Similarity 100.

Matches 10; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK
RUNGROUNG E., BEJCHANDRA S.;
Submitted (Jul.1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF014785; AAB67823.1;
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 51; DB 7; Length 83; 100.0%; Pred. No. 0.013;
                                           0; Indels
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Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AFO14787; AAB67825.1; -.
FFAM: PF00129; MHC_I: 1.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-INOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
HLA-B.
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
         Query Match 100.0%; Score 51; DB 7; Best Local Similarity 100.0%; Pred. No. 0.013; Matches 10; Conservative 0; Mismatches 0;
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83 83
83 AA; 9731 MW; 24BBD666 CRC32;
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83 83
83 AA; 9731 MW; 24B8D666 CRC32;
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01-JAN-1998 (TIEMBLEEL. 05, Last seq
01-NOV-1998 (TIEMBLEEL. 08, Last ann
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Best Local Similarity 100.
Matches 10; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                      Query Match 100.0%; Score 51; DB 7; Length 81; Best Local Similarity 100.0%; Pred. No. 0.013; Matches 10; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Score 51; DB 7; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels
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CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK
RUNGROUGE., BEJCHANDRA S.;
SUDMILLEG (JUL. 1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF014783; AAB67821.1;
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                            01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
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01.JAN-1998 (TIEMBLIEL. 05, Last Sequence update)
01.NOV-1998 (TIEMBLIEL. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
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81 81
81 AA; 9405 MW; 073087CE CRC32;
                                           073087CE CRC32;
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81 81
81 AA; 9405 MW;
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01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-1997 (TrEMBLrel. 08, Last sequence update)
MHC. CLASS I HLA-B (FRAGMENT).
HOMO Saplens (Human).
Elwaryota, Metazoa, Chordata; Cranlata; Vertebrata; Mammalla;
Eutharyota, Primates; Catarrhini; Hominidae; Homo.
                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                  7; Length 89;
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CHOPEK M., CAO K., ZHANG G.H.;
SUDMILTEG (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U88249; AAB48493.1; -.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. CHOPEN M.A. CHOPEN M., CAO K., ZHANG G.H.;
CHOPEN M., CAO K., ZHANG G.H.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 1088254; AAB484881.; -.
PFAM; PFO0129; MHC_I: 1.
                                  01-MAY-1997 (TrEMBLrel. 03, Created)
1-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I HIA-B (FRAGMENT).
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 51; DB 7; 100.0%; Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                           89 AA; 10489 MW; A7D3DF93 CRC32;
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PRT;
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Best Local Similarity 100.
Matches 10; Conservative
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Matches 10; Conservative
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PRELIMINARY;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. CHANDANAYINGYONG M., LUANGTRAKOOL K., SRINAK RUNGROUNG E., BEJCHANDRA S.; SUNGROUNG E., BEJCHANDRA S.; Submitted (JUL-1997) to the EMBL/Genbank/DDBJ databases. EMBL; AF014789; AAB67827.1; -. PFAM; PF00129; MHC_1; 1.
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"Identification of a novel HLA-B*07 allele.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AJ237594; CAB40714.1; -.
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83 83
83 AA; 9731 MW; 24B8D666 CRC32;
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89 AA; 10609 MW;
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OC Butheria; Primates; Catarrhini; Hominidae; Homo.
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RP SEQUENCE FROM N.A.
RA CAO K., BURDETT L., ZHANG H., FERNANDEZ-VINA M.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF016299; AAB69444.1; -.
RW MHC.
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FT NON_TER 89 89
SQ SEQUENCE 89 AA; 10550 MW; 11452E40 CRC32;
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 Score 51;
 DB 7;
 Length 89;

 Best Local Similarity 100.0%;
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! U52177 Human MHC class I ant
! U88249 Human MHC class I HLA
! AF181842 Homo saplens MHC cl
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eutheria; Primates; Catarrhini; Hominidae; Homo.
El (Abases I to 243)
Elsalieles (B*1221)
Upublished
2 (bases I to 243)
Chandanayingyong,De, Sirikong,M., Srinak,D., Longta,K.,
Rungroung,E. and Bejchandra,S.
Direct Submission
L. Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSHLABM1 243 bp DNA PRI 26-MAR-1997 Human cell line THAI DCH023 MHC class I HLA-B gene (allele HLA-B*1525), exon 2.
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DEFINITION Human cell line THAI DCH022 MHC class I HLA-B gene (allele HLA-B*1521), exon 2.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DEFINITION Human cell 11
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gb_pr2:HSHYUNA1
gb_pr2:HSU88249
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Database length: -1518192014
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 246)

2 Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Bl5 alleles (B*1502)

L Unpublished

2 (bases 1 to 246)

E 1 (bases 1 to 246)

Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.

Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.

Direct Submission

Submitted (18-UUL-1997) Transfusion Medicine, Faculty of Medicine, Siriral, Hospital, Mahidol University, Prannok Road, Bangkok 10700,
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US-08-653-294-34 x HSHLABO1
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                   Chandanayingyog, D., Sirikong, M., Srinak, D., Longta, K.,
Rungroung, E., Bejchandra, S., Juji, T., Tokunaga, K. and
Grosse-Wille, H.

1 (Daves) 1 to 243

Chases 1 to 243

Chases 1 to 243

Chases Vilde, H.

Rungroung, E., Bejchandra, S., Juji, T., Tokunaga, K. and
Grosse-Wilde, H.

Direct Submission

Submitted (26-FFB-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
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1 (bases 1 to 243)
Chandanayingyong, D., Sirikong, M., Srinak, D., Longta, K., Rungroung, E., Bejchandra, S., Juji, T., Tokunaga, K. and Grosse-Wilde, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 . 243
/gene="HLA-B"
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Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. 243
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Unpublished
     (bases 1 to 243)
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US-08-653-294-34 x HSHLABM1
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AF014773 246 bp DNA PRI 27-AUG-1997 Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele), exon 2 and partial cds.
AF014773 GI:2345111
                                                                                  Length: 10 Gaps: 0 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                           198 CGAGAGCCTGCGGAACCTGCGCGGCTAC 227
                                                                                                                                                                                                                                                                                                                                                       1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
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1. .246
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/gene="HLA-B"
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/number=2
                                                                                     Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
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Ratio: 5.100
Percent Similarity: 100.000
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                                                                                                                                                                                                     alignment_block:
US-08-653-294-34 x AF014771
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LOCUS AF014773
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82 q 28 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:

LOCUS AF014771 246 bp DNA PRI 27-AUG-1997

DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),

ACCESSION AF014771

VERSION AF014771 GI:2345107
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L (bases 1 to 246)

Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.

Bl5 alleles (B*1502)

Unpublished

Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Chandanaying, E. and Bejchandra, S.
                                                                                                                                                                                                                                                                                          Length: 10
Gaps: 0
Percent Identity: 100.000
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1. 246
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/chromosome="6"
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<1. .>246
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/gene="HLA-B"
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US-08-653-294-34 x AF014769
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 246)

S Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.

L Unpublished

L Opablished

C 2 (bases 1 to 246)

C Andanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.

Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Sunfitted (18-011-1997) Transfusion Medicine, Faculty of Medicine, Sirital, Hospital, Mahidol University, Prannok Road, Bangkok 10700,
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Gaps: 0
Percent Identity: 100.000
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SOURCE ORGANISM

TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

REFERENCE AUTHORS

DEFINITION

ACCESSION

VERSION KEYWORDS

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82 g
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ChandanayIngyong, D., Strikong, M., Luangtrakool, K., Srinak, D.,
Kungroung, E. and Bejchandra, S.
Direct Submission
Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                          Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele), excon 2 and partial cds.
AF014777 GI:2345119
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LOCUS
LOCUS
AF014779 246 bp DNA
DEFINITION Homo saptens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
exon 2 and partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 246)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., B15 alleles (B*1502)
Unpublished
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Ratio: 5.100
Percent Similarity: 100.000
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US-08-653-294-34 x AF014777
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LOCUS AF014777
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1 (bases 1 to 246)

2 (bases 1 to 246)

2 (bases 1 to 246)

3 (bases 1 to 246)

4 (bases 1 to 246)

5 (bases 1 to 246)

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7 (bases 1 to 246)

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Homo saptens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
exon 2 and partial cds.
AF014775 GI:2345115
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Percent Identity: 100.000
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                                                                             from: 1
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                                                                         Align seg 1/1 to: AF014773
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US-08-653-294-34 x AF014773
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Ratio: 5.100
Percent Similarity: 100.000
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US-08-653-294-34 x AF014775
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LOCUS AF014775
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FEATURES

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exon

CDS

BASE COUNT ORIGIN

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Andanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
Rungroung,E. and Bejchandra,S.
Direct Submission
Direct Submission
Submitted (18-JUD-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele), exon 2 and partial cds.

AF014783
AF014783.1 GI:2345131
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.
B15 alleles (B*1502)
Unpublished
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 246)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.
Unpublished (B*1802)
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Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D.,
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Gaps: 0
Percent Identity: 100.000
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Percent Similarity: 100.000
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US-08-653-294-34 x AF014781
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Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D.,
Rungroung, E. and Bejchandra, S.
Direct Submission
Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
Siriral Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele), exon 2 and partial cds. AF014781 GI:2345127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 246)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.
B15 alleles (B*1502)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 10
Gaps: 0
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Percent Similarity: 100.000
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US-08-653-294-34 x AF014779
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Locus AF014781
                                                                                                              Homo sapiens
                                                                                                                                                                                                                                 Unpublished
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DEFINITION
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KEYWORDS
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                                    ACCESSION
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JOURNAL
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                      AUTHORS
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ORIGIN

TITLE JOURNAL

FEATURES

gene

exon

CDS

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (Abases I to 250)

Elsaleles (B*1525)

L (Apases I to 250)

E (Abases I to 250)

S Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.

Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.

Direct Submission

L Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine, Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700, Thailand
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Gaps: 0
Percent Identity: 100.000
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Percent Similarity: 100.000
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US-08-653-294-34 x AF014785
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LOCUS AF014787
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                          Faculty of Medicine,
Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (18-UUL-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1525 allele), exon 2 and partial cds. AF014785 GI:2345135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chandanayingyon, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.
B15 alleles (B*1525)
Unpublished
2 (bases 1 to 250)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 250)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-AUG-1997
Rungroung, E. and Bejchandra, S.
Direct Submission
Submitted (18-JUL-1997) Transfusion Medicine,
Siriral Hospital, Mahidol University, Prannok
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps: 0 Gaps: 0 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                   /allele="HLA-B*1502"
                                                                                             Location/Qualifiers
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1. .250
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US-08-653-294-34 x AF014783
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LOCUS AF014785
                                                                            Thailand
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BASE COUNT ORIGIN

source

FEATURES

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

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REFERENCE AUTHORS

TITLE JOURNAL REFERENCE

AUTHORS

TITLE JOURNAL

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 254)
Mitsuishi,Y.
Direct Submission
Submitted (04-JUN-1996) Tissue Typing Laboratory, UCLA School of Medicine, 950 Veteran Ave., Los Angeles, CA 90095, USA
Location/Qualifiers
1 . 254
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LOCUS
BERINITION Human MHC class I protein HLA-B heavy chain (B*1501new allele)
ACCESSION U59965
VERSYON
VERYWORDS
HLA B antigen; major histocompatibility complex.
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Gaps: 0
Percent Identity: 100.000
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VERSION
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TITLE
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81 c 84 g 31 t
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Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
Rungroung,E. and Bejchandra,S.
Direct Submission
Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS AF014789 250 bp DNA PRI 27-AUG-1997
DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1525 allele),
exon 2 and partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 250)

Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D.,

Rungroung, E. and Bejchandra, S.

Unpublished
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AUTHORS
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A. thermophilum thermostabl
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pHLA-B7 expression vector.
perpression vector; pHLA-B7; heavy human HLA-B7; bicistronic mRNA;
expression vector; pHLA-B7; heavy human HLA-B7; bicistronic mRNA;
light beta-2 microglobulin; class I major histocompatibility complex;
MHC; human leukocyte antigen; HLA; covalently closed circular DNA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reading frame;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F 22-SEP-1991.

R 22-SEP-1999; JP-247697.

22-SEP-1998; JP-247697.

R WPI; 91-182991/25.

R WPI; 91-182991/25.

R HAA-B35 gene - used in DNA probe and transformant cells for immunishing animals, for developing monoclonal antibody.

S Claim i Page i; 11pp; Japanese.

C Tolaim i Page i; 11pp; Japanese.

C Tolaim i Page i; 11pp; Japanese.

C Probes comprising part of the sequence can be used to identify Class I genes. The DNA can be expressed for immunisation of canimals and prodn. of monoclonal antibodies specific for the HAA-B35 antigen. Sealso J03112485 and J03112487.

Sequence 1089 BP; 221 A; 336 C; 359 G; 173 T;
                                                                                                                                                                                                                                                                       HLA-B35 exon. Human leukocyte antigen; probe; major histocompatibility complex; MHC; class I; ss. Homo saplens.
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/note= "pBR322 backbone contg. bacterial origin
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/note= "SV40 polyA signal sequence"
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012115;
29-AUG-1991 (first entry)
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ID Q75974 standard; cDNA; 4059
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US-08-653-294-34 x Q12115
                                                                                                                                                                           seq_documentation_block
  N_Geneseq_36:V43032
N_Geneseq_36:V32620
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N_Geneseq_36:V29686
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110000 | Continuation (8 of 10) of
| Human leukocyte antigen class I
| HuntL coding sequence. HuntL an
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| Mouse TNRL3 DNA. New Tumor Necx
| Isopentenyl transferase ipt gen
| Mus musculus tumour necrosis i
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-Q-Cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.2
-Q-Cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.2
-Q-Cgn1_1/USPTO_spool/US08653294/runat_04D0000
-QAPOP=12.000
-GAPEXTT-4.000 -MINMATCH-0.100 -LOOPEXT-0.000
-GAPEXTT-4.000 -MINMATCH-0.100 -LOOPEXT-0.000
-GAPEXT-4.000 -MINMATCH-0.100 -CAPPOP-10.000 -YGAPEXT-0.500
-FGAPOP=4.500 -PGERTT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-ALIGN=15 -MODE-LOCAL -OUTFWT-pfs -NORM-ext -MINLEN-0
-MAXLEN-1000000 -USER-US08653294 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
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  OM of: US-08-653-294-34 to: N_Geneseq_36:*
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Database sequences: 311585
Database length: 125096042
Search time (sec): 873.190000
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N_Geneseq_36:X08414
N_Geneseq_36:X14193
N_Geneseq_36:V30458_0 +
N_Geneseq_36:V30459_0 +
N_Geneseq_36:V30459_0 +
N_Geneseq_36:V30459_0 +
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Query: US-08-653-294-34
Query length: 10
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                                                     Date: Feb 8, 2000 7:31
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N_Geneseq_36:T94815 +
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N_Geneseq_36:N81608
N_Geneseq_36:Q52673
N_Geneseq_36:Q47076
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N_Geneseq_36:X22446
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N_Geneseq_36:X23425
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/note- "bovine growth hormone 3'UTR and transcriptional terminator; it starts at a blunt-ended BglI site within the 3'UTR of the mRNA coding sequence" 2979. .2984
/*tag- m 3112. .3151
                                                                                                                                                                                                                                                                                                                              /*tag= g //note= "multiple cloning site, forms a junction between the HiA-B7 sequence and the EMCV-CITE sequence, and is used to facilitate subcloning" 1889. 2479
/*tag= h //note= "murine encephalomyocarditis CAP-independent translational enhancer (EMCV-CITE); taken from nucleotides 255-843 of Choned EMCV genomic DNA. It is a non-coding regulatory sequence functioning as an internal entry point for the eukaryotic ribosomal subunits when located within a mRNA mol. It enables the translational start codon of the beta-2 microglobulin, downstream of the HIA-B7 stop codon on this biscistronic mRNA to be recognised by the ribosome"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= o
//rtag= o
//note= "kanamycin resistance gene open reading frame;
the gene is taken from the transposable element
The THO93"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= p
/note= "pBR322 backbone contg. bacterial origin of
replication, it represents nucleotides 2244-3193"
                                                                                                                                                                                                                                      "encodes putative HLA-B7 heavy chain mature
                         sequences. The oligonuclectide removes a polyadenylation signal sequence originally found in the RSV DNA sequence.
                                                                                                         535. .1620
/*tag= c
/note= "HLA-B7 heavy chain open reading frame"
                                                                                                                                                                            /note- "encodes putative signal peptide of the HLA-B7 heavy chain" 607...1620 /*tsg- e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note = "synthetic linker to facilitate cloning"
  modifies this regulatory sequence to effect
higher level of expression of downstream
                                                                                                                                                                                                                                                                                           HLA-B7
                                                                                  /*tag= b
/label= consensus_Kozak_signal_sequence
                                                                                                                                                                                                                                                                                             οţ
                                                                                                                                                                                                                                                                                           untranslated sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "synthetic linker"
'UTR 3111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (3151. .3967)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= n
                                                                                                                                                                                                                                                  peptide"
1621, .1853
/*tag= f
/note= "3' u
                                                                                                                                                                                                                                                                                                       chain mRNA"
                                                                                                                                                                                                                                                                                                                     1854. .1888
                                                                                                                                                    909.
                                                                   531. .534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                    *tag=
                                                                                                                                                                                                                                        /note-
                                                                                                                                                    signal_peptide
                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                      misc_signal
                                                                                                                                                                                                            mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9429469-A.
22-DEC-1994.
                                                                                                                                                                                                                                                                3'utr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3'utr
                                                                                                             cds
  Lew D. Marquet M. Nabel EG, Nabel GJ;

Lew D. Marquet M. Nabel EG, Nabel GJ;

New Vectors for gene therapy, partic for tumours - comprising

New vectors for gene therapy, partic for tumours - comprising

New vectors for gene therapy, partic for tumours - comprising

Proposed For Garden Coding one or more cistron(s) which express

Time HIA-B7 antigen encoding plasmid was developed to incorporate many
advantageous features, eg. the kanamycin resisitance gene. The

cradication of two open reading frames encoding portions of SV40 viral

proteins lowers the risk of tumourigenicity. The vector may also operate

as a cassette into which cistrons may be inserted and removed at will

for the transcription and subsequent translation of peptides of interest.

The vector is used partic. for the treatment of neoplastic disease,

in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualiflers
1. .529
/*tag= as //ote= "Rous sarcoma virus LTR promoter domain, derived for the Schmidt-Rupin strain nucleotides 8673-9146. This region also includes a 56 bp region of a synthetic oligonucleotide which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-AUG-1995 (first entry)
pHLA-B7/beta-2 microglobulin expression vector.
expression vector; pHLA-B7/beta-2 microglobulin; heavy human HLA-B7;
light beta-2 microglobulin; class I major histocompatibility complex;
mHC; bicistronic mRNA; human leukocyte antigen; HLA;
covalently closed circular DNA; ds.
                                                                                                                                                     /*tag= g
/note= "Rous sarcoma virus 3' LTR promoter region"
                                                     /*tag" e
/note= "3' untranslated region of HLA-B7
heavy chain mRNA"
complement (1795. .2880)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1033 G;
                                                                                                                      /note= "HLA-B7 open reading frame" complement (2886. .3415)
                       /note= "SV40 small t intron" complement (1561. .1794)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: Q75974 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1051 C;
complement (1412. .1560)
                                                                                                                                                                                              /*tag= h
/note= "pBR322 backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2589 CGAGAGCCTGCGGAACCTGCGCGGCTAC 2560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             documentation_block:
Q75973 standard; cDNA; 4965 BP.
Q75973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 975 A;
                                                                                                                                                                               .4059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-34 x Q75974/rev
                                                                                                                                                                                                                                   22-DEC-1994,
27-MAY-1994, U06069,
07-JUN-1993, US-074344,
(UDMI ) UNIV MICHIGAN,
(VICA-) VICAL INC.
           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seg_name: N_Geneseg_36:Q75973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.00
                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4059 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
 intron
                                        3'utr
                                                                                               cds
                                                                                                                                        ltr
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alignment_scores
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PI Lew D, Marquet M, Nabel EG, Nabel GJ;

New vectors for gene therapy, partic for tumours - comprising

New vectors for gene therapy, partic for tumours - comprising

New vectors for gene therapy, partic for tumours - comprising

PPT genetic material encoding one or more cistron(s) which express

PPT immunogenic or therapeutic peptide(s)

PPT genetic material encoding one or more cistron(s) which express

PPT genetic material encoding one or more cistron(s) which express

PPT genetic material encoding the plasmid so the plasmid by the plasmid sequence deriv. From the bovine growth bornone

CC cap-dependent protein start site. Translation of the plasmid in posterial cells is controlled by the plasmid in paterial cells is controlled by the presence of a bacterial origin of replication. The vector is used partic. for the treatment of neoplastic for in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA-C gene, DNA probe and transformant cells - for immunisation of animals and monoclonal antibody development.

Claim 1; Page 1; 13pp; Japanese.

Probes comprising part of the sequence can be used to identify class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HLA-C anitigen. See also 012117 (same patent) and J03112486 and J03112487. Sequence 1101 BP; 211 A; 337 C; 377 G; 176 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      012116;
29-AUG-1991 (first entry)
HLA-C exon Cb-1.
Human leukocyte antigen; probe; major histocompatibility complex;
MHC; class I; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1338 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouality: 51.00 Length: 10 Ratio: 5.100 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1293 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
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1. .1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1171 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID Q12116 standard; DNA; 1101 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAY-1991.
22-SEP-1989; 247695.
22-SEP-1989; JP-247695.
(OLXU ) OLYMPUS OPTICAL KK.
WPI; 91-182989/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: N_Geneseq_36:Q12116
27-MAY-1994; U06069.
07-JUN-1993; US-074344.
(UNMI ) UNIV MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-34 x Q75973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4965 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; R12465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J03112485-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores
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CPRM1; human; chemoprotector regulated modifier; genotoxin; cytotoxin; CPRM2; CPRM3; mCPRM1; allele s; allele r; gene therapy; antibody; detoxification; detection; mutant; cancer; carcinogenic; aflatoxin; treatment; neurodegeneration; Alzheimer's disease; malondialdehyde; cyclo-oxygenase reaction; prostaglandin metabolism; ss. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIA-C gene, DNA probe and transformant cells - for immunisation of animals and monoclonal antibody development.

Claim 2; Page 1; 13pp; Japanese.

Probes comprising part of the sequence can be used to identify class I genes. The DNA can be expressed for immunisation of animals and produ. of monoclonal antibodies specific for the HIA-C antimals and produ. of second patent) and J03112486 and J03112487.

Sequence 1101 BP; 215 A; 335 C; 379 G; 172 T;
                                                                                                                                                                                                                                                                                                                                  29-AUG-1991 (first entry)
HLA-C exon Cb-2.
Human leukocyte antigen; probe; major histocompatibility complex;
MHC; class I; ss.
Homo sapiens.
Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps: 00
Percent Identity: 90.000
                                                                                                                                                 Align seg 1/1 to: Q12116 from: 1 to: 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: Q12117 from: 1 to: 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 CGAGTGAGCCTGCGGAACCTGCGCGCGGTAC 324
                                                                                                                                                                                         1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 74. .994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID X22446 standard; DNA; 1323 BP.
                                                                                                                                                                                                                                                                                                                seq_documentation_block:
ID Q12117 standard; DNA; 1101 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAY-1991.
22-SEP-1989; 247695.
22-SEP-1989; JP-247695.
(OLYU ) OLYMPUS OPTICAL KK.
WPI; 91-182989/25.
P-PSDB; R12466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X22446;
20-MAY-1999 (first entry)
Human CPRM2 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 44.00
Ratio: 4.889
Percent Similarity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: N_Geneseq_36:X22446
  44.00
4.889
90.000
                                                                                                                                                                                                                                                                           seq_name: N_Geneseq_36:Q12117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-34 x Q12117
                                                                                    alignment_block:
US-08-653-294-34 x Q12116
      Quality:
Ratio:
                                           Percent Similarity:
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Align seg 1/1 to reverse of: T32217 from: 1
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                                                                                                                                                                                                                                                                refusion to the protector regulated modifier proteins - useful in the detaxification of metabolites, particularly aflatoxins

detaxification of metabolites, particularly aflatoxins

laim 2: Fig 8: Jipp; German

This sequence encodes a novel protein designated CPRM2 (chemoprotector coulated modifier) that inhibits the effects of genotoxic and/or regulated modifier) that inhibits the effects of genotoxic and/or cytotoxic substances. The invention describes the isolation of CPRM1, CPRM3, mcPRM1, allele s. dam dCPRM1, allele r. Transformants containing such proteins are used to produce recombinant proteins and uncleic acids for use in gene therapy and to raise antibodites which are used to (1) detaxify geno - and/or cyto-toxic metabolites and (11) detect presence of CPRM proteins (or nucleic acid encoding them, including presence of CPRM proteins and used to eliminate carcinogenic aflatoxins and to treat neurodegeneration, e.g. Alzheimer's disease, associated with production of malondiadenyde, a toxic product or the cyclo-oxygenase reaction and prostaglandin metabolism.

Sequence 1323 BP; 331 A; 368 C; 338 G; 286 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New chemoprotector regulated modifier proteins - useful in the detoxification of metabolites, particularly aflatoxins bisclosure; Fig 12; 31pp; German.
This sequence encodes a novel protein designated CPRM2 which is a mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CPRM1; mouse; chemoprotector regulated modifier; genotoxin; cytotoxin; CPRM2; CPRM3; mCPRM1; allele s; allele r; gene therapy; antibody; detoxification; detection; mutant; cancer; carcinogenic; aflatoxin; treatment; neurodegeneration; Alzheimer's disease; malondialdehyde; cyclo-oxygenase reaction; prostaglandin metabolism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: X22446 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/product= "CPRM2 mutant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1058 AAAGAAAGTGTGAAAACAAAAGAGGTTAC 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                      24-JUN-1998; D01796.
24-JUN-1997; DE-026823.
(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JUN-1997; DE-026823.
(DEKR.) DEUT KREBSFORSCHUNGSZENTRUM.
Praml C, Schwab M;
WPI; 99-081282/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
  /*tag= a
/product= "CPRM2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID X22450 standard; DNA; 1324 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAY-1999 (first entry)
Human CPRM2 mutant DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-653-294-34 x X22446/rev
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24-JUN-1998; D01796
                                                                                                                                                                                         Praml C, Schwab M; WPI; 99-081282/07.
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                            P-PSDB; W93087
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                                                   WO9859055-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9859055-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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Claim 2; Page 6; 7pp; Japanese.

This sequence represents the coding sequence for the Cuphea leptopoda acyl-ACP-thiosesterase (AAT). This sequence was isolated by synthesising a AAT cDNA, and using that sequence to probe for a fragment of the AAT gene, which was then amplified. AAT is a key enzyme in the synthesis of middle chain aliphatic acids, and as such is useful in pharmaceutical preparations, and foods.

Sequence 1490 BP; 351 A; 332 C; 402 G; 405 T;
chemoprotector regulated modifier that inhibits the effects of genotoxic and/or cytotoxic substances. The invention describes the isolation of CPRMI, CPRMI, CPRMI, allele s, and mCPRMI, allele r. Transformants containing such proteins are used to produce recombinant proteins and nucleic acids for use in gene therapy and to metabolites and including detect presence of CPRM proteins (or nucleic acid encoding them, including detection of mutations indicative of increased risk of cancer, e.g. prenatally). The proteins can be used to eliminate acrinogenic aflatoxins and to treat neurodegeneration, e.g. Alzheimer's disease, associated with production of malondialdehyde, a toxic product or the cyclo-oxygenase reaction and prostaglandin metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cuphea leptopoda; aliphatic acid synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding Cuphea leptopoda Hemsl. acyl-ACP-thio:esterase - for synthesis of middle chain aliphatic acids, useful in pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 1324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 39.00 Length: 10
Ratio: 4.333 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-DEC-1994; JP-320547.
(NOR) NORINBUISANSHO CHUGOKU NOGYO SHIKENBACH
WPI; 96-365584/37.
P-PSDB; W02020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= Acyl-ACP-thloesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T32217 standard; cDNA to mRNA; 1490 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acyl-ACP-thioesterase coding sequence. Acyl-ACP-thioesterase; AAT; cuphea leg middle chain aliphatic acid; ss. Cuphea leptopoda hemsi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 30. .1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to reverse of: X22450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-34 x X22450/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-FEB-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-34 x T32217/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: N_Geneseq_36:T32217
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Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUL-1996,
22-DEC-1994; 320547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
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to: 1490

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DNA encoding calcium-activated potassium channel - useful in assays
to identify compounds which increase or decrease potassium ion flux
Claim 3; Page 112; 151pp; English.

Claim 3; Page 112; 151pp; English.

Chis sequence encodes the human small conductance calcium-activated
This sequence encodes the human small conductance calcium-activated
Corpussium channel protein 3 (h8X3) of the invention. The proteins of the
invention are monomers of a calcium-activated potassium channel, where
Corpus and (ii) has a calculated molecular weight of between 10 and
Corpus and (ii) has a unit conductance of between 2 and 60 pS when the
monomer is in the functional polymeric form of a pocassium chain and is
expressed in a Xenopus occyte. Antibodies specific for the protein, and
Corpus specific for the DNA can be used to detect the presence of the
Corpus specific for the DNA can be used to detect the presence of the
Corpus and so be used for the recombinant production of the protein. The
DNA sequences can also be used for the recombinant productions in the SK and IK
Genes in a computer system. The proteins encoded by the SK and IK
Genes in a computer system for determining their three dimensional
corpus and the corpus of the protein of the protein. The protein of the protein of the protein of the corpus of the corpus of the corpus of the computer system for determining their three dimensional
corpus of the corp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1998 (first entry)
Rat rSK3 coding sequence.
Small conductance calcium-activated potassium channel protein 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       352 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 1674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity: 18.00 Fercent Identity: 70.000
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                                                                                                                                               (ICAS-) ICAGEN INC.
(UYOR-) UNIV OREGON HEALTH SCI.
PP. Bond CT, Maylle J, Silvia CP;
WPI; 98-207332/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ICAG-) ICAGEN INC.
(UVOR-) UNIV OREGON HEALTH SCI.
Adelman JP, Bond CT, Maylle J, Silvia CP;
WPI; 98-207332/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       521 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
2. .2200
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ID V35472 standard; cDNA; 2224 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-34 x V35458/rev
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                      19-MAR-1998.
10-SEP-1997; U16033.
17-APR-1997; US-045233.
11-SEP-1996; US-026451.
07-MAR-1997; US-040052.
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17-APR-1997; US-045233.
11-SEP-1996; US-026451.
07-MAR-1997; US-040052.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
DNA encoding calcium-activated potassium channel - useful in assays

To identify compounds which increase or decrease potassium ion flux

to identify compounds which increase or decrease potassium ion flux

Claim 3: Page 105: 151pp; English.

Claim 3: Page 105: 151pp; English.

Chis sequence encodes the rat small conductance calcium-activated

Conductance calcium-activated proteins of the invention are monomers of a calcium-activated potassium channel, where the monomer: (i) has a calculated molecular weight of between 2 and 60 ps when the monomer is in the functional polymeric form of a potassium chain and is monomer is in the functional polymeric form of a potassium chain and is capressed in a Xenopus socyte. Antibodies specific for the protein, and protein or DNA sequences in a sample. Host cells expression of the protein can be used for the recombinant production of the protein. The content or DNA sequences in a sample host cell can also be used for the recombinant production of the protein. The cell can also be used for determine mutations in the SK and IK genes in a computer system. The proteins encoded by the SK and IK genes in a computer system. The proteins encoded by the SK and IK genes can also be used for determining their three dimensional proteins which is useful for determining ligands that bind to the
                                                                                                                                                                                                                                                             01-OCT-1998 (first entry)
Rat truncated rSK3 coding sequence.
Small conductance calcium-activated potassium channel protein 1;
rSK3; rat; potassium ion flux; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1998 (first entry)
Truncated human hSK3 coding sequence.
Small conductance calcium-activated potassium channel protein 3;
hSK3; human; potassium ion flux; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 1659
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Ratio: 3.800 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 398 G;
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10-SEP-1997; U16033.
11-APR-1997; US-045233.
11-SEP-1996; US-026451.
07-MAR-1997; US-040052.
(ICAG-) ICAGEN INC.
(UCAG-) ICAGEN INC.
Adelman JP, BONG CT, Maylie J, Silvia CP; WPI; 98-207332/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
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ID V35458 standard; cDNA; 1674 BP.
AC V35458;
                                                                                                                                                                                                       V35447 standard; cDNA; 1659 BP. V35447;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-34 x V35447/rev
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                                                                                                                              seq_name: N_Geneseq_36:V35447
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                                                                                                                                                                                    seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
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to identify compounds which increase or decrease potassium ion flux

Claim 3: Page 123-124: 151pp; English.

This sequence encodes the rat small conductance calcium-activated
potassium channel protein 3 (rsS3) of the invention. The proteins of the
invention are monomers of a calcium-activated potassium channel, where
the monomer: (i) has a calculated molecular weight of between 40 and
80 kDa; and (ii) has a unit conductance of between 2 and 60 ps when the
monomer is in the functional polymeric form of a potassium chain and is
expressed in a Xenopus cocyte. Antibodies specific for the protein, and
probes specific for the DNA can be used to detect the presence of the
protein or DNA sequences in a sample. Host cells expression of the
protein can be used in assays to identify compounds which increase or
protein also be used for the recombinant production of the protein. The squences can also be used for determine mutations in the SK and IK
genes in a computer system. The proteins encoded by the SK and IK
can be used in a computer system for determining their three dimensional
can be used in a computer system for determining that three dimensional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding calcium-activated potassium channel - useful in assays to identify compounds which increase or decrease potassium ion flux claim 3; page 128-129; 151pp; English.

This sequence encodes the human small conductance calcium-activated potassium channel protein 3 (hSK3) of the invention. The proteins of the invention are monomers of a calcium-activated potassium channel, where the monomer: (i) has a calculated molecular weight of between 40 and 80 kDa; and (ii) has a unit conductance of between 2 and 60 pS when the monomer is in the functional polymeric form of a potassium chain and is probes specific for the DNA can be used to detect the presence of the protein or DNA sequences in a sample. Host cells expression of the protein can be used in assays to identify compounds which increase or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human hSK3 coding sequence.
Small conductance calcium-activated potassium channel protein 3;
hSK3; human; potassium ion flux; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                            445 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 2224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 38.00 Length: 10
Ratio: 3.800 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                         537 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: V35472 from: 1
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Adelman JP, Bond CT, Maylle J, Silvia CP;
WPI; 98-207332/18.
                                                                                                                                                                                                                                                                                                                                                                                                                            711 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
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252. .2462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
ID V35473 standard; cDNA; 2462 BP.
AC V35473;
                                                                                                                                                                                                                                                                                                                                                                                                                            531 A;
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US-08-653-294-34 x V35472/rev
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17-APR-1997; US-045233.
11-SEP-1996; US-026451.
07-MAR-1997; US-040052.
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                                                                                                                                                                                                                                                                                                                                                                                                                            2224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                       proteins
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           F_{N}^{N}
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decrease the potassium ion flux through the protein. The transfected host cell can also be used for the recombinant production of the protein. The DNA sequences can also be used for determine mutations in the SK and IK genes in a computer system. The proteins encoded by the SK and IK genes can be used in a computer system for determining their three dimensional structure, which is useful for determining ligands that bind to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human small conductance calcium activated potassium channel.3 useful for diagnosis, treatment and prevention of particularly useful for diagnosis, treatment and prevention of particularly schizophrenia and bipolar disorders

Claim 3; Figure 5; 95pp; Bnglish.

Cloandarcance calcium-activated potassium channel.3 (hKCa3/KCNN3) comprise neuropsychiatric, neurological, neuromuscular and immunological disorders, specifically bipolar disease and schizophrenia. Transgenic animals comprising the hKCa3/KCNN3 gene as a transgene in their somatic and germ cell lines can be used as models for studying these conditions and their treatments.

C Antibodies (Ab) directed against the hKCa3/KCNN3 polypeptide can be used to conservative variants of the polypeptide can be used to detect those at risk from these disorders and also in therapy against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human small conductance calcium activated potassium channel gene. Human small conductance calcium activated potassium channel; hKCa3/KCNN3, bipolar disease; schizophrenia; treatment; diagnosis; detection; transgenic animal; gene therapy; neuropsychiatric disorder; neurological disorder; neuromuscular disorder; immunological disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               such disorders. Use of the wild type gene in gene therapy to treat these disorders is also contemplated.
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287. 2482
/*tag= a
/*product= "Small conductance calcium activated
2482. 2487
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                                                                                                                                                                                                                                                    479
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Chandy KG, Fantino E, Gargus JJ, Gutman G, Kalman K;
WPI; 99-132165/11.
P-PSDB; W96312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 2462
                                                                                                                                                                                                                                                                                                                                                                              Ratio: 3.800 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 70.000
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                                                                                                                                                                                                                                                617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                814 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label- Poly-A signal
2509. .2521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   850 CGGGAGGCGCTGAGGCGGCTGAGGGGCCTTC 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to reverse of: V35473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X08414 standard; cDNA; 2521 BP.
                                                                                                                                                                                                                                                552 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-34 x V35473/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: N_Geneseq_36:x08414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
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15-JUL-1997; US-052556
                                                                                                                                                                                                                                                BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JUL-1998; U14902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                             2462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9903889-A1
                                                                                                                                                                                                                                                                                                                                                     alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polyA_site
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                                                                                                                                                                                                                   proteins.
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       888888888
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1 ArgGluSerLeuArgAsnLeuArgGly 9
                                                                                     seq_name: N_Geneseq_36:V30458_0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                  V30458_0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                             Prepared acids encoding human secreted proteins - obtained from the nucleic acids encoding human secreted proteins - obtained from type and libraries derived from umbilical cord, lymph ganglia, I brace derived from umbilical cord, lymph ganglia, I brace sand placental itssue claim 1; Page 268-269; 411pp; English.

X41379 to X41526 represent 5' expressed sequence tags (ESTS) for human secreted proteins, and encode the proteins given in Y12521 to Y12668, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producting secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiating activity, haematopoiesis regulating activity, tissue growth regulating activity, nemotocitive hormone regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/content activity, manifulammatory activity, tumour inhibition activity and chromosome mapping promoter sequences. The nucleic acids encoding the signal peptide can be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide or the insertion of a polypeptide into a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human: secreted protein, EST: expressed sequence teg; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; antiinflammatory; tumour inhibition; antitumour; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-1999 (first entry)
Human secreted protein 5' EST SEQ ID NO: 152 from WO 9906553
  490 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
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Gaps: 0
Percent Identity: 88.889
                                                                                     Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                  to: 2521
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    ö
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  624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-FEB-1999.
31-JUL-1998: IB1237.
01-AGC-1997; US-90S051.
(GEXT ) GENSET.
Duclert A, Dumas Milne Edwards J, Lacroix B;
WPI; 99-153783/13.
                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: X08414 from: 1
    833 C;
                                                                                                                                                                                                                                                                                                                                     870 CGGGAGGCGCTGAGGCGGCTGAGGGGCTTC 841
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                                                                                                                                                                                                                                                                                          1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
ID X41493 standard; cDNA; 416 BP.
    574 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-08-653-294-34 x X41493/rev
                                                                                                                                                                             alignment_block:
US-08-653-294-34 x X08414/rev
                                                                                                            Ratio: 3.800
Percent Similarity: 100.000
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4.625
88.889
                                                                                                                                                                                                                                                                                                                                                                               seq_name: N_Geneseq_36:X41493
  2521 BP;
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                                                                                          Quality:
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WO9906553-A2.
                                                                   alignment_scores:
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      Sequence
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/product-"(semi)aldehyde dehydrogenase-like protein"
complement (426949. .428028)
                                                                                                                                                                                                                                                                                  14-oCT-1998 (first entry)
Rhizobium species plasmid pNGR234a.
Symbiosis; open reading frame; ORF; plasmid; vector; transportation;
degradation; metabolism; host range; nitrogen fixation; nodulation;
legume; plant; ds.
Rhizobium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "glutamate dehydrogenase-like protein"
                                                                                                            COCUS V30458 Accession V30458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product- "aminotransferase-like protein"
/note= "homologous to the BioA gene"
/4+2.76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product= "encapsulation-like protein'
note= "homologous to the CapA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "homologous to the GLUD1 gene"
complement (430538. .431284)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product- "oligopeptide permease" /note- "homologous to the OppC gene" 418673. ,419680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /standard_name= "ORF K2"
/product= "oligopeptide permease"
/note= "homologous to the OppD gene"
419677. .420738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product "oligopeptide permease" note "homologous to the OppF gene" 20774, .422159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="transposase homologue"
/note= "homologous to the Tnp gene"
complement (433880. .434110)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'product= "transposase homologue" 'note= "homologous to the Tnp gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="transposase homologue"
complement (431296, 432840)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_name= "ORF K10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'standard_name= "ORF K3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'standard_name= "ORF K1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'standard_name= "ORF K4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= g
/standard_name= "ORF K7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'standard_name= "ORF K6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /standard_name= "ORF K9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /standard_name= "ORF K8"
                                                                                                                                                                                                 310000
                                                                                                                                                                                                                                             510000
                                                                                                                                                       10000
284 AGAGAATCGCTCAGGAATCCCCGAGGG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        417796. .418671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22628. .424031
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                                                                                                                                                                   V30458_1 100001
V30458_2 200001
V30458_3 300001
V30458_4 400001
V30458_5 standard; DNA; 534720 BF
                                                                                                     Sequence split into 6 fragments
Fragment Name Begin
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/gene= "nIfD"
/product= "alpha-subunit of FeMo protein of nitrogenase"
454590. .456131
                                                                                                                                                                                                                                                                                                                                    /gene= "nifk"
/product= "beta-subunit of FeMo protein of nitrogenase"
456187. ,457677
                                                             /standard_name= "ORF L3"
/product= "putative protein with degradative function"
450341, .451396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /standard_name= "ORF 112"
/product= "protein similar to part of the Fe protein
                                                                                                                                        /standard_name= "ORF L4"
/product= "luciferase alpha-subunit-like protein"
//note= "homologous to the LuxA gene"
452980. .454494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /standard_name= "ORF L9"
/product= "protein involved in FeMo co-factor blosynthesis"
/note= "homologous to the FixF gene"
459093. .459575
                                                                                                                                                                                                                                                                                                                                                                                                     /standard_name= "ORF L8"
/product= "protein involved in FeMo co-factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /standard_name= "ORF L15"
/product= "processing protease-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_name= "ORF L10"
/product= "protein of unknown function"
/note= "homologous to the Nifx gene"
459579, .460067
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/*tag= ag
/stendard_name= "ORF L11"
/product= "protein of unknown function"
460501. .460920
/*tag= ah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /standard_name= "ORF L13"
/product= "protein of unknown function'
163201. .464739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /standard_name- "ORF I.14"
/product- "peptidase-like protein"
/note- "homologous to the bi-MPP gene"
/*t4736. .466079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of nitrogenase"
/note= "homologous to the NifH gene"
461228. 461545
                  /note= "homologous to the LinA gene" 448497. .450203
                                                                                                                                                                                                                                                                                                                                                                                                                                biosynthesis"
/note- "homologous to the Nifa gene"
457687, .459096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 9
Gaps: 0
Percent Identity: 88.889
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                                                                                                                                                                                                                               /standard_name= "ORF L6"
 protein"
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4.625
88.889
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US-08-653-294-34 x V30458_0
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Ratio:
Percent Similarity:
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                                                                                                         CDS
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/standard_name= "ORF L2"
/product= "gamma-hexachlorocyclohexane-dechlorinase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "protein required for nitrogenase activity"
complement (439923. .441032)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "protein required for nitrogenase activity"
complement (438605. .439912)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product- "protein required for nitrogenase activity"
complement (441042, .441899)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "protein required for nitrogenase activity"
complement (442316. 442636)
                                                                                                                                                                                                                                                                                                                                                                                                 /product- "positive regulator of nif, fix and other genes"
                                                                                                                                                                   /standard_mame="ORE K13"
/product="ferrodoxin/ferrodoxin-like protein"
/note="homologous to the FdxN gene"
complement (434753, 436234)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene= "dctA"
/product= "C4-dicarboxylate transport protein"
/product= "homologous to the DctAI gene"
146599. .447843
                                                                                                                                                                                                                                            /*tag= n
/standard_name= "ORF K14"
/standard_name= "ORF K14"
/product= "nifb"
/product= "protein involved in FeMo co-factor
blosynthesis"
complement (436460. .438130)
                             /product="protein of unknown function"
/note= "homologous to the FixU gene"
complement (434107. .434433)
                                                                                     /*tag* 1
/standard_name= "ORF K12"
/product= "protein of unknown function"
complement (434517. 434711)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /standard_name= "ORF L1"
/product= "cytochrome P450-11ke protein"
/note="homologous to the CamC gene"
447844. .448500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /standard_name= "ORF K20
/product= "protein of unknown function"
complement (443313. .443879)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'standard_name= "ORF K21"
|product= "protein of unknown function
| 144337. .445029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /standard_name= "ORF K22"
/product= "ferrodoxin-like protein"
/note= "homologous to the Nifo gene"
445088. .446602
                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (438297. .438590)
                                                                                                                                                                                                                                                                                                                                                    /*tag= o
/standard_name= "ORF K15"
/gene= "nifA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= p
/standard_name= "ORF K16"
/gene= "fixx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /standard_name= "ORF K17"
/gene= "fixC"
/*tag= k
/standard_name= "ORF K11"
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/gene= "fixA"
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'standard_name= "ORF K23"
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15658 CGCGAAAGTCTTAGGAATCTCTTGGGG 15684

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AQ468916 HS_5140_B2_H09_T7A
AA203261 zx55d11.r1 Soares_f
F14616 SSO4H02 Porcine small
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutherial Primates; Catarrhin!; Hominidae; Homo.

Eutherial Primates; Catarrhin!; Hominidae; Homo.

I (bases 1 to 103)

Bult,C.J., Lee,N.H.; Kirkness,E.F., Weinstock,K.G.; Gocayne,J.D., White,O., Sutton,G., Blake,J.A.; Brandon,R.C., Man-Wai,C.

Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J.; File,L.D., Fitzgerald,L.M.; Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.; Gnehm,C.L., Hanna,M.C.; Hedblom,E.; Hinkle,P.S.Jr., Kalley,J.M., Kelley,J.C., Lui,L.I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F.; McDonald,L.A., Nguyen,D.T.; Pelligrino,S.M., Phillips,C.A., Trydey,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Ulterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Tearle,A., Terrie,A., Testher C., Hastings,G.A., Losen,H., Meison,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Walt,Y.F., Rosen,C.A., Hasseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence
Nature 377 (6547 Suppl.), 3-174 (1995)
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9712 Medical Center Drive, Rockville, MD 20850 USA
19712 Medical Center Drive, Rockville, MD 20850 USA
19712 Medical Center Drive, Rockville, MD 20850 USA
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
For clone availability, additional sequence and expression
For clone availability, additional sequence and expression
For clone availability additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.hfml)
Seq primer: M13 Reverse.
Location/Qualifiers
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dev_stage="adult"
/dev_stage="adult"
/note="Organ: adrenal gland; Vector: pBluescript SK-;
site_1: EcoRI; Site_2: XhoI"
35 c 29 g 13 t
                                                                                                                                                                       seq_documentation_block:
LOCUS
AA319533
LOCUMENTION EST21772 Adrenal gland tumor Homo sapiens cDNA 5' end similar similar to major histocompatibility complex, class I, B
(GB:M16102), mRNA sequence.
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Other_ESTs: THC169519
Contact: Kerlavage, AR
Bioinformatics
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Gaps: 0
Percent Identity: 100.000
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gb_gss13:AQ468916
gb_est11:AA203261
gb_est4:F14616
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AW060987 UI-M-BH1-amn-c-01-0-UJ
AA083156 zn08d04.rl Stratagene
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zo57h10.s1 Stratagene
zo77e11.r1 Stratagene
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-WODEL-framet-p2n.model -DEV-Xlp
-Q-/Cgnl_1/USFTO_spool/USO8653294/runat_04022000_160700_15770/app_query.fasta.2
-Q-/Cgnl_1/USFTO_spool/USO8653294/runat_04022000_160700_15770/app_query.fasta.2
-DB-EST -OFMT-fastap -SUFFIX-rst -GAPOP=12.000 -GAPDT-4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP=6.000
-GAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-LIST-A5 -DOCALIGN=20 -THR_SCORE-PCT -ALIGN=15 -MODE-LOCAL
-GOUTPHT=pfs -NORM-SXT -MINLEN=0 -MALTEN-1000000 -USER-USO8653294
-NCPU-6 -ICPU-3 -NO_XLPXY -WAIT -THREADS=1
                                                                                                                          About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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query length: 10
batabase: EST:*
Database sequences: 4538634
batabase length: 1887831982
Search time (sec): 7600.090000
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gb_est13:AA351477
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gb_est10:AA158109
gb_est10:AA160714
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (Dases 1 to 189)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult.C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man Wal.C., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fittchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L. I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligarino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Utcreback, T.R., Weidman, J.T., Lollins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melssner, P.S., Olsen, H., Fracer, C., Mand, Varer, T., Raymond, L., Wei, Y., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fracer, C. M. and Varer, T. R., Restine, T. R., Fields, C., Fracer, C. M., Haseltine, W.A., Fields, C.,
                                                                                                                                                                                                                            A3361477 189 bp mRNA EST 21-APR-1997 EST70761 T-cell lymphoma Homo sapiens cDNA 5' end similar to similar to major histocompatibility complex, class I, Bw62.3, mRNA
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgl/hgl.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. 189
//organism="Homo sapiens"
//db_xref="tarcc (inhost):165623"
//db_xref="tarcc (inhost):165623"
//dbone_lib="T-cell lymphoma"
//cell_type="T-lymphocyte"
//note="Vector: pBluescript SR-; Site_1: EcoRI; Site_2: XhoI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Sep 12, 1996 this sequence version replaced gi:1404737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9712 Medical Center Drive, Rockville, MD 20850 USA
Rel: 3018699056
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Gaps: 0
Percent Identity: 100.000
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     to: 103
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                                                                            1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
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                                                                                                                                                                                                                                                                                                                                                          AA361477.1 GI:2013795
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Ratio: 5.100
Percent Similarity: 100.000
to: AA319533
                                                                                                                                                  seq_name: gb_est13:AA361477
                                                                                                                                                                                                       seq_documentation_block:
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                                                                                                                                                                                                                                                                                                             sequence
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Align seg 1/1
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                      DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
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COMMENT
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E 1 (bases 1 to 218)
S Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Kalton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Honkle, P.S. Jr.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.I., Marnaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednartk, D.P., Cao, L.,
Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dinke, D., Feng, D.-F., Ferife, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.W., Gruber, J., Hudson, P., Kim, A.K.,
Raymond, L., Wel, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Pallion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                         Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_fype="T-lymphocyte"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On May 8, 1995 this sequence version replaced gi:800964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
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/db_xref="taxon:9606"
/clone_lib="Activated T-cells xx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism-"Homo sapiens"
                                                                                                                               cocation/Qualifiers
                                                               from: 1
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AA352603.1 GI:2004923
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0
                                                               to: AA361477
US-08-653-294-34 x AA361477
                                                                                                                                                                                                                                                                      seq_name: gb_est13:AA352603
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 270)

Bult,C.J. Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkie,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., Heywow,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Callins,E.J., Kozak,D.L., Kunsch,C., Hugjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Well,Y.F., Wing,J., Yu,C., Yu,G.L., Ruben,S.M., Traser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
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Exactly availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hg1/hg1.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA352960 270 bp mRNA EST 21-APR-1997 EST61101 Activated T-cells XX Homo sapiens cDNA 5' end similar t similar to major histocompatibility complex, class I, B61, mRNA
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The Institute for Genomic Research
Tylz Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
                                                                                                                                                   Length: 10
Gaps: 0
Percent Identity: 100.000
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/db_xref="ATCC (inhost):153240"
/db_xref="taxon:9606"
/clone_lib="Activated T-cells XX"
/cell_type="T-lymphocyte"
                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
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AA352960.1 GI:2005353
                                                                                                                                                       Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AA294911
                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-34 x AA294911
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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COMMENT
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 259)

Buthcul, C.J., Lee, N. H., Kirkness, E.F., Wethstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Philligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Tischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Maksner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Ming, J., Xu, C., Yu, G.L., Ruben, S.M., Fraser, C.M., and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS AA224911 259 bp mRNA EST 18-APR-1997
DEFINITION EST100074 Pancreas tumor I Homo sapiens cDNA 5' end similar to
similar to major histocompatibility complex, class I, Bw62.3, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
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On Nov 29, 1993 this sequence version replaced g1:430148.
Other_ESTS: THC172938
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Tel: 3018699056
                                                                         Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .259
                                                                                                                                                                                                                                                                                                                       from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: M13 Reverse
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AA294911
AA294911.1 GI:1947266
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                                                                         Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AA352603
                                                                                                                                                                                        alignment_block:
US-08-653-294-34 x AA352603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_est12:AA294911
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alignment_scores:
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VERSION
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                                                                                                                                                   alignment_scores
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BASE COUNT
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/db_xref="tobs:3813009"
/db_xref="tobs:3813009"
/db_xref="tobs:3813009"
/clone="IMAGE:509677"
/clone="IMAGE
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 373)

(Dases 1 to 373)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,

Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le-M., Le-M., Le-M., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J.,

Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.,

and Marra, M.
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Genome Res. 6 (9), 807-828 (1996)
97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK Washington University School of Medicine Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the Insert Length: 1592 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 268.
                                        Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block: 01-DEC-1996
LOCUS AA058454 373 bp mRNA EST 01-DEC-1996
DEFINITION z167407.r1 Stratagene colon (#937204) Homo sapiens cDNA clone INAGE:509677 5' similar to gb:MZ4039_cds1 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA (HUMAN);, mRNA
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                                                                                                              5 others
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Gaps: 0
Percent Identity: 100.000
   /dev_stage="adult"
/note="Vector: pBluescript SK-;
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CTCGAGITITITITITITITI 3'
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Ratio: 5.100
Percent Similarity: 100.000
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US-08-653-294-34 x AA352960
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DEFINITION
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 397)

Hillari,, Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Markins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le, N., Le, N., Chan, Le, N., Chan, Chan,
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Genome Res. 6 (9), 807-828 (1996)
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This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: -28ml3 revi ET from Amersham
High quality sequence stop: 295.
Localin/Qualifiers
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Contact: Wilson RK
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444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1810
Fax: 314 286 1810
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                                                                                 Percent Identity: 100.000
Length:
                                           Gaps:
                                                                                                                                                                                                                                                                                                                    to: 373
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/db_xref="GDB:5588245"
/db_xref="taxon:9606"
/clone="IMAGE:648507"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 CGAGAGACCTGCGGAACCTGCGCGCTAC 258
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AA224068.1 GI:1844610
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                                      Ratio: 5.100
Percent Similarity: 100.000
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US-08-653-294-34 x AA058454
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Quality:
Ratio:
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Auloul, 400 pp mkna EST 09-MAR-1998 zo56c07.rl Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:590892 5' similar to gb:Ull265 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3501 ALPHA (HUMAN);, mRNA sequence. AA160317 GI:1734956
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fea: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 315 280 1810
Fax: 315 280 1810
Fax: 316 58 200 1810
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1 (bases 1 eq.405)

1 (lasses 1 eq.405)

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                                            Length: 10 Gaps: 0 Gaps: 0 Percent Identity: 100.000
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Gaps: 0
Percent Identity: 100.000
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                                                 Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
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Ratio: 5.100
Percent Similarity: 100.000
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US-08-653-294-34 x AA224068
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US-08-653-294-34 x AA160317
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LOCUS AA160317
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alignment_scores
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/organism="Homo saplens"
/db_xref="GDB:126313"
/db_xref="GDB:126313"
/db_xref="Tacker="Jeff"
/clone="Ibb"Fancreatic Islet"
/clone="Ibb"Fancreatic Islet"
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/iab_host="SolR cells (kanamyoin resistant)"
/note="Organ: pancreas; Vector: pBluescript Sr.; Site_1:
/note="Organ: pancreas; Sr.; Site_1: pancreas; Sr.; Site_1:
/note="Organ: pancreas; Sr.; Site_1: pancreas; Sr.; Site
                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:

LOCUS W40489

MAG1489

DEFINITION 2684001.r1 Pancreatic Islet Homo sapiens CDNA clone IMAGE:328969'5'

SIMILAR to gb:U11265 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35

B-5501 ALPHA (HUMAN);, mRNA sequence.

VERSION W40489.1 GI:1324496
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 427)
Hiller,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dierrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Mardis,E., Moorris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Fravaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generation and analysis of 280,000 human expressed sequence tags Genome_Res. 6 (9), 807-828 (1996)
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This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
ThAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGH+ET
High quality sequence stop: 397.
Localion/Qualifiers
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On Jan 25, 1995 this sequence version replaced gi:637865.
On Jan 25, 1995 this sequence version replaced gi:637865.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 18100
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Gaps: 0
Percent Identity: 100.000
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Ratio: 5.100
Percent Similarity: 100.000
to: AA160317
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US-08-653-294-34 x W40489
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    Align seg 1/1
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rel: 0886-65-2888
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Ratio: 5.100
Percent Similarity: 100.000
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US-08-653-294-34 x C18310
                                                                                                                                                   seq_documentation_block:
                                                                                                       seq_name: gb_est9:C18310
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AUTHORS
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AUTHORS
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KEYWORDS
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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Bult. C.J., Lee, N. H., Kirkness, E.F., Wenistock K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man Wal, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P. S.Jr.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanquees, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,

Kozak, D.L., Welly, T.W., Wing, J.M., Gruber, J., Hudson, P., Kim, A.K.,

Baymond, L., Welly, T., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Blillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,

Frascr, C.M., and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                      For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Jurkat T-cells V"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                     Vertebrata; Mammalla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Sep 12, 1996 this sequence version replaced g1:1397854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    others
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Gaps: 0
Percent Identity: 100.000
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/db_xref="taxon:9606"
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279 CGAGAGACCTGCGAAACCTGCGCGGCTAC 308
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                                                                                                                                                                                           AA310808
AA310808.1 GI:1963136
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Contact: Kerlavage, AR
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US-08-653-294-34 x AA310808
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                                       seq_name: gb_est12:AA310808
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Ratio:
Percent Similarity:
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin; Hominidae; Homo.
Eutheria; Primates; Catarrhin; Hominidae; Homo.

I (bases 1 to 475)

Sulvai, Magata, M., Ckuno, S., Ozaki, K., Shimizu, F., Shimda, Y., Shinomiya, H., Suzuki, M., Takaichi, A., Takeda, S., Watanabe, T., Maekawa, H., Nakamura, Y. and Takahashi, E.

Otsuka CDNA project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1393837.
Contact: Tsutomur Fullwara
Otsuka GEN Research Institute
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 kagasuno Rawauchi-cho, Tokushima, Tokushima, 771-01 Japan
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LOCUS AA663896 479 bp mRNA

DEFINITION ae74d401.s1 Strategene schizo brain S11 Homo sapiens cDNA clone
IMAGE:969889 3' similar to gb:M28203 HIA CLASS I HISTOCOMPATIBILITY

ANTIGEN, B-62 B*1504 ALPHA (HUMAN);, mRNA sequence.

ACCESSION AA653896
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
C18310 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-560D07 5', mRNA sequence.
C18310
EST
C18310.1 GI:1579912
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="GEN-560D07"
/clone_11b="Human placenta cDNA (TFujiwara)"
/tissue_type="placenta"
in 161 c 154 g 68 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 10
Gaps: 0
Percent Identity: 100.000
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Maria Caraca

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alignment_scores
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                           source
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DEFINITION
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ORIGIN
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MEDLINE
COMMENT
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AUTHORS
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          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_rype="schizophrenic brain S-11 frontal lobe"
/dev_stage="34 years old"
/dev_stage="34 years old"
/lab_host="solR (kanamycin resistant)"
/note="vector: Bluescript SR:; Site_1: EcoRI; Library
/note="vector: Bluescript SR:; Site_1: EcoRI; Library
constructed from S-11 frontal lobe, male, 34 years old,
50% caucasian, 50% Aleutian. Schizophrenic suicide.
Random primed into EcoRI site of ZAP II vector. Mass
excised. Custom library. Avg insert length 1.4kb.
Material obtained by Johnston N.; Torrey, Er.; Volken R.,
and the Stanley Neuropathology Consortium - Analysis of
RNAs from the Brains of Individuals with Psychiatric
Diseases (Unpublished) Stanley Neurovirology Laboratory,
Johns Hopkins School of Medicine, Baltimore MD."
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project

L. Unpublished (1997)

On Sep 12, 1996 this sequence version replaced gi:1394858.

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Email: estewatson.watl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: polyT not found Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:

LOCUS AL039796 503 bp mRNA EST 29-SEP-1999
DEFINITION DKF2p434B1912_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKF2p434B1912 5', mRNA sequence.

ACCESSION AL039796 1 GI:5408804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 503)
Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                           1. 479
// Organism-"Homo sapiens"
// Ab_xref="taxon:9606"
// Clone="IMAGE:969889"
// Clone=lib="Stratagene schizo brain Sll"
// Sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 10
Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 CGAGAGAGCCTGCGGAACCTGCGCGGCTAC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
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Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
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Ratio: 5.100
Percent Similarity: 100.000
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US-08-653-294-34 x AA663896
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JOURNAL
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KEYWORDS
SOURCE
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                                                                                                                              COMMENT
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Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s. Wiemann(dkfz- heidelberg.de;
Research Center (DKF2); Email s. Wiemann(dkfz- heidelberg.de;
Sequenced by Qiagen within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers
rce / Organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA263135 710 bp mRNA EST 02-JUL-1998
PMY0598 KGJ-a Lambda Zap Express CDNA library Homo sapiens CDNA 5',
mRNA sequence.
AA263135.1 GI:1898941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human.

Human.

Human.

Human.

Homo sapiens

Hukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 710)

Claudio, 7.0., Libuw, C.C., Dempsey, A.A., Cukerman, E., Stewart, A.K.,

Na, E., Atkins, H.I., Iscove, N.N. and Hawley, R.G.

Identification of sequence-tagged transcripts differentially

Genomics 50 (1), 44-52 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :: pSportl; Site_1: NotI; Site_2: SalI"
165 g 68 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Hawley RG
Conclogy Research Laboratories
The Toronto Hospital
CRCS-424, 67 College St., Toronto, Ontario M5G 2M1, Canada
Frax: 416 340343
Email: r.hawley@utoronto.ca
On Jun 2, 1999 this sequence version replaced g1:4967270.
Contact: Duesterhoeft A
MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone was randomly picked from KGla primary library.
Seq primer: 5. GAAATTAACCCTCACTAAAGGG 3'
High quality sequence stop: 710.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio: 5.100 Length: 10 Ratio: 5.100 Gaps: 0 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="DKFZP434B1912"
/clone_llb="434 (synonym: htes3)"
/tssue_type="testis"
/dev_stage="adult"
/lab_nost="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 CGAGAGACCTGCGGAACCTGCGCGGCTAC 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 c
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US-08-653-294-34 x AL039796
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63
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                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                              ORIGIN
                                                                           /clone_lib="KGl-a Lambda Zap Express cDNA library"
/cell_type="promyeloblast"
/cell_type="promyeloblast"
/cell_type="promyeloblast"
/cell_type="promyeloblast"
/note="wector: Lambda Zap Express (Stratagene); Site_l:
ECORI; Site_2: XhoI; Unidirectional cloning sites:
ECORI; Site_2: XhoI; Unidirectional cloning sites:
ECORI-XhoI. mRNA was purified from KGl-a cell line, cDNA was synthesized using an XhoI-OligodT linker primer. ECORI adaptors were ligated, followed by digestion with XhoI for directional cloning into predigested Lambda Zap Express"
224 c 227 g 109 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI424623 209 bp mRNA EST 30-MAR-1999
LT34901.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2098128 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1to 209)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index

Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Apr 21, 1998 this sequence version replaced g1:3072294. Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .209
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2098128"
/clone="IMAGE:2098128"
/clone="ID="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 10
Gaps: 0
Percent Identity: 100.000
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1. .710
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Seq primer: -400P from Gibco
High quality sequence stop: 208.
Location/Qualifiers
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A1424623
A1424623.1 GI:4270554
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Ratio: 5.100
Percent Similarity: 100.000
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US-08-653-294-34 x AA263135
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LOCUS AI424623
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        source
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VERSION
KEYWORDS
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AUTHORS
TITLE
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COMMENT
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/note-"Organ: brain; Vector: p17T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                                                                                                                                                                                                                                                                            to: 209
                                                                                                                                                                                                          Percent Identity: 100.000
                                                                                                                                                                                                                                                                            from: 1
                                                                                                                                                                                                                                                                                                                 to reverse of: AI424623
                                                                                                                                                                                                                                                                                                   1 ArgGluSerLeuArgAsnLeuArgGly 9
                                                                                                                                                                                                                                                     :
                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-34 x AI424623/rev
                                                                                                                                                                                 Quality: 44.00
Ratio: 4.889
Percent Similarity: 100.000
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Search time 133.56 Seconds (without alignments)
3.547 Million cell updates/sec February 8, 2000, 04:05:44 Run on:

US-08-653-294-35 Title:

Perfect score:

102 1 YGRLNRLSERRESLRNLRGY 20 Sequence: 188963 seqs, 23686106 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. A_Geneseq_36:* Database :

H. pylori GHPO 144 Consensus sequence	Human L5/3 tumour Human L5/3 tumour	Human L5/3 partial Human L5/3 partial	Macrophage stimula Human L5/3 tumour	Macrophage stimula Human growth facto	Human MSP protein.
W98326 P80911	R66597 R66598	W14266 W14267	W07691 R66602	W07692 W14270	W82789
					7
219	705 705	705	710	711	711
40.2	40.2	4 4 6 7 7	40.2	40.2	40.2
4 1 1 1	41	4 4	414	4 4 1	41
35 36	37 38	e 4 0 0	417	<b>4</b> 4	. 42

## ALIGNMENTS

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Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-BY. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs)
                                                                          16-MAY-1996 (first entry)
HLA-B7 CTL modulating peptide (B7.84-75/75-84).
CYtotoxic T Lymphocyte; CTL; major histocompatibility complex; MHC; imminosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B7.
                                                                                                                                                                                                                                                                                                                 Clayberger C, Krensky AM, Parham P; WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                       05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
                                       R92913 standard; peptide; 20 AA.
                                                                                                                                                                                                                                  12-OCT-1995.
05-APR-1995; U04349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the patient.
                                                                                                                                                                                        Synthetic.
WO9526979-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
RESULT
                     R9291
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Gaps ó 100.0%; Score 102; DB 1; Length 20; 100.0%; Pred. No. 1.3e-09; Ive 0; Mismatches 0; Indels Ouery Match Best Local Similarity 100. Matches 20; Conservative

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1 YGRLNRLSERRESLRNLRGY 20 1 YGRLNRLSERRESLRNLRGY 20 à

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7

185415 standard; peptide; 20 AA.
R95415.
R95415.
R95415.
R95415.
R95415.
R95415.
R95415.
R954175.
R955175.
R955 RESULT R95415 ID R9 AC R9 DD 12 DD H11 KW HIL KW TT-KW B KW CY OS SY PD 18

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Seguence
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                                                                                                                                Composes. Comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example: Page 18: 29pp: English.

Example: Page 20pp: Engli
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Example 1; Page 19; 41pp; English.

Peptides Wa3784-99 and Wa3778-9 were assayed for their immunomodulating activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or (aa80 = 1 or N; aa81, aa84 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B alphal domain (positions)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Peptide B7.84-75-75-84 tested for immunomodulating activity.
Immunomodulating dimer. Immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
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22-NAX-1997, U08689.
24-NAX-1996, US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                      STRD ) UNIV LELAND STANFORD JUNIOR
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                                                                                        Krensky AM;
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Best Local Similarity 100.
Matches 20; Conservative
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
                                                                                                          WPI; 95-194027/25
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WO9744351-A1.
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PF 2-MAY-1997.

PF 2-MAY-1997.

PF 2-MAY-1997.

PF 2-MAY-1997.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.

P Beulow R, Clayaberger C, Krensky AM;

PD Beulow R, Clayaberger C, Krensky AM;

PT MPI; 98-086530/08.

PT alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases.

PT treating autoimmune diseases.

PR Ample 1; Page 19; 41pp; English.

PR Example 1; Page 19; 41pp; English.

PR Example 1; Page 19; 41pp; English.

CC ctivity. A peptide-type compound or variant is claimed which has cimmunomodulating activity, including the N-terminal acylated and/or comprises the peptide-type compound computing the N-terminal acylated and/or comprises the formula; A=8, Where A; B= CC terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A=8, Where A; B= CC T R; and an represents amino acid; aa87 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or compliant amino acid; aa82 = R or L; aa83 = G or R; and an represents amino acid; acid; aa82 = R or L; aa83 = G or R; and an expresents amino acid; acquences related to a class I HLA-B alphal domain (positions of an any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B alphal domain (positions of a major activate CTLS. They can also inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, chemister, and allowers and lump and the products can also be continuated atthirties and lumpus erythematosis. The products can also be continuated.
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79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rhemmatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
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Peptide B7.84-75-75-84 tested for immunomodulating activity.
Immunomodulating diam: immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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100.0%; Pred. No. 1.3e-09;
cive 0; Mismatches 0;
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100.0%; Pred. No. 1.3e-09;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 20; Conservative
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WO9744351-A1.
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Matches 20;
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100.0%; Pre
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100.00; Pre
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                                              Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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12-MAY-1995; US-440504.
                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MX-1996 (first entry)
HLA-B7 CTL modulating peptide (B7.75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B7.
                                                                                                                                                                                                                                  Mer, 35 Joint 187.

Mer, 35 Joint 187.

Medulating cytotoxic T-lymphocyte activity towards targets claim 11; Page 54; Elpp. English.

The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplashs and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition. This peptide sequence is more commonly found within larger peptide compounds of not more than 30 amino acids in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                         15-MAR-1994 (first entry)
Peptide fragment of Class I HLA peptide.
Human leukocyte antigen: HLA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic I lymphocyte; modulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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05-ARR-1995; U04349.
05-ARR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
                                                                                                                                              16-SEP-1993.
25-FEB-1993: U01758.
02-MAR-1992: US-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
CLAYDEFGER CA, Krensky AM;
WPI; 93-303134/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; Page 66; 80pp; English.
                             R41209 standard; peptide; 10 AA
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Best Local Similarity 100.
Matches 10; Conservative
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W09526979-A1.
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RESULT
R41209
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R83061
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Ouery Match

Matchess 10: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

Matchess 10: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

Dr. 11 RESIGNARRY 10

11 RESIGNARRY 10

MATCHES 10: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

MATCHES 10: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

MATCHES 10: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

MATCHES 10: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

MATCHES 10: Missocompetable 10 AA.

MATCHES 10: Missocompetable 10 AA.

MATCHES 10: Missocompetable 10 AA.

MATCHES 10: Missocompetable 10: Mismatches 0: Gaps 10: Mismatches 0: Missocompetable 10: Mismatches 0: Mismatc
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                                                                                                                      Per leulow R. Clayberger C. Krensky AM;

WPI: 98-086530/08.

WPI: 98-086530/08.

WPI: 98-086530/08.

WPI: 98-086530/08.

WPI: 98-086530/08.

WPI: 98-086530/08.

Treating autoimmune diseases

Example I; Page 19; 41Pp; English.

Example I; Page 19; 41Pp; 41Pp;
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22-MAY-1997; U08689.

23-MAY-1997; U08689.

24-MAY-1997; U08689.

25-MAY-1997; U08689.

25-MAY-1997; U08689.

25-MAY-1997; U08689.

27-MAY-1997; U08689.

27-MAY-1997; US-C53294.

28-MAY-1997; US-C53294.

28-MAY-1997; US-C53294.

29-MAY-1997; US-C53294.

20-MAY-1997; US-C532
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Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51; DB 1; Length 10;
Pred. No. 0.043;
0; Mismatches 0; Indels
                            22-MAY-1997; U08689.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 50.0
Best Local Similarity 100.
Matches 10; Conservative
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WO9744351-A1.
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amino acid sequences related to a class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLS. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIA-Bw62 CTL modulating peptide (Bw62.60-84).
Yordoxola T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HIA-Bw62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptide(s) based on class I HLA antigen domains - used for modulating cytotoxis. Tymphocyte activity towards targets modulating cytotoxic T-lymphocyte activity towards targets.

Claim 10; Page 54; 61pp; English.

The peptide (or a fragment of at least 10 amino acids, joined at at least one terminus to a sequence other than that of wild type HLA antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAR-1994 (first entry)
peptide tragment of class I HLA peptide.
Human leukocyte antigen: HLA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic T lymphocyte; modulation.
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25-FEB-1993; U01758.
02-MRR-1992; US-844716.
(STR.) UNIY LELAND STANFORD JUNIOR.
Clayberger CA. Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R41207 standard; peptide; 25 AA.
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16-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 50.0
Best Local Similarity 100.
Matches 10; Conservative
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05-APR-1995; U04349.
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Best Local Similarity
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WO9526979-A1.
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Conservative
                      Query Match
Best Local Similarity
Matches 10; Conserv
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WPI; 95-194027/25
                                                                                                                                                                 16 RESLRNLRGY
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                                                                                                                                                                                                                                                                                                                                         12-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Will solidate to comparison lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example 12, 20pp; English.

Example 26.84

Example 26.84

These sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein p74 is associated with T-cells of ell types, but is particularly expressed on memboteric detergent, and then passed through an affinity column correct amphoteric detergent, and then passed through an affinity column correct amphoteric detergent, and then passed through an affinity column correct containing a covalently bound HLA-B7702 palindromic oppidate

Compounds can be screened for their effect on the cytolysis. Candidate

CT-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74.

Containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete containing T-cells and antigen presenting cells (APCS), by adding to the conners.
                                                                                                                                                  Example 13; Page 32; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC mHA-Bw62. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the settivity of the cytotoxic T lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLA: D74: alphal-helix; human-leucocyte-associated antigen; inhibitor; T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                             Clayberger C, Krensky AM, Parham P;
WPI; 95-538882446.
Extension of acceptance period of transplants from MHC unmatched
donor hosts. using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 51; DB 1;
Pred. No. 0.11;
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05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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100.0%; Pre
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R95431;
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Best Local Similarity
Matches 10; Conserv
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WPI; 95-194027/25
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HLA-B7.60-84.
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WWI! 99-19402//25.

PT compans. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example: Page 9; 29pp; English.

Example: Page 9; 29pp; English.

CC R95413, and R95418-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the HLA-BW62.60-84. These sequences can be used to isolate the protein protein arcell lyaate. p74 is a T-cell surface membrane protein p74 is associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. p74 is found in a limited number of cell types, but is particularly expressed on and T cells. p74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide.

C mapositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits corpounds can be screened for their effect on the cytolytic activity of treells, by combining them with the extracellular portion of p74 and etermining the amount of binding between the candidate compound and p74.

Modulation of CTL activity can be inhibited in a cellular composition mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.

Sequence 25 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
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                                                                                Gaps
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                                                                                0; Indels
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                                                    0.11;
50.0%; Scor.
100.0%; Pred. No. v...
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10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                                                                                                                                                                                                                                                   R95419 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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29-AUG-1991 (first entry)
HLA-B35 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krensky AM;
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                      Claim 1; Page 1; Ilpp; Japanese.

Probes comprising part of the sequence encoding this sequence can be used to identify Class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HIA-B35 antigen. See also J03112485 and J03112487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel anti-microbial protein from e.g. Macadamia integrifolia - useful for controlling microbial infestations of plants or mammals Claim 1: Page 63-65; 96pp; English.

The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammalian animals.
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Θ
                                                                              N-PSDB; Q12115.
HLA-B35 gene - used in DNA probe and transformant cells for
immunising animals, for developing monoclonal antibody.
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                                                                                                                                                                                                                                                              Query Match 50.0%; Score 51; DB 1; Length 362; Best Local Similarity 100.0%; Pred. No. 1.8; Matches 10; Conservative 0; Mismatches 0; Indels
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20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
Bower II. Coulter KC, Green JL, Manners JM, Marcus JP;
WPI; 98-377279/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                W62838;
27-OCT-1998 (first entry)
Glycine max antimicrobial protein.
antimicrobial protein; infestation; control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 46.6%; Score 47.5; I Best Local Similarity 47.8%; Pred. No. 11; Matches 11; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               W62838 standard; Protein; 605 AA.
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                                  22-SEP-1989; JP-247697.
(OLYU ) OLYMPUS OPTICAL KK.
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                 22-SEP-1989; 247697
22-SEP-1989; JP-247
                                                                  WPI; 91-182991/25.
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WO9827805-A1.
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Search completed: February 8, 2000, 04:05:44 Job time: 9361 sec

211 YGRIRVLORFNORSPOLONLRDY 233

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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	February 7, 2000, 18:04:41; Search time 111.22 Seconds (without alignments) 8.482 Million cell updates/sec		
OM protein - protein search, using sw model	February 7, 2000, 18:04:41	US-08-653-294-35 102 1 YGRLNRLSERRESLRNLRGY 20	BLOSUM62 Gapop 10.0 , Gapext 0.5
OM protein - pr	Run on:	Title: Perfect score: Sequence:	Scoring table:

142080 Total number of hits satisfying chosen parameters:

142080 seqs, 47169319 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

PIR_62:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	class I	MHC class I antige	MHC class I antige	class I	ä	class I	Ė	ໝ	l sur	Chla cha	class I ly	77	class I histocompa	н	H	н	н	ılst		н		MHC class I histoc	ss I hi		н	class I	class I	υ	HLA-B*5602 - human	lymphocyte antigen
SUMMARIES																															
SUM	Ð	138875	138876	138860	138874	159188	HLHU40	I68774	S24439	168701	I36956	I68747	I54308	S24436	524437	S24438	S24440	S24433	S03538	I54418	HLHUB7	<b>311966</b>	G01230	S16789	A45880	137519	375	137522		7	⋖
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	Score	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51
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362 2 172752 362 2 172753 362 2 172754 362 2 134437 362 2 134437 362 2 134505 362 2 136962 362 2 136962 362 2 156149 362 2 156149 362 2 156149 362 2 156149 362 2 161865	HLA-B*5501 - human HLA-B*5502 - human HLA-B*5502 - human MHC class I histoc HLA-B alpha-chain lymphocyte antigen HLA-B*5401 - human MHC class I protei HLA-B*5401 - human MHC slass I protei HLA-B*5401 - human MHC slass I protei lymphocyte antigen lymphocyte antigen lymphocyte antigen MHC HLA-BW42, HLA- MHC HLA-B14 chain MHC HLA-B18 chain	
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## ALIGNMENTS

RESULT 138875

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A; Gene: GDB:HLA-B
A; Cross-references: GDB:120048; OMIM:142830
A; Map position: 6p21.3-6p21.3
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterodimer; membrane protein; transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: 168774
R;Mueller, C.A.; Engler Blum, G.; Gekeler, V.; Stelert, I.; Weiss, E.; Schmidt, H.
Immunogenetics 30, 200-207, 1989
A;Title: Genetic and serological heterogeneity of the supertypic HIA-B locus specific
A;Reference number: 154463; MUID:89379286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: A02186
R; Lopez de Castro, J.A.; Bragado, R.; Strong, D.M.; Strominger, J.L.
Blochemistry 22, 3961-3969, 1983
A; Title: Primary structure of papain-solubilized human histocompatibility antigen HLA A; Reference number: A02186; MUID: 84000412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Comment: Comparison of a number of class I allelic sequences (-B40 vs. -B7 and -A2 y restricted to the alpha-1 and alpha-2 domains. The most conspicuous clustering of v ossible alloantigenic determinants of these antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHC class I histocompatibility antigen HLA-B40 alpha chain - human (fragment) C;Species: Homo sapiens (man) C;Date: 28-Aug-1985 #text_change 02-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
A;Map position: 6p21.3-6p21.3
A;Introns: 90/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: glycoprotein
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A;Residues: 1.274 KRES.
A;Coss.references: GB:M29865; NID:g187676; PIDN:AAA36223.1; PID:g187677
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                        Gaps
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F;195-260/Domain: immunoglobulin homology <IMM>
F;86/Binding site: carbohydrate (Asn) (covalent) *status experimental
F;101-163,202-258/Disulfide bonds: *status predicted
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1.8;
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1.8;
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1.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 1-270 <LOP>
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les 10; Conserv
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Best Local Similarity
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                                                                                                   MHC class I antigen - human (fragment)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Species: O7-Un-1996 #sequence_revision O7-Jun-1996 #text_change 23-Jul-1999

C;Accession: 138860

R;Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stefand Immunogenetics 42, 19-27, 1995

A;Title: HLA-B alleles of the Cayapa of Ecuador: new B39 and B15 alleles.

A;Reference number: 138860; MUID:95317819

A;Reference number: 138860

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-137 <RES

A;Cross-references: EMBL:U14756; NID:9930328; PIDN:AAC50171.1; PID:9930329

C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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Cipecies: Homo sapiens
Cipecies: Natl. 1998
Cipecies: Natl. 1999
Cipecies: Natl. 
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Pred. No. 0.91;
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MHC cell surface glycoprotein - human (fragment)
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100.0%; Pre
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 10; Conservative
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C;Genetics: A;Gene: GDB:HLA-B

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C; Species: Homo saplens (man)
C; Species: Homo saplens (man)
C; Species (2-101-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C; Accession: I54308
R; Rodriguez, S.G.; Johnson, A.H.; Hurley, C.K.
Hum. Immunol, 37, 1993
A; Title: Molecular Characterization of HLA-B71 from an African American Individual.
A; Reference number: I54308; MUID:94064392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 07-Jun:1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C;Date: 07-Jun:1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C;Accession: 16847
R;Pobla, H: Kuon, W: Tabaczewski, P.; Doerner, C.; Weiss, E.H.
Immunogenetics 29, 297-307, 1989
A;Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the B A; Reference number: 154457; MUID:89233295
A;Accession: 168747
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                      A) Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross:1-308 < RES>
A;Cross-references: GB:MZ4044; NID:g176812; PIDN:AAA35423.1; PID:g176813
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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A;Cross-references: GB:M28204; NID:9576472; PIDN:AAA53257.1; PID:9576473
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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A;Cross-references: GB:L07950; NID:g307236; PIDN:AAA59683.1; PID:g307237
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                                                             R.Parham, P., Lawlor, D.A.; Lomen, C.E.; Ennis, P.D. J. Immunol. 142, 3937-3950, 1989
A.Fitle: Diversity and diversification of HLA-A,B,C alleles. A;Reference number: 136956; MUD:89235215
A;Accession: 136956
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A, Status: preliminary: translated from GB/EMBL/DDBJ
A, Molecule type: mRNA
A, Residues: 1-350 <RES>
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llarity 100.0%; Pred. No. 2.3;
Conservative 0; Mismatches
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154308
MHC HLA B71 - human (fragment)
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Matches 10; Conserv
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Best Local Similarity
Matches 10; Conserv
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C;Date: 02-Jul-1996
C;Accession: 136956
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R:Arnot, D.; Lillie, J.W.; Auffray, C.; Kappes, D.; Strominger, J.L.
R:Arnot, D.; Lillie, J.W.; Auffray, C.; Kappes, D.; Strominger, J.L.
Immunogenetics 20, 237-252, 1987
Immunogenetics 20, 237-252, 1987
A; Reference number: 154412; MUID:84287690
A; Reference number: 1548101
A; Reference number: 1548101
A; Residue; preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-300 CRES-
A; Residues: 1-300 CRES-
A; Residues: 1-300 CRES-
B; Cross-references: GB:MA7540; NID:9187733; PIDN:AAA59638.1; PID:9386890
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Keywords: surface antigen
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Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                          class I histocompatibility antigen HLA-B-3901 - human (fragment)
C.Species: Homo sapiens (man)
C.Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 07-Nov-1997
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C;Species: Pan troglodytes (chimpanzee)
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R;Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garbe Nature 357, 329-333, 1992
A;Title: Arecombinant HLA-B alleles in a tribe of South American Amerindians indicate A;Reference number: S24437
A;Accession: S24437
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C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Superfamily: class I histocompatibility antigen
E; 1-17/Domain: signal sequence #status predicted <SIG>
E; 17-394/Product: class I histocompatibility antigen HLA-B-4802 #status predicted <AXI>
E; 107-198/Domain: alpha-2 #status predicted <EXI>
E; 107-198/Domain: alpha-2 #status predicted <EXI>
E; 212-277/Domain: immunoglobulin homology <IMM>
E; 300-323/Domain: transmembrane #status predicted <IMM>
E; 324-354/Domain: intracellular #status predicted <INI>
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live 0; Mismatches
Best Local Similarity 100.0%; P. Matches 10; Conservative 0;
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A; Residues: 1-354 <WAT>
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C;Accession: S24438
R;Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Ga Nature 357, 329-333, 1992
A;Title: New recombinant HLA-B alleles in a tribe of South American Amerindians indic A;Reference number: S24027; MUID:92269956
A;Accession: S24438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Superfamily: class I histocompatibility antigen; immunoglobulin homology C; Superfamily: class I histocompatibility antigen; immunoglobulin homology C; Keyvords: glyroprotein; transmembrane protein his signal sequence #status predicted <SIG> F: 17-354/Product: class I histocompatibility antigen HIA-B-4801 #status predicted <WA F: 17-99/Pommain: extracellular #status predicted <EXT> F: 17-99/Pommain: alpha-2 #status predicted <EXT> F: 107-198/Pommain: immunoglobulin homology <IMM>
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C;Date: 22-Nov-1993 #sequence_revision 18-Jul-1997 #text_change 07-Nov-1997
                                                                                                                                                                                                                                                                                                                                                                                                             class I histocompatibility antigen HLA-B-4801 precursor - human (fragment)
                                                                             Gaps
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7:343-354/Domain: intracellular #status predicted <INT>
F;102/Binding site: carbohlular #status predicted <INT>
F;107-180,219-275/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%; Score 51; DB 2; Length 354; 100.0%; Pred. No. 2.4; cive 0; Mismatches 0; Indels
Length 354;
DB 2;
2.4;
                                                                         0; Mismatches
Score 51;
Pred. No.
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glycine max pseudomonas homo sapien glycine max homo sapien homo sapien homo sapien homo sapien homo sapien

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Title: Perfect score:

Run on:

ΜO

Sequence:

Scoring table:

Searched:

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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-APT-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-60(B-40) B*4001 ALPHA CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE: 84000412.
LOPEZ DE CASTRO J.A., BRAGADO R., STRONG D.M., STROMINGER J.L.;
"Primary structure of papain-solubilized human histocompatibility
antigen HLA-B40 (-Bw60). An outline of alloantigenic determinants.";
Biochemistry 22:3961.3969(1983).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE INMUNE SYSTEM.

-1-FUNCATION: ANYOLYEE IN THE FRESENIALION OF COLLEGE ANYONE SYSTEM.

-1-SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).

R PISA, A02186; HILHUAO.

R MIN; 142830.

R PRAM; PFO0047; 19; 1.

R PFAM; PFO0047; 19; 1.

MMC I; Glycoprotein.

T DOMAIN

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T DOMAIN

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T SEQUENCE 270 AA; 31205 MW; BFE44EFF CRC32;
 P30498
P13916
Q05395
P30499
P11827
P10321
P30484
P30686
P30508
P30508
P30508
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 10; Conservative 0; Mismatches
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Last annotation update)
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1863_HUMAN
GLCA_SOYBN
HRPJ_PSESY
1001_HUMAN
1CXX_HUMAN
1CXX_HUMAN
1C01_PANTR
1C02_HUMAN
1C05_HUMAN
1C06_HUMAN
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 11 RESLRNLRGY
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1B24_HUMAN
1D 1B34_HUMAN
AC P30470;
DT 01-APR-1993 (
DT 15-7UL-1999 (
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P01890;
 SEQUENCE.
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1B33_HUMAN
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               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                              8, 2000, 01:26:01;
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1B02_HUMAN
1B02_PANTR
1B04_HUMAN
1B07_HUMAN
1B08_HUMAN
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1B28_HUMAN
1B31_HUMAN
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1834_HUMAN
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1848_HUMAN
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1B24_HUMAN
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1B25_HUMAN
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1B39_HUMAN
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1B56_HUMAN
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                                                                   protein - protein search, using sw model
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1 YGRLNRLSERRESLRNLRGY 20
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Gapop 10.0 , Gapext 0.5
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Listing first 45
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Maximum DB seq length: 1000000
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Match Length
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Result No.

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P01889;
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01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-5 ALPHA CHAIN PRECURSOR.
Pan troglodytes (Chimpanzee).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Primates; Catarrhini; Hominidae; Pan.
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HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3504 ALPHA CHAIN PRECURSOR (FRAGMENT).
HLA-B OR HLAB.
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                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                 MEDLINE; 92269956.
WATKINS D.I., MCADAM S.N., LIU X., STANG C.R., MILFORD E.L.,
LEVINE C.G., GARBER T.L., DOGON A.L., LORD C.I., GHIM S.B.,
TROUP G.M., HUGHES A.L., LETVIN N.L.;
"New recombinant HIA-B alleles in a tribe of South American
Amerindians indicate rapid evolution of MHC class I loci.";
Nature 357:329-333(1992).
                                                                                                                                                                    THE IMMUNE SYSTEM.
SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.0%; Score 51; DB 1; Length 354; 100.0%; Pred. No. 0.8; ive 0; Mismatches 0; Indels
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EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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BY SIMILARITY.
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BY SIMILARITY.
; 6564795A CRC32;
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PFAM; PF00129; MG_I; 1.
MC_I; Transmembrane; Glycoprotein; Signal.
SIGNAL
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HSSP; P30685; 1A1N.
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MIM; 142830; -.
PROSITE; PS00290; IG_MHC; 1.
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                             Homo sapiens (Human).
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354 AA;
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SEQUENCE FROM
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P16210;
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SEQUENCE
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ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
Rapid cloning of HLA-A,18 cDNA by using the polymerase chain
"Rapid cloning of HLA-A,18 contains the produced in amplification.";
Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
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SEQUENCE FROM N.A.
MEDLINE; 90315860.
PARHAM P., BENJAMIN R.J., CHEN B.P., CLAYBERGER C., ENNIS P.D.,
KRENSKY A.M., LAWLOR D.A., LITTMAN D.R., NORMENT A.M., ORR H.T.,
SALTER R.D., ZEMMOUR J.;
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01-FEB-1991 (Rel. 17, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-7 B*0702 ALPHA CHAIN
PRECURSOR (B7.2).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
SignAL
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1802_PANTR
1B02_PANTR
1D 1802_PANTR
AC P13751;
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                                                 MEDLINE; 85287366.
SOOD A.K., PAN J., BIRO P.A., PEREIRA D., SRIVASTAVA R., REDDY V.B.,
DUCEMAN B.W., WEISSMAN S.M.;
"Structure and polymorphism of class I MHC antigen mRNA.";
Immunogenetics 25101-121(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                    MEDLINE; 8008278.

MEDLINE; 8008278.

MEDLINE; 8008278.

"Complete anno acid sequence of a papain-solubilized human histocompatibility antigen, HLA-B7. 2. Sequence determination and search for homologies."

Biochemistry 18.5711-5720(1979).

-- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
"Diversity of class I HLA molecules: functional and evolutionary interactions with T cells.";
                                                                                                                                                                                                                                              THE IMMUNE SYSTEM.
                                                                                                                 SEQUENCE FROM N.A.
ELLEXSON M.E., ZHANG L., HILDEBRAND W.H.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AALA -> GPW (IN REF. 3).

Q -> E (IN REF. 5).

W -> S (IN REF. 3).

R -> G (IN REF. 3).

GL -> RP (IN REF. 3).
                     Cold Spring Harb. Symp. Quant. Biol. 54:529-543(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B-7 B*0702 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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87B2ED84 CRC32;
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EMBL; M16102; AAA56522.1; ALT_SEQ.
EMBL; U29057; AAA91229.1; -.
PIR; A02185; HLHUB7.
PIR; B35997; B35997.
HSSP, P04660; 1AGB.
MIN; 142830; -.
PROSITE: PS00290; IG_MHC; 1.
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PFAM; PF00129; MHC_I; 1.
MHC_I; Transmembrane; Gl
                                                                                                                                                             SEQUENCE OF 25-295.
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                                                                                                                                                                                                                                                                     MICROGLOBULIN)
                                         SEQUENCE FROM N.A.
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CARBOHYD
DISULFID
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CONFLICT
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TRANSMEM
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ALEIN 0.;
*Nucleotide sequences of chimpanzee MHC class I alleles: evidence for
*Trans-species mode of evolution.";
EMBO J. 7:2765-2774(1988).

[2] REVISIONS.

MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G., KLEIN J.;

SEQUENCE FROM N

01-JAN-1990 (Rel. 13, Created) 01-JAN-1990 (Rel. 13, Last sequence update) 01-APR-1993 (Rel. 25, Last annotation update) CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-2 ALPHA CHAIN PRECURSOR.

STANDARD;

Pan troglodytes (Chimpanzee). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.

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                                                                                                                                                                                                                                                                                                                                                                                                             CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Submitted (FEB-1989) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             CHLA CLASS I HISTOCOMPA:
B-2 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 4BF65A6C CRC32;
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100.0%; Pred. No. 0.82;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                   PIR; SUSSER, THE STAIN.
HSSPITE; PS00290; IG_MHC; 1.
PRAM; PF00047; ig; 1.
PFAM; PF00129; MHC_I; 1.
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                       -1- SUBUNIT: DIMER C
MICROGLOBULIN).
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P30460:
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DISULFID
CARBOHYD
SEQUENCE
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SIGNAL
CHAIN
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1B04_HUMAN
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Gaps

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Indels

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50.0%; Score 51; DB 1; Length 362;

Query Match 50.0%; Score 51; DB Best Local Similarity 100.0%; Pred. No. 0.8 Matches 10; Conservative 0; Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-14 B*1401 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE: FROM N.1.

MEDLINE: 89235215.

PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;

PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;

Diversity and diversification of HLA-A,B,C alieles.";

J. Immunol. 142:3937-3950(1989).

-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INMUNE SYSTEM.

-!- SUBDINIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                           01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-14 B*1401 ALPHA CHAIN
                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 9BED8199 CRC32;
                     362 AA.
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PFAM; PF00047; 1g; 1.

PFAM; PF00129; MHC_I; 1.

MHC I; Transmembrane; Glycoprotein; Signal.

24
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                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM MEDLINE, 89235
                                                                                                                                                                                                                              HLA-B OR HLAB.
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P30463;
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                           NO STATE THE TENT OF THE PROPERTY OF THE PROPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Antagonist HIV-1 Gag peptides induce structural changes in HLA B8.";
J. Exp. Med. 184:2279-2286(1996).
-!-FUNCTION: INVOLUDED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REID S.W., MCADAM S., SMITH K.J., KLENBRMAN P., O'CALLAGHAN C.A., HARLOS K., JAKOBSEN B.K., MCMICHAEL A.J., BELL J.I., STUART D.I.,
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-8 B*0801 ALPHA CHAIN
PRECURSOR.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.82;
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PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal; 3D-structure.
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                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE: 89235215.
MEDLINE P., LAWLON. LOMEN C.E., ENNIS P.D.;
PARHAM P., LAWLON. LOMEN C.E., ENNIS P.D.;
"Diversity and diversification of HLA-A,B,C alleles.";
J. Immunol. 142:3937-3950(1989).
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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1467B8EB CRC32;
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1AGC; 16-JUN-97.
1AGD; 16-JUN-97.
1AGE; 16-JUN-97.
1AGF; 16-JUN-97.
                                                                                                                                                                                                Homo sapiens (Human).
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 97130420.
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SEQUENCE
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Best Loca Matches

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01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-65(B-14) B*1402 ALPHA CHAIN
PRECURSOR.
                               ö
                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Length 362;
                               Indels
                               ö
 Score 51; DB 1;
Pred. No. 0.82;
                                                                                                                                                                          362 AA.
Query Match

SO.0%; Score 51; DB
Best Local Similarity 100.0%; Pred. No. 0.6
Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                          HLA-B OR HLAB.
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us-08-653-294-35.rsp

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1811_HUMAN
P30465;
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1811_HUMAN
AC P30465;
DT 01-APR-
DT 15-UUL
DE HLA CLI
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                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P30464:
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-75(B-15) B*1502 ALPHA CHAIN
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
CXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                      MEDLINE; 89235215.
PARHAM P., LAWLOR D.A., LOWEN C.E., ENNIS P.D.;
PARHAM P., LAWLOR D.A., LOWEN C.E., ENNIS P.D.;
July L. LAWLOR System of HLA-A,B,C alleles.";
July and diversification of HLA-A,B,C alleles.";
July and diversification of HLA-A,B,C alleles.";
July and diversification of HLA-A,B,C alleles.";
July Lawlon L. 1937-3950(1989).

THE IMMUNE SYSTEM.

MICROGLOBULIN).
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE; 92196792.
LITTLE A.-M., PARHAM P.;
"THE HLA-BAP5 subtype of B15: molecular characterization and comparison with rossreacting antigens.";
Tissue Antigens 38:186-190(1991).
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  Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BE68AC9E CRC32;
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0.82;
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100.0%; Pred. No. v.
0; Mismatches
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PROSITE; PS00290; IG_MHC; 1.
PFAM: PF00047; 19: 1.
PFAM: PF0129; MHC_I: 1.
MHC I: Transmembrane; Glycoprotein; Signal.
SIGNAL
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227
362 AA;
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Best Local Similarity
Matches 10; Conserv
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                                                   SEQUENCE FROM N.A
MEDLINE; 89235215
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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MADLINE, 93055050
MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
LITTLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
MARTELL R.W., DU TOIT E.D., PARHAM P.,
"Distinctive HLA-A,B antigens of black populations formed by
interallelic conversion.";
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1-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last amotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-72(BW-70) B*1503 ALPHA
TISSUE-BLOOD;
MEDLINE; 96369309.
LIN L., TOKUNAGA K., TANAKA H., NAKAJIMA F., IMANISHI T.,
KASHIMASE K., BANNAI M., MIZUNO S., AKAZA T., TADOKORO K.,
SHIBATA Y., JUJI T.;
"Further molecular diversity in the HLA-B15 group.";
Tissue Antigens 47:265-274 (1996).
--- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
THE IMMONE SYSTEM.
--- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_L; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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... 0; Mismatches
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Best Local Similarity 100.
Matches 10; Conservative
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HLA-B OR HLAB.
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P30466;
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                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its modified ann profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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J. Immunol. 149:3411-3415(1992).
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-62 B*1504 ALPHA CHAIN
PRECURSOR.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDILINE; 92569956.
WATKINS D.I., MADAM S.N., LIU X., STANG C.R., MILFORD E.L.,
LEVINE C.G., GARBER T.L., DOGON A.L., LORD C.I., GHIM S.H.,
TROUP G.M., HUGHES A.L., LETVIN N.L.;
"New recombinant HIA-B allels in a tible of South American
Amerindians indicate rapid evolution of MHC class I loci.",
                               THE IMMUNE SYSTEM.
SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 99D70546 CRC32;
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Pred. No. 0.82;
0; Mismatches
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PIR; S16789; S16789.
HSSP; P30685; 1A1N.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_1; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
SIGNAL
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362 AA;
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Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-62 B*1504 ALPHA CHAIN. EXTRACELLULAR ALPHA-1.
FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE: 89235115.
MEDLINE: 89235115.
MEDLINE: BARHAM P., LAWLOD D.A., LOMEN C.E., ENNIS P.D.;
"Diversity and diversification of HLA-A,B,C alleles.";
J. Immunol. 142:3937-3950(1989).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1993 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA CHAIN
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Eukaryota; Metazoa; Chòrdata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                              DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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0.82;
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PFAM; PF00129; MHC_I; 1.
MHC_I: Transmembrane; Glycoprotein; Signal.
SIGNAL
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llarity 100.0%; Pr
Conservative 0;
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EMBL; U70528; AAB16918.1; --
PIR; S24433; S24433.
HSSP; P30685; IAIN.
MIM; 142830; --
PROSITE; PS00290; IG_MHC; 1.
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                                                                          -!- SUBUNIT: DIMER (MICROGLOBULIN).
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362 AA;
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Best Local Similarity
Matches 10, Conserv
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                   HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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MEDLINE; 89339610.
OOBA T., HAYASHI H., KARAKI S., TANABE M., KANO K., TAKIGUCHI M.;
"Inhe structure of HLA-B35 suggests that it is derived from HLA-Bw58
by two genetic mechanisms.";
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01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3501 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 96209671.
SMITH K.J., REID S.W., STUART D.I., MCMICHAEL A.J., JONES E.Y.,
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MENSSEN R., ORTH P., ZIEGLER A., SAENGER W.;
Submitted (APR-1998) to the PDB data bank.
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BY SIMILARITY.
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038EC3FC CRC32;
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100.0%; Pred. No. 0.82;
ive 0; Mismatches
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                                                                                                    EMBL; M24039; AAA59662.1; -.
HSSP; P30460; IAGB.
MIM: 142830; -.
PROSITE; PS00290; IG_MHC; 1.
PFAM: PF00147; 19: 1.
PFAM: MF01129; MHC_I: 1.
MHC_I; Transmembrane; Glycoprotein; Signal.
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362
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333
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310
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362 AA;
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Best Local Similarity
Matches 10; Conserv
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P30685;
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1993 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3502 ALPHA CHAIN
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CHERTROPE I.P., HERRERA M., FAINBOIM L., SATZ M.L.;
CHERTROPE L.P., HERRERA M., FAINBOIM L., SATZ M.L.;
CHERTROPE L.P., HERRERA M., FAINBOIM L., SATZ M.L.;
"Complete nucleotide sequence of a genomic clone encoding HA-B:
1solated from a Caucasian individual of Hispanic origin.
Identification of a new variant of HLA-B35.";
Hum. Immunol. 31:153-158(1991).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS THE IMMONE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PDB; 1A9B; 18-NOV-98.
MIM; 142830; 18-NOV-98.
PROSITE; PS00290; IG_MHC; 1.
PPRAN; PF001047; 19; 1.
PFRAN; PF00120; MHC_1; 1.
MHC_1; Transmembrane; Glycoprotein; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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. 0.82;
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 51;
Pred. No.
                                                                                                                                                                 EMBL; M28109; AAA59617.1; JOINED.
EMBL; M281110, AAA59617.1; JOINED.
EMBL; M28111; AAA59617.1; JOINED.
EMBL; M28112; AAA59617.1; JOINED.
EMBL; M28113; AAA59617.1; JOINED.
EMBL; M28114; AAA59617.1; JOINED.
EMBL; M28114; AAA59617.1; JOINED.
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100.0%;
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Best Local Similarity 100.
Matches 10; Conservative
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362 AA
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1B22_HUMAN
ID 1B22_HUMAN
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DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

MICROGLOBULIN).

us-08-653-294-35.rsp

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               This SWISS-PROT entry is copyright. It is produced through a collaboration
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J. Exp. Med. 181:2037-2048(1995)
J. Exp. Med. 181:2037-2048(1995)
THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE: 92176661.
ZEMMOUR J., LITLE A.M., SCHENDEL D.J., PARHAM P.;
"The HLA-A.B 'negative' mutant cell line CIR expresses a novel
HLA-B35 allele, which also has a point mutation in the translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3503 ALPHA CHAIN
PRECURSOR.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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J. Immunol. 148:1941-1948(1992)
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PROSITE; PS00290; IG_MHC; 1.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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EMBL; D50299; BAA08828.1; -.
HSSP; P30685; IAIN.
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PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK I KUNGROUNG E., BENCHANDRA S.;
SUDMILTEG (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF014769; AAB67807.1; --
PFAM; PF00129; MHC_I; 1.
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019525 (TEMBLICH. 05, Created)
01-JAN-1998 (TEMBLICH. 05, Last seque
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Copyright (c) 1993 - 2000
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Listing first 45 summaries
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                                                                                          SEQUENCE FROM N.A.
CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGROUNG E., BEJCHANDRA S.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF014771; AAB67809.1;
PFAM; PF00129; MHC_1; 1.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK
RUNGROUNG E., BEJCHANDRA S.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF014773; AAB67811.1;
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 50.0%; Score 51; DB 7; Length 81; Best Local Similarity 100.0%; Pred. No. 1.2; Matches 10; Conservative 0; Mismatches 0; Indels
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK
RUNGROUNG E., BEJCHANDRA S.;
SUBMILTEG (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; aFO14775; AABG/B13.1; -
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CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK
SUNGROUNG E., BEJCHANDRA S.;
SUDMILTEG (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AFO14777; AAB67815.1; -
PFAM; PF00129; MHC_I; 1.
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CHANDANAXINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK ISTUGROUNG E., BEJCHANDRA S.;
SUDMILTEG (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AFO14779; AAB67817.1; -
PFAM; PF00129; MHC_I; 1.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HLA-B.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-07-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HIA-B (FRAGMENT).
                                                                                                                                                                                                                                                 50.0%; Score 51; DB 7;
100.0%; Pred. No. 1.2;
tive 0; Mismatches
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Pred. No. 1.2;
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81 AA; 9405 MW; 073087CE CRC32;
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGROUNG E., BEJCHANDRA S.;
SUBMITTED (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF014787; AAB67825.1; -.
PFAM; PF00129; MHC_I; 1.
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                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. CHANDANAZINGYONG D., LUANGTRAKOOL K., SRINAK RUNGROUNG E., BEJCHANDRA S.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AF014785; AAB67823.1; F. PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 50.0%; Score 51; DB 7; Length 83; Best Local Similarity 100.0%; Pred. No. 1.2; Matches 10; Conservative 0; Mismatches 0; Indels
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                                     Indels
            Length
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-INOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
HLA-B.
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             DB 7;
            50.0%; Score 51; DB 7;
100.0%; Pred. No. 1.2;
.tve 0; Mismatches
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83 AA; 9731 MW; 24B8D666 CRC32;
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83 83
83 AA; 9731 MW; 24B8D666 CRC32;
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             Query Match
Best Local Similarity 100.
Matches 10; Conservative
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CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGROUNG E., BEJCHANDRA S.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AFO14783; AAB67821.1; -.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                            CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D., RUNGROUNG E., BEJCHANDRA S.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases. EMBL, AF014781; AAB67819.1; -PFAM; PF00129; MHC_I: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin1; Hominidae; Homo.
                                                                          Query Match 50.0%; Score 51; DB 7; Length 81; Best Local Similarity 100.0%; Pred. No. 1.2; Matches 10; Conservative 0; Mismatches 0; Indels
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
HLA-B.
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81 81
81 AA; 9405 MW; 073087CE CRC32;
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                                       073087CE CRC32;
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9405 MW;
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81 AA;
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Best Local Similarity
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RESULT 11
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01-MX-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I HLA-B (FRAGMENT).
HUMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%; Score 51; DB 7; Length 89; 100.0%; Pred. No. 1.3; 1.4ve 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. CHANG G.H.;
CHOPEK M., CAO K., ZHANG G.H.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, 108349; AAB48493.1; -.
PFAM; PF00129; MHC_I; 1.
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CHOPEK M., CAO K., ZHANG G.H.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, 1088264; AAB48498 1; -
PFAM; PF00129; MHC_I; 1.
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NAY-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I HLA-B (FFRAGNENT).
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN (FRAGMENT).
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89 89
89 AA; 10501 MW; FA3EFCDC CRC32;
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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PRELIMINARY;
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019548;
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019548
AC 019548 AC 019548 AC 019548 DT 01-JAN
DT 01-JAN
DT 01-NOV
DE MHC CLP
GN HIA-B.
GN HIA-B.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK RUNGROUNG E., BEJCHANDRA S.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AF014789; AAB67827.1; -. PFAM; PF00129; MHC_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 7; Length 83; 1.2;
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CARTER V., DUNN P.P.;

Identification of a novel HLA-B*07 allele.";

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ237594; CAB40714.1; -.
                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
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09Y452;
01.NOY-1999 (TrEMBLrel. 12, Created)
01.NOY-1999 (TrEMBLrel. 12, Last sequence update)
01.NOY-1999 (TrEMBLrel. 12, Last annotation update)
HUMAN LEUCOCYTE ANTIGEN B (FRAGMENT);
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83 AA; 9731 MW; 24B8D666 CRC32;
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OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA CAO K., BURDETT L., ZHANG H., FERNANDEZ-VINA M.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
DR PEML; AF016299; AAB6944.1; -.
DR PFAM; PF00129; MHC_I; 1.
KW MC.
FT NON_TER 89 89
SQ SEQUENCE 89 AA; 10550 MW; 11452E40 CRC32;
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Search completed: February 8, 2000, 19:16:17 Job time: 21504 sec

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i U55022 Human MHC class I ant
i U91330 Homo sapiens MHC clas
i AF181842 Homo sapiens MHC cl
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Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are predicted by tRNAscan-SE (Sean Eddy,
                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
euphyllophytes, Spermatophyta, Magnollophyta, eudicotyledons, core
eudicots, Rosidae, eurosids II, Brassicales, Brassicaceae,
                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis.

(Labsas 1 to 84544)

Lin,X., Kaul,S., Shea,T.P., Fujii,C.Y., Shen,M., VanAken,S.E.,
Lin,X., Kaul,S., Shea,T.P., Fujii,C.Y., Shen,M., VanAken,S.E.,
Barnstead,M.E., Mason,T.M., Bowman,C.L., Ronning,C.M., Benito,M.,
Carrera,A.J., Creasy,T.H., Buell,C.R., Town,C.D., Nierman,W.C.,
Fraser,C.M. and Venter,J.C.
Arabidopsis thaliana chromosome II BAC F7H1 genomic sequence
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The Institute for Genomic Research
9712 Medical Center Dr.

Rockville, MD 20850, USA

e-mail: Xiin@tigr.org

BAC clone F7H1 is from Arabidopsis chromosome II and is near the molecular marker mi398.

The orientation of the sequence is from SP6 to T7 end of the BAC
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Submitted (24-APR-1999) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
4 (Dases I to 84544)
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Submitted (18-JUN-1999) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
5 (bases 1 to 84544)
                                                                                                                         seq_documentation_block:
LOCUS ATACO07134 84544 bp DNA PLN 01-JUL-1999
DEFINITION Arabidopsis thallana chromosome II BAC F7H1 genomic sequence,
complete sequence.
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Submitted (Ol-JUL-1999) The Institute for Genomic Research,
Medical Center Dr., Rockville, MD 20850, USA
On Apr 24, 1999 this sequence version replaced g1:4580447.
Address all correspondence to:
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Lin,X. and Kaul,S.
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AJ2437594 Homo sapiens HLA-B
AJ243433 Homo sapiens HLA-B
AJ243737 Homo sapiens HLA-B
AJ249317 Homo sapiens HLA-B
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-WODEL-frame+_pan.model - DEV-xlp
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-Q=/cgnl_l/USFTO_spool/US08653294/runat_04022000_160701_15779/app_query.fasta.2
-DB-denembl -QFWT-fastap -SUFFTX-rge -GAPOP=12.000 -GAPEXT-4.000
-QGAPEXT-0.050 -KGAPOP=10.000 -KGAPEXT-0.000
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-OUTFWT-pfs -NORM-ext -MINIEN-0 -MAXLEN-1000000 -USER-US08653294
-NCPU-6 -ICPU-3 -NO_XLPXY -WAIT -THREADS=1
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                                                                                      About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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gb_pr2:HSHLAB6N1
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Quality:
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/note="overlap with BAC clone F19G14 (AC006438:1. .4157)."
928. .1330
                                                                                                                                                                                                                                                                                                                               /note="8353 nt before this point were not included in the submitted sequence, due to overlap with another BAC" complement(1. .4157)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSVETVEGYKYFLTIVDDHSRATWMYLLKTKSEVLTVFPAFIQQVENQYKVKVKAVRS
DNAPELKFTSFYAEKGIVSFHSCPETPEQNSVVERKHQHILNVARALALECSGVPELSLW
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SSTISYSKISPSHMCYINNITKIPIPTNYAEAQDTKEWCEAVDAEIGAMEKTNTWEIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGDSLISWRSKKQHTVSRSSAEAEYRALALATCEMVMLFTLLVSLQASPPVPILYSDS
TAAIYIATNPVFHERTKHIKLDCHTVRERLDNGELKLLHVRTEDQVADILTKPLFPYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="GI:4678198"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FNYTNLPRTYNLTQEIQDFRQGTLSLSEXYTRLKTLMDQLDSTEALDEPCTCGKAMRL
QOKAEQAKIVKFLAGLNESYAIVRRQIIAKKALPSLGEVYHILDQDNSQGSFSNYVAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAAFQVSEITQSPSMDPTVCYVQNGPNKGRPICSFYNRVGHIAERCYKKHGFPPGFTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDTSVLSAVNLPTGPTVKISGVGTLKLNDDILLKNVLFIPEFRLNLISISSLTDDIGS
RVIFDKNSCEIQDLIKGRMLGQGRRVANLYLLDVGDQSISVNAVVDISMWHRRLGHAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLLLKVSASKKWFLKQLDVSNAFLNGELEEEIFMKIPEGYAERKGIVLPSNVVLRLKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation-"MVTVARVTRKSTRSKAGTSSVTRKSRSTGAVTTPPNSPPVNRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASRALTSSESGDPTQSPFFLHSADHPGLNIISHRLDETNYGDWSVAMLISLDAKNKTG
FIDGTLSRPLESDLNFRLWSRCNSMYKSWLLNSVSPQIIRSILRMNDASDIWRDLNSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LORLDAISDSLGTTRHKNKGSDFCHVCHLAKQRKLSFPTSNKVCKEIFDLLHIDVWGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIYGLKQASRQWFKKFSSSLLSLGFKKTHGDHTLFLKMYDGEFVIVLVYVDDIVIAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "similar to retroviral aspartyl proteases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="similar to replication protein Al"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note-"similar to reverse transcriptase"
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TSCMKLEASLKHDVHSDVDGEDLFMELKLLKDVLPKEITKPVEVLKFLKIMDSCYPNT
WIAYRILLTIPVSVALAERTFSKLKLIKKYLRSTMSQERLNGLALISV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTHPPRSTODSSPROHLPLPKKNARIWSSGAWKSRLYSFSTYFLRFRDIGFIONHTKA
LCLSAGAGHALMALSQIGLSDVTAVELVDSIPLVKRADPHNLPFFDGVFDFAFTAHLA
EALFPWQFVEEMERTVRRGGFCVVSVDECGGDDVRDIARLFHNSKVVDVANVTLEGSK
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MILKKIKDAKYFSVILDSIPDVSRKEOMTFLIRCVDVSTCSPKIEEFFLIFLHIKDRR
EYTDNPGHRSDVESLTESETHGIGGFFFLFGMIIWYDLLAAVNIVSKSLOFEDMDLEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation-"MERNVEKMLKRVSIVFLSIGTVLMVIMILQTPKTCISPEAPSKP
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                                                                                                                                                                                                                                                                                                                /note="predicted by genscan and genefinder"
21092. .21322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="predicted by genscan and genefinder" complement(21932. .22627)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(<23753. .24059,24489. .>25330)
/gene="F7H1.6"
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Gaps: 0
Percent Identity: 52.941
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join(23753. .24059,24489. .25330)
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<21092. .>21322
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18429. .18462
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1. .203273

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/clone=1b="RPC1-11 Human Male BAC"

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6 203273: contig of 20018 bp in length.
Location/Qualiflers
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of 10549 bp in length
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contig of 11935 bp in length
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gap of unknown length
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contig of 9258 bp in length
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contig of 8907 bp in
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of 7703
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S (bases 1 to 201273)

Baldwin, J, Barna M, Beckelly, R, Boguslavkiy, L, Boukhgaiter, B.,

Baldwin, J, Barna M, Beckelly, R, Boguslavkiy, L, Boukhgaiter, B.,

Brown, A, Castle, A., Colangelo, M., Collins, S., Collymore, A.,

Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,

Ferreira, P., Fitzhghy, M., Forrest, C., Funke, R., Gaçe, D.,

Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Kieln, J.,

McEwan, P., McGurk, A., McKernan, K., Macdonald, P., Marquis, N.,

Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,

Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,

Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Direct Submission

Submitted (28-SEP-1999) Whitehead Institute/MIT Center for Genome

Rosearch, 320 Charles Street, Cambridge, MA 02141, USA

On Nov 30, 1999 this sequence version replaced gl:5931431.

All repeats were identified using RepeatMasker:

Sant, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                             seq_documentation_block:
LOCUS AC010932 203273 bp DNA HTG 30-NOV-1999
DEFINITION Homo sapiens chromosome 15 clone RP11-296E22 map 15, *** SEQUENCING
IN PROGRESS ***, 36 unordered pieces.
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 36 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Center code: WIBR

Web site: http://www.seq.wi.mit.edu

Contact: sequence_submission@genome.wi.mit.edu

Center project Information

Center project name: Li684

Center clone name: 296_E_22
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gap of unknown length
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gap of unknown length
contig of 1671 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 2032/3)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 15, clone RP11-296E22
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gap of
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AC010932.2 GI:6479157
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                                                                                                                 seq_name: gb_htg6:AC010932
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COMMENT

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Direct Submission
Submitted (26-FEB-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSHLABO1 243 bp DNA PRI 26-MAR-1997
HUMAN Cell line THAI DCH012 MHC class I HLA-B gene (allele
HLA-B*1525), exon 2.
                                                                                                                                                                                                Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 24).

Chandanayingyong,D., Sirikong,M., Srinak,D., Longta,K.,

Rungroung,E., Bejchandra,S., Juji,T., Tokunaga,K. and

Grosse-Wilde,H.

Bl5 alleles (B*1525)

Unpublished
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 243)
                                               HSHLABM1 243 bp DNA PRI 26-MAR-1997 Human cell line THAI DCH023 MHC class I HLA-B gene (allele HLA-B*1525), exon 2.
                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 243)
Chandanayingyong, D., Sirikong, M., Srinak, D., Longta, K.,
Rungroung, E., Bejchandra, S., Juji, T., Tokunaga, K. and
Grosse-Wilde, H.
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Acronalsm="Homo sapiens"
Ab_xref="taxon:9606"
Abromosome="6"
Amap="6p21"
Acell_type="lymphoblastoid"
Acell_line="THAI DCH023"
J. .243
Jene="HLA-B"
Ante="similar to exon 2 of B*1501"
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                 U91334.1 GI:1906675
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79 c
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Ratio: 5.100
Percent Similarity: 100.000
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US-08-653-294-35 x HSHLABM1
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human.
Homo sapiens
seq_name: gb_pr2:HSHLABM1
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LOCUS HSHLABO1
DEFINITION Human cell 11
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                                     seq_documentation_block:
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                                                         LOCUS
DEFINITION
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KEYWORDS
SEGMENT
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E 1 (bases 1 to 243)

Chaddanayingyong, D., Sirikong, M., Srinak, D., Longta, K., Rungroung, E. and Bejchandra, S.

L Unpublished

C (bases 1 to 243)

S Chandanayingyong, D., Sirikong, M., Srinak, D., Longta, K., Rungroung, E. and Bejchandra, S.

Chandanayingyong, D., Sirikong, M., Srinak, D., Longta, K., Direct Submission

L Submitted (26-FEB-1997) Transfusion Medicine, Faculty of Medicine, Sirital Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                                                                   HIGHLABKI 243 bp DNA PRI 26-MAR-1997
Human cell line THAI DCH022 MHC class I HLA-B gene (allele HLA-B #1521), exon 2.
U91332
U91332.1 GI:1906671
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Gaps: 0
Percent Identity: 100.000
                                       Gaps: 1
Percent Identity: 52.174
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                     Length:
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/cell_type="lymphoblastoid"
<1. .243
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
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                                                                                           alignment_block:
US-08-653-294-35 x AC010932/rev
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Percent Similarity: 100.000
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US-08-653-294-35 x HSHLABK1
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LOCUS HSHLABK1
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Ratio:
Percent Similarity:
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alignment_scores
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DEFINITION

ACCESSION VERSION KEYWORDS SEGMENT SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL REFERENCE

AUTHORS

TITLE JOURNAL

FEATURES

BASE COUNT ORIGIN

exon

```
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Chandanaylayong, D., Sirikong, M., Luangtrakool, K., Srinak, D.,

E 2 (bases I to 246)

S Chandanaylayong, D., Sirikong, M., Luangtrakool, K., Srinak, D.,

Rungroung, E. and Bejchandra, S.

Direct Submission

E Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,

Sirinaj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
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AF014771 GI:2345107
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Gaps: 0
Percent Identity: 100.000
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Percent Similarity: 100.000
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US-08-653-294-35 x AF014769
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LOCUS AF014771
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
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                                                           BIS alleles (B*1525)
Unpublished
2 (bases 1 to 243)
2 (bases 1 to 243)
Rundroung, D., Sirikong, M., Srinak, D., Longta, K.,
Rungroung, E.,
Bejchandra, S., Juji, T., Tokunaga, K. and
Grosse Wilde, H.
Direct Submission
Submitted (26-FEB-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.
Direct Submission
Submitted (18-ULL-1997) Transfusion Medicine, Faculty of Medicine, Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
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Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
exon 2 and partial cds.
AF014769 GI:2345103
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 246)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.
Unpublished
Chandanayingyong, D., Sirikong, M., Srinak, D., Longta, R., Rungroung, E., Bejchandra, S., Juji, T., Tokunaga, K. and Grosse-Wilde, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 100.000
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Ratio: 5.100
Percent Similarity: 100.000
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VERSION
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
REFERENCE
AUTHORS
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Chases 1 to 246)
Chandanayingyong, D., Strikong, M., Luangtrakool, K., Srinak, D.,
Rungroung, E. and Bejchandra, S.
Direct Submission
Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                                          AFU14775 246 bp DNA PRI 27-AUG-1997
Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
exon 2 and partial cds.
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Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.
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Unpublished
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Percent Identity: 100.000
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Ratio: 5.100
Percent Similarity: 100.000
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LOCUS AF014775
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KEYWORDS
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ChandanayIngyong, D., Strikong, M., Luangtrakool, K., Srinak, D.,
Rungroung, E. and Bejchandra, S.
Direct Submission
Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arul4773 246 bp DNA PRI 27-AUG-1997
Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
exon 2 and partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 246)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D.,
Rungroung, E. and Bejchandra, S.
Unpublished
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Ratio: 5.100
Percent Similarity: 100.000
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US-08-653-294-35 x AF014771
                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AF014771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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VERSION
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from: 1

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 246)

2 (bases 1 to 246)

3 (handanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., B15, alleles (8*152)

4 (pases 1 to 246)

5 (chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.

6 (chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.

7 (bases 1 to 246)

8 (chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.

8 (shiria) Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                             seq_documentation_block:

LOCUS
AF014779 246 bp DNA
DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
exon 2 and partial cds.

ACCESSION AF014779
VERSION AF014779 GI:2345123
                                                                                                                    198 CGAGAGACCTGCGGAACCTGCGCGGCTAC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                          11 ArgGluSerLeuArgAsnLeuArgGlyTyr
                                     to: AF014777
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Ratio: 5.100
Percent Similarity: 100.000
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US-08-653-294-35 x AF014777
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                                       Align seg 1/1
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81 c 82 g 18 t
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Submitted (18-UU-1997) Transfusion Medicine, Faculty of Medicine, Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                          ArU14777 246 bp DNA PRI 27-AUG-1997 Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele), ArO14777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Homo sapiens
Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 246)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D.,
Rungroung, E. and Bejchandra, S.
B15 alleles (B*1502)
Unpublished
                                                            Gaps: 0
Percent Identity: 100.000
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LOCUS AF014777
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ORGANISM

VERSION KEYWORDS SOURCE

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TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 246)

Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Ristaleias (R*152)

L (ppublished

E (bases 1 to 246)

Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.

Rungroung, E. and Bejchandra, S.

Rungroung, E. and Bejchandra, S.

Bliete (18-UUL-1997) Transfusion Medicine, Faculty of Medicine, Sirital, Hospital, Mahidol University, Prannok Road, Bangkok 10700,
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LOCUS AF014785 250 bp DNA PRI 27-AUG-1997

DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1525 allele),

ACCESSION AF014785

VERSION AF014785.1 GI:2345135
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
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Percent Similarity: 100.000
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US-08-653-294-35 x AF014783
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Ratio:
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                                                           human.
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                                                                                                                                                                                                          Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

E. 1 (bases 1 to 246)

S. Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.

E. 1 (bases 1 to 246)

E. 2 (bases 1 to 246)

S. Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.

Direct Submission

E. Submisted (18-UUL-1997) Transfusion Medicine, Faculty of Medicine Siriral, Hospital, Mahidol University, Prannok Road, Bangkok 10700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS AF014781 246 bp DNA PRI 27-AUG-1997
DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
exon 2 and partial cds.
ACCESSION AF014781
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US-08-653-294-35 x AF014781
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gene

exon

CDS

BASE COUNT

ORIGIN

us-08-653-294-35.rge

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                                                                                                  2 (bases 1 to 250)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., 'Srinak, D.,
Rungroung, E. and Bejchandra, S.
Direct Submission
Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF014787 250 bp DNA PRI 27-AUG-1997
Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1525 allele),
exon 2 and partial cds.
AF014787 GI:2345139
1 (bases 1 to 250)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D.,
Rungroung, E. and Belchandra, S.
B15 alleles (B*1525)
Unpublished
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 250)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.
Unpublished
Els alleles (B*1525)
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Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D.,
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Percent Identity: 100.000
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US-08-653-294-35 x AF014785
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LOCUS
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81 C 84 g 31 t
Rungroung, E. and Bejchandra, S. Breet Submission Submission Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine, Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 0
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Ratio: 5.100
Percent Similarity: 100.000
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US-08-653-294-35 x AF014787
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| Human secreted protein 5' ES | Sequence of Opine synthase | Complete nucleotide sequen | Saccharothrix australiensis
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pHLA-B7 expression vector.
expression vector; pHLA-B7; heavy human HLA-B7; bicistronic mRNA;
expression vector; pHLA-B7; heavy human HLA-B7; bicistronic mRNA;
light beta-2 microglobulin; class I major histocompatibility complex;
MHC; human leukocyte antigen; HLA; covalently closed circular DNA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F 22-SEP-1999:

R 22-SEP-1999: JP-247697.

22-SEP-1999: JP-247697.

R (OLVU) OLYMPOS OPTICAL KK.

R WPT: 91-182991/25.

R P-PSDB; R12464.

I HLA-B35 gene - used in DNA probe and transformant cells for immunising animals, for developing monoclonal antibody.

S Claim i: Page i: Ilpp; Japanese.

C Probes comprising part of the sequence can be used to identify claim in language.

C Claim i: Page i: Ilpp; Japanese.

C Probes comprising part of the sequence can be used to identify claim in language.

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C Probes comprising part of the lan
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/note- "pBR322 backbone contg. bacterial origin
replication"
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/*tag- b
/note- "kanamycin resistance gene open reading i
the gene is taken from the transposable element
Tn903"
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Gaps: 0
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1D Q12115 standard; DNA; 1089 BP.
AC 012115;
DT 29-AUG-1991 (first entry)
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ID 075974 standard; cDNA; 4059
AC 075974;
  42.50
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                                                                                                                             seq_name: N_Geneseq_36:Q12115
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Percent Similarity: 100.000
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US-08-653-294-35 x Q12115
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N_Geneseq_36:N50226
N_Geneseq_36:N50182
N_Geneseq_36:X07410
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| HIA-835 exon. HIA-835 gene - u | PHIA-87 expression vector. New | PHIA-87/beta-2 microglobulin e | PHIA-87/beta-2 microglobulin e | Human CRIPPO-related gene CR-3 | DNA encoding human CRIPTO-related gene (CR-1 Coding sequence for the alpha in EST clone GG35. New polynucled clone dn809_5 isolated from human CRIPTO related from human CRIPTO related from human cannot be amylase gene and u coding sequence for the alpha | EST clone CE24. New polynucled i HIA-C exon Cb-1. HIA-C gene, I HIA-C exon 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expression vector pNE223. New Streptococcus pneumoniae genom Expression vector pNE2116. New Mutagenic plasmid pNE2217. New Promoter probe vector pNE2214. New Human protein tyrosine phospha! Polynucleotide sequence from Synthetic glyphosate oxidoredure Modified glyphosate oxidoredure (CPTI-GOX gene fusion. Chemical Glyphosate oxidoreductase gene (Glyphosate oxidoreductase gene (Glyphosate) artificial chromosc (Enterococcus faecalis genome occus continuation (7 of 10) of 9 lebrrella burgdorferi polynuc
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                                                                                                                                                                        Command line parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ! Documentation
                                                                                                     About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
        out_format : pfs
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Search time (sec): 873.190000
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Query length: 20
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N_Geneseq_36:X20250 +
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N_Geneseq_36:T71145
N_Geneseq_36:T80987
N_Geneseq_36:V83924
N_Geneseq_36:Q22495
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N_Geneseq_36:X20556
N_Geneseq_36:Q20835
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N_Geneseq_36:Q75974
N_Geneseq_36:Q75973
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N_Geneseq_36:V69922
N_Geneseq_36:V69927
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N_Geneseq_36:V82783
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N_Geneseq_36:V52426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .Geneseq_36:X12977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N_Geneseq_36:V17563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _Geneseq_36:V90017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _Geneseq_36:T9
_Geneseq_36:T1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N_Geneseq_36:N
N_Geneseq_36:N
N_Geneseq_36:N
N_Geneseq_36:V
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N_Geneseq_36:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genesed_36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  score_list:
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N_Genesed_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N_Genesed_N
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Lew D, Marquet M.

10. Marquet M.

11. Lew D, Marquet M.

12. Marquet M.

13. Mpl: 95-036494/05.

14. Mew vectors for gene therapy, partic for tumours - comprising genetic material encoding one or more cistron(s) which express genetic material encoding one or more cistron(s) which express claim 9: Page 42-43: SOpp: English.

12. This HiA-B7 antigen encoding plasmid was developed to incorporate many advantageous features, eg. the kanamycin resisitance gene. The advantageous features, eg. the kanamycin resisitance gene. The proteins lowers the risk of tumourigenicity. The vector may also operate as cassette into which cistrons may be inserted and removed at will be to the transcription and subsequent translation of peptides of interest.

13. The vector is used partic. for the treatment of neoplastic disease, and and provides enhanced gene delivery and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/note= Rous sarcoma virus LTR promoter domain, derived
for the Schmidt-Rupin strain nucleotides
8673-9146. This region also includes a 56 bp
region of a synthetic oligonucleotide which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-AuG-1995 (first entry) pHLA-B7/beta-2 microglobulin expression vector. expression vector. pHLA-B7/beta-2 microglobulin; heavy human HLA-B7; light beta-2 microglobulin; class I major histocompatibility complex; MHC; bicistronic mRNA; human leukocyte antigen; HLA; covalently closed circular DNA; ds.
                                                                                                                                                                                                                             /*tag= g
/note= "Rous sarcoma virus 3' LTR promoter region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1000 T;
                                                                                /*tag= e
/note= "3' untranslated region of HLA-B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 4059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1033 G;
                                                                                                                                                                             /note= "HLA-B7 open reading frame"
                   /*tag= d
/note= "SV40 small t intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: Q75974 from: 1
complement (1412. .1560)
                                                                                                                       heavy chain mRNA"
complement (1795. .2880)
                                                                                                                                                                                                                                                                  3416. 4059
/*tag= h
/note= "pBR322 backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1051 C;
                                                            complement (1561. .1794)
                                                                                                                                                                                                     complement (2886. .3415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .529
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:

1D 075973 standard; CDNA; 4965 BP.

AC 075973;
DT 23-AUG-1995 (first entry)
DE pHLA-B7/beta-2 microglobulin expression vector; pHLA-B7/beta-2 MCV 19th beta-2 microglobulin; Class KW MC; bicistronic mRNA; human leuko KW covalently closed circular DNA; ds Synthetic.

FT Key Location/Qualifler FT Ltr 1tr /*tag" a /*tag" a /*tag" a /*tag" a /*tag" a /*tag" ET FT LTr 1 - 529 FT /*tag" a /*tag fT FT LTr 1 - 529 FT /*tag 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           975 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-35 x Q75974/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                        27-MAY-1994; U06069.
07-JUN-1993; US-074344.
(UNMI ) UNIV MICHIGAN.
(VICA-) VICAL INC.
                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4059 BP;
                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                   WO9429469-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
intron
                                                            3'utr
                                                                                                                                           cds
                                                                                                                                                                                                          ltr
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/note- "bovine growth hormone 3'UTR and transcriptional terminator; it starts at a blunt-ended BglI site within the 3'UTR of the mRNA coding sequence" 2979. .2984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /"cug-"murine encephalomyocarditis CAP-independent translational enhancer (EMCV-CITE); taken from nuclectides 255-843 of cloned EMCV genomic DNA. It is a non-coding regulatory sequence functioning as an internal entry point for the eukaryotic ribosomal subunits when located within a mRNA mol. It enables the translational start codon of the beta-2 microglobulin, downstream of the HLA-B7 recognised by the ribosome"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= o
/note= "kanamycin resistance gene open reading frame;
the gene is taken from the transposable element
T1903.*
                                                                                                                                                                                                                                                                                                                                                       /*tag- e
/note- "encodes putative HLA-B7 heavy chain mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microglobulin; this cDNA is (differs to the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*teg= p
/note="pBR322 backbone contg. bacterial origin of
replication, it represents nucleotides 2244-3193"
modifies this regulatory sequence to effect a
higher level of expression of downstream
sequences. The oligonucleotide removes a
polyadenylation signal sequence originally found
                                                                                                                                                                                                                                                                                                                                                                                                 peptide"
1621. 1853
7*tag= "3" untranslated sequence of HLA-B7 heavy
chain mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= g // Arag= multiple cloning site, forms a junction // note= "multiple cloning site, forms a junction between the HIA-B7 sequence and the EMCV-CITE sequence, and is used to facilitate subcloning" 1889. .2479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag* n
/note= "synthetic linker to facilitate cloning"
                                                                                                                           /*tag= b
/label= consensus_Kozak_signal_sequence
/355. 1620
/*tag= c
/note= "HLA-B7 heavy chain open reading frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= j
/note= "3' untranslated region of the beta-2
                                                                                                                                                                                                                                                                                 / note- "encodes putative signal peptide of HIA-B7 heavy chain" 607. .1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note- "synthetic linker"
'UTR .3111
                                                                                    in the RSV DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (3151. .3967)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note- "encodes beta-2
deriv. from chimpanzee
cDNA by only 4 bases)"
2840. .2846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         microglobulin mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .2839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    854. .1888
                                                                                                                                                                                                                                       535. .606
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *tag= h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
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                                                                                                                                                                                                                                              signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polya_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
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                                                                                                           misc_signal
                                                                                                                                                                                                                                                                                                                                     mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                           3'utr
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                                                                                                                                                                               cds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cds
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Key
 88888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VUICA-) VICAL INC.

PI Lew D. Marquet M. Nabel EG, Nabel GJ;

DR WIT: 95-036494/05.

New vectors for gene therapy, partic for tumours - comprising

New vectors for gene therapy, partic for tumours - comprising

The properties of therapeutic peptide(s)

The pula-B/Deta-2 microglobulin plasmid expression vector, in addition

CC the kanamycin resistance gene, contains the plasmid DNA encoding the

CC the kanamycin resistance gene, contains the plasmid DNA encoding the

CC the kanamycin resistance gene, contains the plasmid DNA encoding the

CC class I major hisotocompatibility complex (MHC) antigen. The plasmid is

CC class I major hisotocompatibility complex (MHC) antigen. The plasmid is

CC class I major hisotocompatibility complex (MHC) antigen. The plasmid is

CC class I major hisotocompatibility complex (MHC) antigen. The plasmid is

CC class I major hisotocompatibility properties of the mana is dependent

CC class I major hisotocompatibility from the bovine growth hormone

CC designed to express these two proteins via a bicistronic mena is regulated by the

CC controlled by the CTER. Finally the replication of the plasmid in

CC controlled by the CTER. Finally the replication of the plasmid in

CC controlled by the CTER. Finally the replication of the plasmid in

CC controlled by the corter is used partic. for the treatment of neoplastic

CC disease, eg. melanoma, and provides enhanced gene delivery and expression

in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New CREATO gene CR-1 and CRIPTO-related gene CR-3 genomic DNA - CR-3 protein and anti-CR-3 antibodies, useful in immunoassay to detect CR-3 as tumour specific marker

Disclosure: Page 29: 44pp: English.

The CR-3 nucleotide sequence was isolated from a human genomic library using a labelled DNA fragment containing 800bp upstream of the translation initiation site of CR-1. Clones were isolated which contained the 5' cDNA non-coding region of CR-3. One clone was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human CRIPTO-related gene CR-3. cell proliferation; tumour; CR-1; transforming growth factor; epidermal growth factor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                             1338 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                             1293 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: Q75973 from: 1 to: 4965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     829 CGAGAGACCTGCGGAACCTGCGCGGCTAC 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
809. .1375
/*tag= a
/product= CR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-1992.
23-AUG-1991; 749001.
23-AUG-1991; US-749001.
(USSH ) US DEPT HEALTH & HUMAN.
Salomom D, Persico M;
WPI; 92-123675/15.
                                                                                                                                                                                                                                                                                                                                                                                                             1171 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
ID Q22494 standard; DNA; 2675 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: N_Geneseq_36:022494
27-MAY-1994; U06069.
07-JUN-1993; US-074344.
(UNMI ) UNIV MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-35 x Q75973
                                                                                                                                                                                                                                                                                                                                                                                                             4965 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US7749001-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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sequenced and found to include a complete CRIPTO CDNA lacking introns and containing a poly(A) tract at the 3' end. Seven single base pair substitutions were observed in the coding region (c.f., CR-1 sequence in Ciccodicola A. et al., EMBO J.8:1987-1991(1989)), six of which gave rise to amino acid changes. The 3' non-coding c sequence is less similar (97% identical) to CR-1. Most of the differences occur in the inverted Alu sequence. The unusual poly(A) addition site AGTAAA found in the CR-1 gene is also conserved in CR-3. The similarity between CR-1 and CR-3 extends for 697 nucleotides upstream of the initiator AUG where it is possible to observe 7 base pair substitutions and 6 nucleotide deletions. The 14 "Others" in the sequence represent nucleotides whose cidentity, although determined by the inventors, was unclear in the sequence 2675 BP; 738 A; 611 C; 553 G; 759 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:

ID T71145; standard; DNA; 2675 BP.

AC T71145;

DT 19-AUG-1997 (first entry)

DT DN encoding human CRIPTO-related gene product, CR-3.

KW CRIPTO; CR1; CR3; epidermal growth factor superfamily; EGF; mitogen; KW tumour marker; epithelium; mesenchyme; diagnosis; prognosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New DNA encoding the human CRIPTO-related gene product CR-3 - used to produce recombinant protein, useful for preparation of diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tills encodes a human CRIPTO-related gene product CR-3. CR-3 is thought to be a tumour-specific marker and as such DNA and amino acid sequences of CR-3 and derivatives can be used in the diagnosis, prognosis and possibly treatment of some types of cancer. CR-3 includes a region homologous to products of the epidermal growth factor superfamily of genes and it may be a mitogen involved in regulating proliferation, differentiation and transformation of sequence 2675 BP; 618 C; 555 G; 763 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GlyArgLeuAsnArgLeuSerGlu.....ArgArgGluSerLeuArgAs 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.00 Length: 21
3.200 Gaps: 1
71.429 Percent Identity: 57.143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 2675
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23-AUG-1991; 02-74901.
17-NOG-1991; 02-74901.
17-NOG-1991; 03-154198.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
PEFZGLOO MG, SALOMON DS;
PPEZBLOO MG, SALOMON DS;
P-PSDB; W19980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
809. .1375
/*tag= a
/product= CR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Column 17-20; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: Q22494 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: N_Geneseq_36:T71145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2211 CAAAATGGGTTAC 2223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-35 x Q22494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 nLeuArgGlyTyr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibodies
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mutation
                                             mutation
04.NOV-1997 (first entry)
CRIPTO-related gene, CR-3.
CRIPTO-related gene; CR-3; epidermal growth factor; EGF; TGF-alpha; amphiregulin; tumour specific marker; colon cancer cell line; colorectal tumour; mesenchyme; epithelial cell; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= i
/note= "C>T mutation from CR-1 sequence, causes
Ala>Val mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= m
/note= "C>T mutation from CR-1 sequence, causes
Pro>Leu mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            causes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 causes
                                                                                    2 GlyArgLeuAsnArgLeuSerGlu.....ArgArgGluSerLeuArgAs 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= j
/note= "T>C mutation from CR-1 sequence,
val>Ala mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= 1
/note= "T>G mutation from CR-1 sequence,
Tyr>Asp mutation"
1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ^*tag= k
note= "G>A mutation from CR-1 sequence"
       Length: 21
Gaps: 1
Percent Identity: 57.143
                                                                                                                                                                                                                                                                                                                    153. .162
/*tag= e
/note= "Pyrimidine rich stretch"
371. .395
/*tag= f
/note= "Pyrimidine rich stretch"
                                                                                                                                                                                                                                                                                                                                                                               note- "Pyrimidine rich stretch"
641. 1931
*tag- h
                                                             to: 2675
                                                                                                                                                                                                                        Location/Qualiflers
809. .1375
**tag= a
/product= CR-3
2554. .2559
/*tag= b
511. .516
/*tag= c
/bound_moeity= SPI
532. .537
/*tag= d
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                       label- Alu_sequence
                                                            Align seg 1/1 to: T71145 from: 1
                                                                                                                                                    seq_documentation_block:
ID T80987 standard; DNA; 2675 BP.
AC T80987;
                                                                                                                                                                                                                                                                                                                                                            ....482
**tag= ~
ote
      48.00
3.200
71.429
                                                                                                                                        seq_name: N_Geneseq_36:T80987
                                                                                                                         2211 CAAATGGGTTAC 2223
                                      alignment_block:
US-08-653-294-35 x T71145
                                                                                                           16 nLeuArgGlyTyr 20
                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                         polya_signal
                                                                                                                                                                                                                                                                       protein_bind
                                                                                                                                                                                                                                                                                              protein_bind
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                               mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                             mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutation
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This sequence represents the CRPTO-related gene, CR-3. The CR-3 gene sequence is identical to the human CRIPTO gene with the exception of eight base pair substitutions that give rise to six amino acid changes. GR-3 exhibits partial amino acid sequence homology and a tertiary structure within a 38 amino acid sequence homology and a tertiary structure within a 38 amino acid region similar to the epidermal growth factor (EGF) supergens family that includes EGF, TGF-alpha and amphirequilm. Expression of CR-3 may serve as a tumour specific marker as it is expressed in several human colon cancer cell lines and possibly in human colorectal tumours. The assay of the amount of CR-3 in a sample can be used in studies on the regulation of the proliferation, differentiation, and transformation of various mesenchymal and epithelial cells. Study of the expression of CR-3 may also be used in the diagnosis, prognosis and treatment of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assays for CRIPTO-related gene product CR-3 - used in studies on the regulation of the proliferation, differentiation and transformation of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V83924;
03-MAR-1999 (first entry)
03-MAR-1999 (first entry)
Human CRIPTO-related gene (CR-3).
human CRIPTO-related protein; CR-1; antibody; CR-3; proliferation;
differentiation; transformation; mesenchymal cell; epithelial cell;
tumour specific marker; cancer; ds.
Homo saplens.
                                                                                 /*tag= 0
/note= "G>A mutation from CR-1 sequence, causes
G1y>G1u mutation"
1341
                                                                                                                                                                                            /*tag= p
/note= "T>C mutation from CR-1 sequence, causes
Val>Ala mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n
"G>A mutation from CR-1 sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 21
Gaps: 1
Percent Identity: 57.143
                                                                                                                                                                                                                                                                                                    22-JUL-1997.
22-AUG-1991; 74-9001.
23-AUG-1991; US-74-9001.
17-NOV-1993; US-154-198.
05-JUN-1995; US-154-198.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
PETSICA MC, Salomon DS;
PPSDB; W25-667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 2675
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809. .1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Fig 2; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= CR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
ID V83924 standard; DNA; 2675 BP.
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3.200
71.429
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/*tag=
/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: T80987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-35 x T80987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 nLeuArgGlyTyr 20
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Ratio:
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03-MAR-1999 (first entry)
Human CRIPTO-related gene (CR-1).
human CRIPTO-related protein; CR-1; antibody; CR-3; proliferation;
differentiation; transformation; mesenchymal cell; epithelial cell;
tumour specific marker; cancer; ds.
                                                                                                                                                                                         2 GlyArgLeuAsnArgLeuSerGlu....ArgArgGluSerLeuArgAs 16
                    Length: 21
Gaps: 1
Percent Identity: 57.143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
887. .4167
/*tag= a
/note= "contains introns"
                                                                                                                                     to: 5761
                                                                                                                                     Align seg 1/1 to: Q22495 from: 1
                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
ID V83923 standard; DNA; 5761 BP.
AC V83923;
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2064. .2146
/*tag= e
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/*number= 3
2652..2766
/*tag= h
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2865. .2974
/*tag= j
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2011. .2063
/*tag= d
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/*tag= f
/number= 3
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2975. .4048
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/*tag= 1
/number= 6
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2767. .2864
/*tag= 1
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921. .2010
/*tag c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        887. .921
/*tag= b
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/number= !
                    48.00
3.200
71.429
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                                                                                                                                                                                                                                                                                                         seq_name: N_Geneseq_36:V83923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-DEC-1998.
05-JUN-1995; 464023.
23-AUG-1991; US-749001.
17-NOV-1995; US-464023.
(USSH ) US DEPT HEALTH &
                                                                                                                                                                                                                                                                        5010 CAAAATGGGTTAC 5022
                                                                                      alignment_block:
US-08-653-294-35 x Q22495
                                                                                                                                                                                                                                         16 nLeuArgGlyTyr 20
                                      Ratio:
Percent Similarity:
                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
      alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                             Example 3; Columns 17-22; 26pp; English.

The present sequence encodes a human CRIPTO-related protein CR-3. The present sequence encodes a human CRIPTO-related protein CR-3. The specification describes an antibody which has binding affining to CR-3 and not to CR-1. The antibodies can be used for the detection of CR-3. CR-3 is a regulatory molecule involved in regulating the proliferation, differentiation, and transformation of various mesenchymal and epithelial enlar in addition expression of CR-3 may serve as a tumour specific marker that may have applicability in the diagnosis, prognosis and possible treatment of specific types of cancer.

Sequence 2675 BP; 739 A; 618 C; 555 G; 763 T;
                                                                                                                                                                  New antibody to human CRIPTO-related polypeptide-3 - used for the detection of CRIPTO-related polypeptide-3 which is involved in the regulation of the proliferation, differentiation and transformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New CRIPTO gene CR-1 and CRIPTO-related gene CR-3 genomic DNA - CR-3 protein and anti-CR-3 antibodies, useful in immunoassay to detect CR-3 as tumour specific marker

Disclosure: Page 22: 44pp: English.

The CR-1 genomic clone can be used in transgenic animals to examine the effects of overexpression of this gene on development and tumorigenicity and to study regulation of CR-1 gene.

See also 022494.

Sequence 5761 BP: 1529 A; 1306 C; 1227 G; 1699 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-AUG-1992 (first entry)
Human CRIPTO gene CR-1.
cell proliferation; tumour; CR-3; transforming growth factor; epidermal growth factor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GlyArgLeuAsnArgLeuSerGlu.....ArgArgGluSerLeuArgAs 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 1
Percent Identity: 57.143
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
US5854399-A.
29-DEC-1998.
29-DEC-1998.
05-JUN-1999; US-749001.
17-NOV-1993; US-154198.
05-JUN-1995; US-464023.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
PESSH MG, Salomon DS;
WPI; 99-095001/08.
P-PSDB; W87631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: V83924 from: 1 to: 2675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.

US7149001-A.

25-FEB-1992.

23-AUG-1991; 749001.

23-AUG-1991; US-749001.

(USSH ) US DEPT HEALTH & HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
ID Q22495 standard; DNA; 5761 BP.
AC Q22495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.00
3.200
71.429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: N_Geneseq_36:022495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2211 CAAATGGGTTAC 2223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-35 x V83924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salomom D, Persico M; WPI; 92-123675/15. P-PSDB; R22548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 nLeuArgGlyTyr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
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                                                                                                                                                                                                                          of cells
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HEALTH & HUMAN SERVICES

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alignment_block:
US-08-653-294-35 x x12977/rev
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Percent Similarity:
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នូមមន
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence of specific classes of soybean seed protein genes respirately and the sequence of specific classes of soybean seed protein genes respirately to change seed storage protein profiles of transgenic plants bisclosure; page 29-30; SBpp: English.

This sequence represents the coding sequence for the alpha subunit of the soybean seed protein beta-conglycinin. The method of the invention is for reducing the quantity of a soybean seed storage protein (A), such as beta-conglycinin, in soybeans. It comprises: (a) constructing a chimeric gene comprising: (i) a nucleic acid fragment encoding all or a portion of (A) placed in sense or antisense orientation region; (b) creating a transgenic soybean cells of (1); and (11) a transcriptional termination region; (b) creating a transgenic soybean cell the chimeric gene of (a); and (c) growing the transgenic soybean cells of (b) under conditions that result in expression of the chimeric gene of (a); where the quantity of one or more members of a class of (A) subunits is reduced when compared to soybeans not containing the chimeric gene of (a); the method is used to construct transgenic soybean a lines where the expression of genes encoding (A) are modulated to effect a change in seed storage protein profile of transgenic plants.
                                                                                                                                      The present sequence encodes a human CRIPTO-related protein CR-1. The specification describes an antibody which has binding affinity to CR-3 and not to CR-1. The antibodies can be used for the detection of CR-3. CR-3 is a regulatory molecule involved in regulating the proliferation, differentiation, and transformation of various mesenchymal and epithelial cells. In addition expression of CR-3 may serve as a tumour specific marker that may have applicability in the diagnosis, prognosis and possible treatment of specific types of cancer. Sequence 5761 BP; 1529 A; 1304 C; 1229 G; 1699 T;
                                                  New antibody to human CRIPTO-related polypeptide-3 - used for the detection of CRIPTO-related polypeptide-3 which is involved in the regulation of the proliferation, differentiation and transformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JUN-1998 (first entry)
Coding sequence for the alpha subunit of beta-conglycinin.
Beta-conglycinin; soybean seed protein; transgenic plant; seed storage protein profile; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GlyArgLeuAsnArgLeuSerGlu.....ArgArgGluSerLeuArgAs
                                                                                                                                                                                                                                                                                                                                                          Length: 21
Gaps: 1
Percent Identity: 57.143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 5761
                                                                                                                         Example 2; Columns 9-16; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JUN-1997; U09743.
14-JUN-1996; US-019940.
(DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: V83923 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID v17562 standard; cDNA; 1818 BP.
                                                                                                                                                                                                                                                                                                                                                                             3.200
71.429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: N_Geneseq_36:V17562
                                                                                                                                                                                                                                                                                                                                                              48.00
Persica MG, Salomon DS;
WPI; 99-095001/08.
P-PSDB; W87630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5010 CAAAATGGGTTAC 5022
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-653-294-35 x V83923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 nLeuArgGlyTyr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GM, Kinney AJ;
                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycine max.
WO9747731-A2.
                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
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                                                                                                            cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fader
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Claim 1) Page 412-413; 2084pp; English.

A computer readable medium has been developed which has recorded on it
A computer readable medium has been developed which has recorded on it
922 nucleotide sequences isolated from the Enterococcus faecalis genome.
X12938 to X13919 represent these nucleotide sequences which are primary
nucleotide sequences, also known as contigs. The computer based system
can identify fragments of the Enterococcus faecalis genome with
commercial importance. The products can be used to detect the presence
of Enterococcus faecalis in samples. They can also be used for
diagnosing Enterococcus infection in an animal and monitoring
progression of disease, and for identifying agents which can be used to
modulate the growth or pathogenicity of Enterococcus faecalis, or
another related organism, in vivo or in vitro. In particular the
polypeptides encoded by the Enterococcus faecalis nucleotide sequences
can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-NOV-1998.

14-NOV-1997.

15-NOV-1997; US-066009.

16-NAY-1997; US-044031.

16-NAY-1997; US-046655.

16-NAY-1997; US-046655.

18-NOV-1997; US-046655.

Barash SC. Dillon PJ. Kunsch CA:

WPI: 99-045171/04.

New isolated Enterococcus faecalis polynucleotides and polypeptides need to develop products for the detection of Enterococcus and for used to develop products for the actenuation of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
Modification of the seed storage protein profile can result in the production of novel soy protein products with unique and valuable functional characteristics.

Sequence 1818 BP; 581 A; 424 C; 427 G; 386 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAR-1999 (first entry)
Enterococcus faecalis genome contig SEQ ID NO:40.
Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 395 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               631 TATGGTCGCATTCGCGTCCTCCAGAGGTTCAACCAACGCTCCCCACAACT 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TyrGlyArg.....LeuAsnArgLeuSerGluArgArgGluSerLe 14
                                                                                                                                                                                                                                                                   47.50 Length: 23
2.794 Gaps: 1
73.913 Percent Identity: 47.826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: V17562 from: 1 to: 1818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X12977 standard; DNA; 1346 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 395, A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  681 TCAGAATCTCCGAGACTAC 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 uArgAsnLeuArgGlyTyr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: N_Geneseq_36:X12977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterococcus faecalis. WO9850555-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-35 x V17562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1346 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seg_documentation_block:
                                                                                                                                                                                                                                                                                                           Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                   alignment_scores;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
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Gaps: 0 Percent Identity: 42.105

47.00 2.938 84.211

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The present sequence encodes a secreted protein. The polynucleotide and secreted protein are predicted to have biological activities which would make them suitable for treating, preventing neclical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating activity, issue growth activity, activity, haematopolesis regulating activity, tissue growth activity, activity,inhibin activity, chemotactic/chemokinetic activity, activity, inhibin activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity (no data is given in the specification to support these activities). The polynucleotide is also stated to be useful for gene therapy.

Sequence 745 BP; 179 A; 229 C; 176 G; 161 T;
   chemokinetic activity; haemostasis; thrombolytic activity; receptor; ligand; anti-inflammatory; cadherin; tumour invasion suppressor; tumour inhibition; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding TIE 11gands 3 and 4 - useful for, e.g. blocking blood vessel growth and promoting neovascularisation, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides encoding secreted human proteins - derived fro human foetal brain, adult brain, foetal kidney, placenta or adult pineal gland cDNA 11braties. Claim 26; Page 80; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tyrosine kinase; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JUN-1998 (first entry)
Mouse TIE-2 receptor ligand 3 cDNA.
TIE-2 receptor ligand; TIE ligand-3; tyrosine kinase; mouse, anglogenesis; vascularisation; blood vessel growth; tumour;
                                                                                                                                                                           20-WAR-1998; U05653.
19-WAR-1998; US-044466.
21-WAR-1997; US-82167.
(GEMA ) GENETICS INC.
AGOSTION MJ, Jacobs K, Lavallie ER, MCCOy JM, Merberg D,
RACHE LA, Spaudding V, Treacy M;
P-PSDB; W85461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 13
Gaps: 0
Percent Identity: 76.923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 ArgLeuAsnArgLeuSerGluArgArgGluSerLeuArg 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 AGAGTCAACAGGCTAAGTGAGAGGAGGGATGCTACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to reverse of: V82783 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-DEC-1997.
19-JUN-1997; U10728.
02-JUN-1996; US-022999.
19-JUN-1996; US-655926.
02-JUL-1996; US-021087.
(REGE-) REGENERON PHARM INC.
JONES PF, VALENZUELA DM, Yancopoulos GD;
WPI; 98-063143/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
ID T99594 standard; cDNA; 1849 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-35 x V82783/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy; receptorbody; ss. Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . .1576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.00
4.182
84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: N_Geneseq_36:T99594
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                   Homo sapiens.
WO9842739-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9748804-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T99594;
22-JUN-1998
                                                                                                                                                                    01-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
   DD PRESENTATION OF THE PROPERTY OF THE PROPERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST clone CG336. Indiana: expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides encoding human secreted proteins - derived from
e.g. human blood, kidney, foetal lung, placenta, testes, brain,
ovary, pitutary, retina and colon cDNA libraries.
To claim 1: Page 171; 618pp: English.
The present sequence represents a human expressed sequence tag (EST).
The polynucleotide, which is a secreted EST, and the encoded protein
are predicted to have useful biological activities which would make
them suitable for treating, preventing or ameliorating medical
conditions in humans and animals, although no supporting data is
given: Suggested activities include nutritional activity, immune
stivity, tissue growth activity, activin/inhibin activity,
chemotactic/chemokinetic activity, haemacopolesis regulating
activity, tissue growth activity, activin/inhibin activity,
cativity, receptor/ligand activity, anti-inflammatory activity,
activity, tumour invasion suppressor activity, tumour inhibition
activity. The polynucleotide may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-1999 (first entry)
Clone dn809_5 isolated from human foetal brain cDNA library.
Secreted protein; nutritional activity; immune stimulating; vaccine; suppressing activity; hamatopolesis regulating activity; tissue growth activity; activin; inhibin activity; chemotactaxis;
                                                                                                   1 TyrGlyArgLeuAsnArgLeuSerGluArgArgGluSerLeuArgAsnLe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D, Racie LA, Spaulding V, Treacy M; 99-070077/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100
   to: 1346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 13
Gaps: 0
Percent Identity: 76.923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 AGAGTCAACAGGCTAAGTGAGAGGAGGGGATGCTACGC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 ArgLeuAsnArgLeuSerGluArgArgGluSerLeuArg 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 G;
   from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: V89291 from: 1 to: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 C;
Align seg 1/1 to reverse of: X12977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V82783 standard; cDNA; 745 BP. V82783;
                                                                                                                                                                                                                                                                                                                                                                                                                               V89291 standard; cDNA; 289 BP.
V89291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.00
4.182
84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                               seq_name: N_Geneseq_36:v89291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-1998.
10-APR-1998; U06955.
10-APR-1997; US-838821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-35 x V89291
                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy; ss.
Homo sapiens.
WO9845436-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                       1152 TAAAGGC 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                         17 uArgGly 19
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/*tag= b
/note= "This region is 4.7-5.3 kilobases in length
/note= sequence of this region has not been
deduced."
                                                               homology domains. It was obtained by PCR amplification of CDNA derived from mouse cell lines C2C12ras and MGB7 using primers (see T9955-96) specific for mTL3. A host-vector system for the production of mTL-3 is claimed, as well as an antibody which specifically binds mTL-3, a receptorbody which specifically binds mtl-3, a conjugate comprising mTL-3 and a cytotoxic agent, and an isolated nucleic acid (see T99593) coding for human TIE ligand 4 blocking blood vessel growth, promoting for human tie ligand 4 blocking or blocking the growth of differentiation of a cell expressing the TIE receptor and attenuating or preventing tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour rejection antigen precursor coding sequence.
Tumour rejection antigen precursor; TRAP, TRA, melanoma; cancer;
tumour; treatment; detection; vaccine; HLA-A2; adoptive transfer;
T cell; T lymphocyte; human leukocyte antigen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic DNA encoding a tumour rejection antigen precursor processed to antigen presented by HLA-A2, useful for treating or
Claim 23; Fig 6A-B; 86pp; English.
This couns sequence includes a coding region for novel mouse TIE ligand-3 (mTL-4, see W26792), a TIE-2 receptor ligand that is a tyrosine kinase with immunoglobulin and epidermal growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             707 CAGCTTAACAGCCTCCAAGAGAAGAGGGAACAACTGCACAGTCTCCTGGG 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 18
Gaps: 0
Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                           507 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag- a
/note= "Unidentified nucleotide."
9422. .9456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11539
/*tag= c
/note= "Unidentified nucleotide."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: T99594 from: 1 to: 1849
                                                                                                                                                                                                                                                                                           549 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coulie P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wolfel T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Page 18-22; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUL-1994; US-272351.
10-JAN-1995; US-370319.
(LUDW-) LUDWIG INST CANCER RES.
BOOD-falleur T. Brichard V. C.
Traversari C. Van PEL A, Wolf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
ID T11549 standard; DNA; 13585 BP.
AC T11549;
                                                                                                                                                                                                                                                                                         451 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                               2.875
88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: N_Geneseq_36:T11549
                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-35 x T99594
                                                                                                                                                                                                                                                                                           1849 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -JUN-1995; U08153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosing melanoma
                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9601557-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   757 CCAT 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
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                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 yTyr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -JAN-1996
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A1794877 sb72h01.yl Gm-c1010
A1795011 sb75a10.yl Gm-c1010
AQ873097 V59C8 mTn-3xHA/lac2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 103)

8 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgeraldi,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm.C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.J., Kelley,J.M., Mcrancy-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Phillipps,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weldman,J.F., Li,Y., Dimke,D.P., Feng,D.-F., Feorie,A.M., Aruber,C., Hastings,G.A., Hew,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Welly,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Inital assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
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For clone availability, additional sequence and expression
for clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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/db_xref="taxon:9606"
/docone_lib="Adrenal gland tumor"
/dev_stage="adult"
/note="Organ: adrenal gland; Vector: pBluescript SK-;
site=1: EcoR1; Site=2: XhoI"
35 c 29 g 13 t
                                                                                                                                                                                                                               seq_documentation_block:
LOCUS AA319533 103 bp mRNA EST 19-APR-1997
DEFINITION EST21772 Adrenal gland tumor Homo sapiens CDNA 5' end similar similar to major histocompatibility complex, class I, B (GB:M16102), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Sep 12, 1996 this sequence version replaced gi:1393672 Other_ESTs: THC169519
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
1711: 3018699056
Fax: 3018699423
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Percent Identity: 100.000
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US-08-653-294-35 x AA319533
                                                                                                                                                          seq_name: gb_est12:AA319533
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gb_est34:AI794877
gb_est34:AI795011
gb_gss6:AQ873097
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MEDLINE
COMMENT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Documentation
| AA319533 EST21772 Adrenal gland
| AA319533 EST21772 Adrenal gland
| AA319531 EST21775 Activated T-
| AA319531 EST10761 T-cell lympho
| AA329501 EST60621 Activated T-
| AA32960 EST61101 Activated T-
| AA32960 EST61101 Activated T-
| AA52960 EST61101 Stratagene
| AA160317 2c56c07.r1 Stratagene
| AA160317 2c56c07.r1 Stratagene
| AA160317 2c56c07.r1 Stratagene
| AA160318 EST181593 Jurkat T-cel
| C18310 C18310 Human Placenta cC
| AA663896 ac74d01.s1 Stratagene
| AA663896 ac74d01.s1 Stratagene
| AA663896 ac74d01.s1 Stratagene
| AA675632 C1781-E1-2590116.TF C1781015 AC C17810 C1781
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-MINMATCH=0.100 -LOOPCI=0.000 -LOOPEXT=0.000 -GGAPOP=6.000
-GGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -DELOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
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-UST=45 -NORM=ext -MINLEN-0 -MAXLEN=1000000 -USER-US08653294
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gb_est37:AW008453
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Homo sapiens
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                                                                         Align seg 1/1
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia; Eukaryota: Metazoa: Catarrhin; Hominidae: Homo.

Eutheria: Primates: Catarrhin; Hominidae: Homo.

Eutheria: Primates: Catarrhin; Hominidae: Homo.

Sadams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

Mhite, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghaqen, N.S.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Sprigs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Colleman, T.A., Collins, E.J.,

Dimke, D., Fenrie, A., Fischer, C., Hastings, G.A.,

Rymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Praser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of CDNA sequence
                                                                                                                                                                                 seq_documentation_block:
LOCUS
LOCUS
AA361477
DEFINITION EST70761 T-cell lymphoma Homo sapiens cDNA 5' end similar to
similar to major histocompatibility complex, class I, Bw62.3, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
for clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Sep 12, 1996 this sequence version replaced gi:1404737 Other_ESTs: THC169519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
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Percent Identity: 100.000
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to: 103
                                             Location/Qualifiers
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Align seg 1/1 to: AA319533
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Ratio: 5.100
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VERSION
KEYWORDS
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COMMENT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

E Adams, M.D., Kerlavage, A.R., Fleischmann, B.D., Fuldher, R.A.,

Bull, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

Whiteo., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,

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Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

Gloddk, A., Ghehm, C.L., Hanna, M.C., Hadblom, E., Hinkle, P.S., J.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

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Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Ho, W., Hu, J.S., Greene, J.M., Gruber, J., Hastings, G.A.,

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Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melssner, P.S., Olsen, H.,

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Fraser, C.M., Pannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,

Fraser, C.M., R.M., R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
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index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse
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Other_ESTs: THC172938
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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    .218
    ^coganism="Homo sapiens"
    /db_xref="ATCC (inhost):152802"
    /db_xref="taxon:9606"

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                                                                                                                                                  to: 189
                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                              from: 1
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AA352603.1 GI:2004923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 C
                                                                                                                                         to: AA361477
alignment_block:
US-08-653-294-35 x AA361477
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from: 1
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AA352960.1 GI:2005353
                                                                                                                                                                                                                                                                                Align seg 1/1 to: AA294911
                                                                                                  Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                      alignment_block:
US-08-653-294-35 x AA294911
                                                                                                                                                                                                                                                                                                                                                                                                                               seg_name: gb_est13:AA352960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
LOCUS AA352960
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  ORIGIN
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Eutheria, Primates; Catarini; Hominidae; Homo.

State 1 (Dases 1 to 259)

Bult, C.J., Lee, N. H., Kirkness, E.F., Wehnstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wal, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geophagen, N.S.,

Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblon, E., Hinkle, P.S., Tr.,

Kelley, J.M., Kelley, J.C., Liut, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,

Kozak, D.L., Kunsch, C., Hunglun, J., Li, H., Meissner, P.S., Olsen, H.,

Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of CDNA sequence

N. Nature 377 (6547 Suppl), 3-174 (1995)

On Nov 29, 1993 this sequence version replaced gi:430148.
                                                                                                                                                                                                                                                                                                                                                                                                                             AA294911 259 bp mRNA EST 18-APR-1997 EST100074 Pancreas tumor I Homo sapiens cDNA 5' end similar to similar to major histocompatibility complex, class I, Bw62.3, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
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ECORI; Site_2: XhoI"
87 c 75 g 30 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Tel: 3018699056
Fax: 3018699423
                     Length: 10
Gaps: 0
Percent Identity: 100.000
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/db_xref="ArCC (inhost):190413"
/db_xref="taxon:9606"
/clone_lib="Pencreas tumor I"
/dev_stage="adult"
                                                                                                                                                                                                      to: 218
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AA294911
AA294911.1 GI:1947266
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                  Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                       alignment_block:
US-08-653-294-35 x AA352603
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alignment_scores:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Catarrhin; Hominidae; Homo.

1 (basa 1 to 270)

2 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, D.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palaques, R.F., McDonald, L.A., Nquyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Kozak, D.L., Kunsch, C., Hunglun, J., Li, H., Weissner, P. S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
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Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
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For clone availability, additional sequence and expression
For clone availability, additional sequence and expression
Information related to this EST, please check the TiGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA352960 270 bp mRNA EST 21-APR-1997 EST61101 Activated T-cells XX Homo sapiens cDNA 5' end similar t similar to major histocompatibility complex, class I, B61, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On May 8, 1995 this sequence version replaced gi:801269.
Other_ESTs: THC172938
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
121: 3018699056
Fax: 3018699423
Length: 10
Gaps: 0
Percent Identity: 100.000
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/cell_type="T-lymphocyte"
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/db_xref="ATCC (inhost):153240"
/db_xref="taxon:9606"
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us-08-653-294-35.rst

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Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 373)

Hiller,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,

Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,

Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,M., Le,M.

Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Riffin,L.,

Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,

Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
97044478
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                     Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@thmage.llnl.gov) for further information.
Insert Length. 1592 Std Error: 0.00
Seq primer: -28MJ rev2 from Amersham
High quality sequence stop: 268.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Stratagene colon (#937204)"
/lab_host="Sofix cells (kanamycin realstant)"
/note="Organ: colon; Vector: pBluescript SK-; Site_l:
EcoR; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. T-84 colonic epithelial cell line. Average
insert size: 10 kb: Uni-ZaP XR Vector; -5' adaptor
sequence: 5' GAATTGGCACGAG 3' -3' adaptor sequence: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Sep 12, 1996 this sequence version replaced g1:1393357
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63108
                                                              5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Fel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                Length: 10
Gaps: 0
Percent Identity: 100.000
  /dev_stage="adult"
/note="Vector: pBluescript SK-;
Xho!"
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                                                              35
                                                                                                                                                                                                                                                                                                               to: 270
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/organism="Homo sapiens"
/db_xref="GDB:3813009"
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                                                                                                                                                                                                                                                                                                                                                                             182 CGAGAGGCTNCGGAACCTTCGCGGCTAC 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:509677"
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Ratio: 5.100
Percent Similarity: 100.000
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US-08-653-294-35 x AA352960
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                                                                62
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seq_documentation_block:
100CUS AA224068 397 bp mRNA EST 19-FEB-1997
LOCUS AA224068
DEFINITION ZIIIf02.T1 Stratagene hNT nuron (#937233) Homo sapiens cDNA clone
IMAGE:648507 5' similar to 9b:L22549_cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, B-39 B*3901 ALPHA (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9666"
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/clone="IMAGE:648607"
/dev_stage="har neurons"
/lab_host="SOLR (kanamycin resistant)"
/note="vector: pBluescript SK-; Site_1: EcoRI; Site_2: Note="vector: pBluescript SK-; Site_1: EcoRI; Site_2: Differentiated, post mitotic har neurons. Average insert size: 1.5 kb; uni-ZAP XR vector; -5' adaptor sequence: 5' GAATTGGGCACGAG 3' -3' adaptor sequence: 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 397)

1111ler,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Rucaba,T., Lacy,M., Le,N., Le,N., Mardis,E., Moore,B., Morris,M., Parson,J., Prange,C., Rikin,L., Rohliting,T., Schellenberg, K., Soares,M.B., Tan,F., Thierry Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -ZBm13 revl ET from Amersham High quality sequence stop: 295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Nov 29, 1993 this sequence version replaced gi:430429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
   others
                                                                                                                                                                                 Gaps: 0
Percent Identity: 100.000
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57
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   116
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      O
                                                                                                                                            Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
   113
                                                                                                                                                                                                                                                                                                                                                            to: AA058454
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US-08-653-294-35 x AA058454
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to: AA160317
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 405)

Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
Washu-NCI human EST Project
Unpublished (1997)

Confact: Wilson RK
Washington university School of Medicine
Vashington university School of Medicine
12, 1996 this sequence version replaced gi:1406818.

Confact: Wilson RK
Washington university School of Medicine
Tel: 314 286 1800

Fax: 314 286 1800

Fax: 314 286 1800

Fax: 314 286 1800

Fax: 314 286 1810

Fax: 314 286
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LOCUS AA160317
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Percent Identity: 100.000
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US-08-653-294-35 x AA160317
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AUTHORS
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Eukaryotti.

Eukaryotti.

Eukaryotti.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 419)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,

Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,

Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,

Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J.,

Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (infoelmage.llnl.gov) for further information.
Insert Length. 1534 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 275.
Location/Qualifiers
                                                                                                                                                                                  AA100680 419 bp mRNA EST 31-JUL-1997 21980b2.r1 Stratagene colon (#937204) Homo sapiens CDNA clone ILMAGE:511851 5' SIMILAR to gb:NZ4039.cds1 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK Washington University School of Medicine Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 others
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                      281 CGAGAGAGCCTGCGGAACCTGCGCGGCTAC 310
11 ArgGluSerLeuArgAsnLeuArgGlyTyr
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US-08-653-294-35 x AA100680
                                                                                                       seq_name: gb_est9:AA100680
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225 CACAGACTTACCGAGAGA.

seq_documentation_block: LOCUS W40489

DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE

Homo sapiens

ORGANISM

REFERENCE

human.

seq_name: gb_est7:W40489

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Laurentia Frinances, Cararinin; Hominidae, Homo.

Eutheria Frinances, Cararinin; Hominidae, Homo.

Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man Wai, C.,

Klayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Fitzgerald, E.M., Fitzhugh, W.M., Fritchman, J.L., Geoglagen, N.S.,

Glodek, A., Gnehm, C.L., Hanne, M.C., Hedblom, E., Hinkle, P.S., Jr.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., WcDonald, L.A., Nollyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Dinke, D., Ferrie, A., Fischer, C., Hastings, G.A.,

Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melssner, P.S., Olsen, H.,

Raymond, L., Wei, Y.F., Wing, J., Li, H., Melssner, P.S., Olsen, H.,

Fraser, C.M., and Venter, J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence
Email: arkerlav@tigr.org

Email: arkerlav@tigr.org

Emoil: arkerlav@tigr.org

Information related to this EST, please check the TIGR Human Gene

Index (http://www.tigr.org/tdb/hgi/hgi.html)

Seq primer: M13 Reverse.

Incation/Qualifiers

1. 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Jurkat T-cells V"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1996 this sequence version replaced gi:1397854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="ATCC (inhost):156811"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 CGAGAGAGCCTTCGGAACCTGCGCGCGCTAC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 ArgGluSerLeuArgAsnLeuArgGlyTyr
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                                                                                                                               AA310808
AA310808.1 GI:1963136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Other_ESTs: THC180721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 C
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Percent Similarity: 100.000
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US-08-653-294-35 x AA310808
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                                                                                                                               ACCESSION
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ORIGIN
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                  2C84b01.rl Pancreatic Islet Homo sapiens CDNA clone IMAGE:328969 5' similar to gb:U11265 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3501 ALPHA (HUMAN);, mRNA sequence.
W40489.1 GI:1324496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 427)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Glsh,W., Mardis,E., Moore,B., Morris,M., Parsons,J., Pernge,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Jan 25, 1995 this sequence version replaced g1:637865.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality. sequence stop: 397.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 others
Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="IMAGE:328969"
```

/db_xref-"GDB:12631

1. .427 /organism="Homo

FEATURES

and Marra, M.

97044478

TITLE JOURNAL MEDLINE COMMENT

11 ArgGluSerLeuArgAsnLeuArgGlyTyr

seq_name: gb_est12:AA310808

to: W40489 from: 1

Align seg 1/1

51.00

Quality:

alignment_scores:

87

BASE COUNT ORIGIN

Ratio: 5.100 Percent Similarity: 100.000

alignment_block: US-08-653-294-35 x W40489

LOCUS

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

```
/tissue_type="schizophrenic brain S-11 frontal lobe"
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/dev_stage="34 years old"
/lob_host="SolR (kanamycin resistant)"
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/note="Vector: Bluescript SR.; Site_1: EcoRI; Library
constructed from S-11 frontal lobe, male, 34 years old,
50% caucasian, 50% Aleutian. Schizophrenic suicide.
Random primed into EcoRI site of ZAP II Vector. Mass
excised. Custom library. Avg insert length 1.4kb.
Material obtained by Johnston N.; Torrey, E.F.; Volken R.,
and the Stanley Neuropathology Consortium - Analysis of
RNAs from the Brains of Individuals with Psychiatric
Diseases (Unpublished) Stanley Neurovirology Laboratory,
Johns Hopkins School of Medicine, Baltimore MD."
165 c 158 g 64 t lothers
                                                                   Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 315 est@watson.wustl.edu
Finis clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Fossible reversed clone: polyT not found
Seq primer: -40ml3 fwd. ET from Amersham
High quality, sequence stop: 430.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL039796 503 bp mRNA EST 29-SEP-1999
DKF2p4481912_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKF2p434B1912_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 503)
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Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1394858.
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST (Duesterhoeft, et al.)
Unpublished (1999)
On Jun 2, 1999 this sequence version replaced gi:4967270.
Contact: Duesterhoeft A
                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 10
Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL039796.1 GI:5408804
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Ratio: 5.100
Percent Similarity: 100.000
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US-08-653-294-35 x AA663896
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LOCUS AL039796
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JOURNAL
COMMENT
JOURNAL
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AUTHORS
                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                      [ (bases 1 to 475) [ Superior 1 to 475] [ (bases 1 to 475) [ Superior 2 to 475] [ Fujiwara, T., Hirano, H., Hishigaki, H., Horie, M., Kawai, A., Kuga, Y., Kyushiki, H., Nagatta, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Sainomiya, H., Suzuki, M., Takaichi, A., Takeda, S., Watanabe, T., Maekawa, H., Nakamura, Y. and Takahashi, E. Otsuka cDNA project Unpublished (1996) [ On Sep 12, 1996 this sequence version replaced gi:1393837. Contact: Tsutomu Fujiwara Otsuka GEN Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 479)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Otsuka Pharmaceutical Co., Ltd
463-10 kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
                                                                                               C18310 475 bp mRNA EST 02-OCT-1996 C18310 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-560D07 5', mRNA sequence.
C18310 C18310 GI:1579912
                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. 475
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a 161 c 154 g 68 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 10
Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 0886-65-2888
Fax: 0886-37-1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio: 5.100
Percent Similarity: 100.000
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US-08-653-294-35 x C18310
                                                                         seq_documentation_block:
                        seq_name: gb_est9:C18310
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source

FEATURES

BASE COUNT ORIGIN

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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                                                                                                                                                                                                                                                                                                                                                BASE COUNT
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1 (bases 1 to 583)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Tumor Gene Index

Tumor Gene Index

On May 7, 1998 this sequence version replaced gi:3121511.

Contact: Robert_Strausberg* Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg* Ph.D.

Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever, M.D., Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NOI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thig03.x1 NCI_CGAP_CLLI Honos sapiens cDNA clone IMAGE:2118100 3/
similar to SW:MY16_MOUSE P17564 WYELOID DIFFERENTIATION PRIMARY
RESPONSE PROTEIN MYD116. ;, mRNA sequence.
              Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by Qiagen within the cDNA sequencing consortium of the
                                                                                                          No sI sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                    :: pSport1; Site_1: Not1; Site_2: Sal1"
165 g 68 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 100.000
This is the 5' sequence of the clone insert
                                                                                                                                                                                                                                                                                                                   /clone_lib="444 (synonym: htes3)"
/tissue_type="testis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ww-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
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                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKF2p434B1912"
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High quality sequence stop: 4
Location/Qualifiers
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                                                                                         German Genome Project
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Ratio: 5.100
Percent Similarity: 100.000
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US-08-653-294-35 x AL039796
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/Grganiam="Homo sapiens"
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//clone='Inaxon:9606"
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//clone='Inaxon:9606"
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//clone='Inaxon:9606"
//clone='Inaxon:0606"
//clone='Inaxon:0606"
//db_host="B-cell, chronic lymphotic leukemia"
//db_host="Pullog"
//db_
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 8, 2000, 04:05:44; Search time 133.56 Seconds (without alignments) 2.128 Million cell updates/sec Run on:

US-08-653-294-36 58 1 YRLAIRRIALRY 12 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

188963 seqs, 23686106 residues Searched:

188963 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 08 Listing first 45 summaries

A_Geneseq_36:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	2 84-	Peptide B2702.84-7	Immunomodulating d	HLA-B2702 CTL modu	œ	Immunomodulating d	HLA-B2702 CTL modu	E I	Peptide B2702.84-7	Peptide B2702.84-7	HLA-B2702 84-75T/7	Human MHC 1 alpha	Human neuronal nic	HLA-B2702 CTL modu	Immunomodulating d	HLA-B2702 CTL modu	Peptide B2702.84-7	Human DNAX toll-11	Curvularia verrucu	Curvularia verrucu	Human neuronal nic	χŢ	Hepatitis GB virus	Xanthosine N7 meth	Coffee xanthosine	Coffee XMT protein	Corn p-hydroxyphen	Neuronal nicotinic	Human secreted pro	Human ligase IV. M	DNA-ligase-III. Ne	eryA region polype	Human cytostatin I	Human cytostatin I
SUMMARIES		ID	R95429	W33798	W33799	R92907	R95428	W33778	R92909	R92908	W33791	W33792	R95430	R71429	W44156	R92911	W33779	R92910	W33793	W86351	W12037	W12042	W44152	R82249	R81449	W31535	W65768	W76641	W41940	W09022	W74762	W69561	R95634	R44431	2658	26
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		Length	12																							371	371	371	444	504	520	844	911	3567	107	107
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Gaps

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Query Match
100.0%; Score 58; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels

1 YRLAIRRIALRY 12 |||||||||||||||| 1 YRLAIRRIALRY 12

ò 임 W33798 standard; peptide; 12 AA. W33798;

RESULT 2 W33798 ID W33798 AC W33798;

### 100 51.7 107 1 W83929  36 30 51.7 347 1 W72169  38 30 51.7 454 1 W72165  44 30 51.7 546 1 W72165  45 30 51.7 546 1 W72165  46 30 51.7 546 1 W72165  47 30 51.7 546 1 W72165  48 52 50.0 6 1 W47263  FRIGHTON OF THE CONTROL OF	Human growth inhib Human cytostatin i HSV-2 strain SB5 C HSV-2 strain SB5 C W. rosa truncated HSV-2 strain SB5 C W. rosa fourth adh Human telomerase. Immunomodulatory p Immunomodulatory p Peptide #1 used in	ALIGNMENTS  1 1 1 2 1 1 1 240429 standard; peptide; 12 AA. 12-NOV-1996 (first entry) 12-NOV-1996 (first entry) 14-82702 84-79-64 palindrome. 14-82702 84-79-64 palindrome. 15-NOV-1996 (first entry) 15-NOV-1996 (first entry) 16-NOV-1996 (first entry) 17-10 1/99-14-14 in mannal: heat shock protein; Hsc70; APC; Breal: Jordium influx: cytotoxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell. 16-NOV-1994; U12985. 10-NOV-1994; U12985. 11-NOV-1994; U1	. igand.
004 6000000444444 119	W83929 W30891 W72145 W92336 W72165 W72165 W72165 W47263 W47263	ALIG The control of the control of	the
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With a compound of the peptide(s) - based on a Class I HiA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases.

Example 1; Page 19; 41pp; English.

Communomodulating activity, including the N-terminal acylated and/or currential antiated or esterified forms of up to 60 amino acids, where compound comprises the formula; A-B, where A, B = comming and a compound comprises the formula; A-B, where A, B = compound compound comprises the formula; A-B, where A, B = compound compound comprises the formula; A-B, where A, B = compound compound comprises the formula; A-B, where A, B = compound c
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WPI: 98-086530/08.
WPI: 98-086530/08.
WPI: 98-086530/08.
WPI: 98-086530/08.
WPI: 98-086530/08.
WPI: 98-086530/08.
WPI: Pacating dimer peptide(s) - based on a Class I HLA-B
alpha-1 domain, used for preventing rejection of transplants or
treating autoimmune diseases
treating autoimmune diseases
Claim 17; Page 35; 41pp: English.
This sequence represents a specifically claimed immunomodulating
dimer peptide of the invention. A peptide-type compound or variant is
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19-JUN-1998 (first entry)
Peptide B2702.84-79/79-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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                                                                                                                                                                                                                                                             24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
WPI: 98-086530/08.
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22-NAY-1997.
24-NAY-1996. US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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Matches 12; Conservative
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22-MAY-1997; U08689.
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WO9744351-A1.
                                                                                                                                                                Homo sapiens
                                                                                                           rejection.
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W33799
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claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula: A-B, where A, B = (R aaf6-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a represents amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytocoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proliferation of I cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis.
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R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration for a limited period of time (compared to the lifetime modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA-B2702 CTL modulating peptide (B2702.84-75/75-84). Cytotoxic I lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched
donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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60.0%; Pred. No. 0.024;
vative 0; Mismatches
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(STRD ) UNIV LELAND STANFORD JUNIOR.
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Best Local Similarity 60.0
Matches 12; Conservative
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Matches 12; Conservative
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05-APR-1994; US-2228
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R92907
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1 YRLAIR-----RIALRY 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
WO9526979-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
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R92909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PT companies comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs.

Example: Page 12; 29pp: English.

Example: Page 21; 29pp: English.

Example: Page 22; 29pp: English.

Example: Page 21; 29pp: English.

Example: Page 21; 29pp: English.

Example: Page 22; 20pp: English.

Example: Page 
                                                                                                      12-NOV-1996 (first entry)
HLA-B2702 84-75-84 palindrome.
HLA-B2702 84-75-84 palindrome.
HLA-B2702 194-75-84 palindrome.
HLA: P74: alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;
cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUN-1998 (first entry)
Immunomodulating dimer peptide #1.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
6
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                                                                                                                                                                                                                                                                                                                                         18-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
CLAYDEFGER C, Krensky AM;
WPI; 95-194027/25.
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(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R. Clayberger C, Krensky AM;
WPI; 98-086530/08.
                                                      R95428 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W33778 standard; peptide; 20 AA
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22-MAY-1997; U08689.
                                                                                                                                                                                                                                                                                        Synthetic.
WO9513288-A1.
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WO9744351-A1.
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RESULT
R95428
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treating autoimmune diseases

Claim 16; Page 35; 41pp; English.

This sequence represents a specifically claimed immunomodulating
dimer peptide of the invention. A peptide-type compound or variant is
claimed which has immunomodulating activity, including the N-terminal
acylated and/or C-terminal amidated or esterified forms of up to 60
acylated and/or C-terminal amidated or esterified forms of up to 60
acylated and/or C-terminal amidated or esterified forms of up to 60
acylated and/or C-terminal amino acids, where the peptide-type compound comprises the formula; where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = L). S or N; aa79 = R or G; aa80 = I or N; aa81, aa48 = E or V; aa77 = L). S or N; aa78 = R or G; aa80 = I or N; aa81, aa48 = E or N; aa81 and a a and a as a represents amino acid; The sequence in the brackets may optionally be a compounds comprise amino acid sequences related to a Class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the used for products of interest to activate CTLs. They can also inhibit the used for products or a service o
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R83061-R83085, R8309-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of The peptides are administered to a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime modulate (or limited period of time (compared to the lifetime modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)). Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.2%; Score 39; DB 1; Length 20; 55.0%; Pred. No. 0.21; 1. Indels ive 0; Mismatches 1; Indels
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05-ARR-1994; US-222851.
(STRD) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
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Best Local Similarity 55.0°
Matches 11; Conservative
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Best Local Similarity 60.0
Matches 12; Conservative
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Homo sapiens.
WO9744351-A1.
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R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administered to time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
                                                                                                                     16-MAY-1996 (first entry)

HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).

Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases.

Example 1, Page 19; 41pp, English.

Peptides W33784-98 and W33778-9 were assayed for their immunomodulating activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUN-1998 (first entry)
Peptide B2702.84-75r/75-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                              Extension of acceptance period of transplants from MHC unmatched donor hosts – using Class I B75-84 MHC antigen of the recipient
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55.0%; Pred. No. 0.21;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                       05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
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(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
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                                                                                                      R92908 standard; peptide; 20 AA
W33791 standard; peptide; 20
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05-APR-1995; U04349.
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                                                                                                                                                                                                                                                                                                                                          Clayberger C, Kren
WPI; 95-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 98-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 AA;
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the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-771) [aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa11, aa84 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HiA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of Interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, insending atthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
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Peptide B2702.84-75/75-84T tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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22-NAX-1997, U08689.
24-NAX-1996, US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W33792 standard; peptide; 20 AA.
W33792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YRLAIR-----RIALRY 12
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Best Local Similarity 55.0
Matches 11; Conservative
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1 YRLAIRRIALRY 12
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08-MAR-1994; U02447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc_difference 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc_difference 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                          Goldstein A, Good
WPI; 95-098577/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc_difference
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                                                                                                                                                                                                                                                     receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
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W44156
       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ON MARKET THE PROPERTY OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This composes comparising lymphoid surface membrane proteins - which may finhibit cytolytic activity and differentiation of CTLS.

Example: Page 12: 29pp; English.

Example: Page 12: 29pp; English.

R94313, and R95415-R9543 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the car and 12: 20pp; English.

CC R0413, and R95415-R9543 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the car associated protein p74 from a T-cell lyses equences can be used too isolate the protein p74 from a T-cell lyses equences can be used too and is also immunologically cross reactive with the heat shock protein R70. p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or the cytolytic combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or the cytolytic cactivity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by sequence 20 AA; the extracellular portion of p74, in an amount sequence 20 AA; the p74 ligand.
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                                                                                                                                                                                                                                                                                                                                                                                 R95430;
L92-NOV-1996 (first entry)
HZ-NOV-1996 (first entry)
HZ-B2702 84-75T/75-84T palindrome.
HZ-B2702 84-75T/75-84T palindrome.
HZ-B2702 84-75T/75-84T palindrome.
HZ-C-11 lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
T-C-11 lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
T-C-11 lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                          Gaps
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R71429;
12-OCT-1995 (first entry)
Human MHC 1 alpha 1 domain peptide [Ala81]-Dk-(69-85).
Major histocompatibility complex class 1; MHC 1; cell receptor; alpha 1 domain; peptide [Ala81]-Dk-(69-85); interaction modulation; arthritis; neoplasias; lupus erythematosus.
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Pred. No. 0.51;
0; Mismatches 0; Indels
                                   1; Indels
Pred. No. 0.21;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAY-1995.
10-NOY-1994; U12985.
10-NOY-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                              R95430 standard; peptide; 20 AA.
R95430;
                                                                                                       1 YRLAIR-----RIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.8%;
57.9%;
                                                                                                                                                                       1 YRLAIRLNERRENLRTALRY 20
   55.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 63.8
Best Local Similarity 57.9
Matches 11; Conservative
                                   Conservative
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9513288-A1.
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WO9505189-A.
23-FEB-1995.
                                                                                                                                                                                                                                                                          RESULT 11
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                                                                                                                                                                                                                                                                                                              R95430
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Human neuronal nicotinic acetylcholine receptor alpha-3 subunit.
Human; neuronal nicotinic acetylcholine receptor; alpha-3 subunit;
brain tissue; screening; NRChR; antibody.
                                                                                                                                                                                  Example 4: Page 45: 103pp; English.
R71424-R71438 are human major histocompatibility complex class 1
(MHC 1) alpha 1 domain derived peptides and peptide mutants, they were used to modulate interactions between MHC 1 and cell surface receptors. Via competitive inhibition the peptides diminish the receptors response, this feature may be useful for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                   Regulating cell surface receptor response - by modulating interaction between MHC class I antigen and the cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 1; Length 18; Pred. No. 1.1; 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                             of neoplasias, lupus erythematosus and arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159. .480
/label= TMD4
/note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "encoded by WWC"
240. .265
/label= TWDl
/note= "transmembrane domain"
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/label- cytoplasmic_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label unspecified 'note" encoded by AMC"
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/note= "encoded by AWC"
273. .296
/label= TMD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "encoded by TGY" 102. .326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "encoded by WWC"
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'note= "encoded by TWC"
                                                                         Olsson L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'label = unspecified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W44156 standard; Protein; 504 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label- signal
Misc_difference 235
                                                                                                                                                                                                                                                                                                                                                                                                                                       60.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- TMD3
12-AUG-1994; U09189.
12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA.
Goldstein A, Goodenow RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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Indels

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Mismatches

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Conservative

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Matches

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Example 2: Page 72-73; 99pp; English.

The present sequence represents a human neuronal nicotinic acetylcholine receptor (NAChR) subunit. The cells expressing the alpha and/or beta neceptor (NAChR) subunit. The cells expressing the alpha and/or beta NAChR subunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal NAChR.

Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits or specific receptor subunit combinations with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with one or more receptor subtypes. The resulting direraction with one or more receptor subtypes. The resulting density should exhibit fewer unwanted side effects than drugs identified e.g. screening with cells
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R83061-R83085, R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to about the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.MAY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).
CYLOCOXIC T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                Human neuronal nicotinic acetylcholine receptor subunits and DNA also transformed cells useful for screening cpds. which modulate
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                                   (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC. (SIBI-) SIBIA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.3%; Score 35; 58.3%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         that express a variety of subtypes.
Sequence 504 AA;
                                                                                                          Elliott KJ, Ellis SB, Harpold MM;
WPI; 94-303024/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R92911 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 58.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 | | ||::| |
232 YSLXIRRLSLFY 243
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WPI; 95-358582/46.
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R92911
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Synthetic:

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Wey14451-A1.

PF 27-MAY-1996; US-653294.

PF 24-MAY-1996; US-653294.

RAY-1996; US-653294.

PR 24-MAY-1996; US-653294.

RAY-1996; US-653294.

RAY-1996; US-653294.

RAY-1996; US-653294.

PI Beulow R, Clayberger C, Krensky AM;

WPI; 98-086530/08.

RAY-1996; US-653294.

RAY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                               Immunomodulating dimer peptide #2.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
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Pred. No. 1.5;
2; Mismatches 0; Indels
                                                                                                                                                                              20 AA.
                                                                                                                                                                                                                               19-JUN-1998 (first entry)
                                                                                                                                                                           W33779 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||||||
| YRLAIRLNERYRLAIR 16
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                                                                                                                                                                                                                                                                                                                                     rejection.
                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                            15
                                                                                                                            RESULT
W33779
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Search completed: February 8, 2000, 04:05:45 Job time: 9362 sec

Score 34.5; DB 1; Length 20; Pred. No. 1.5;

59.5%; 56.2%;

Query Match Best Local Similarity

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

February 7, 2000, 18:04:41 Run on:

Search time 111.22 Seconds (without alignments) 5.089 Million cell updates/sec

1 YRLAIRRIALRY 12 US-08-653-294-36 58 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

142080 seqs, 47169319 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45

pirl:* pir2:* pir3:* PIR_62:* 1: pir1: 2: pir2: 3: pir3: 4: pir4: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

ALES.	Description	probable oxidoredu		histocompatibility	ABC-type transport		protein -	hypothetical prote	chetical	protein	strf protein - Str	conserved hypothet	probable fumarate	dynein heavy chain	hypothetical prote	ribosomal protein	hypothetical prote	thioether S-methyl	beta-glucosidase h	hflx protein - Myc	~~	524	bosoma.	G	hypothetical prote	~	hypothetical prote	-~1	conserved hypothet	hypothetical prote
SUMMAKIES	e e	G70882	JC5342	S29990	S74745	S44230	7	S15593	D72507	S44228	S44225	C69460	F72691	B54802	S69745	H71504	F70410	S52102	G69760	S72938	A41798	D65032	C72053	S50980	T16542	148120	E75055	148119	F72323	D72509
	DB	7	~	~	~	~	~	7	~	N	~	7	ď	~	~	~	~	~	~	~	~	N	7	ч	7	~	7	7	7	~
	Length	309	313	348	276	281	281	388	178	267	267	469	573	4367	128	141	190	264	477	518	682	1124	142	203	215	252	253	259	306	339
đ	Query Match	69.0	62.1	62.1	60.3	60.3		60.3	28.6	58.6	58.6								56.9						٠.	55.2	- 4	٠.	٠.	٠.
	Score	40	36	36	35	35	35	35	34	34	34	34	34	34	33	33	33	33	33	33	33	33	32	32	32	32	32	32	32	32
	Result No.	1	7	٣	4	5	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote chloride peroxidas hypothetical prote hypothetical prote hypothetical prote p-glycoprotein iso nonstructural poly hypothetical prote DNA directed RNA p 3-dehydroquinate d probable dapB prot hypothetical prote hypothetical prote	hypothetical prote hypothetical prote
704960 269334 105172 1105172 1106616 1148122 1708822 1709822 1709822 170982 171567	S74282 T02119
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434 609 857 1010 1281 19281 77 78 153 245 264	265 286
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	31
88888884444 888888884444 8888888888888	44 45

ALIGNMENTS

A.Status: preliminary; nucleic acid sequence not shown; translation not shown A.Status: preliminary; nucleic acid sequence not shown; translation not shown A.Molecule type: DNA A.Molecule type: Molecule type: M

ö 0; Gaps Score 40; DB 2; Length 309; Pred. No. 2; 1; Mismatches 0; Indels 69.0%; 88.9%; Query Match
Best Local Similarity 88.9
Matches 8; Conservative

||:|||||| | 65 YRIAIRRIA 73 1 YRLAIRRIA 9 ô

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Na+/H+ antiporter cdu2 - clostridium difficile
(Spaces): Jose: 27-May-1997
(Spaces): Jose: 28-May-1997
(Spaces): Jose: Jos

0; Gaps

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R; Mansouri, K.; Piepersberg, W. Mol. Gen. Genet. 228, 459-469, 1991
A; Title: Genetics of streptomycin production in Streptomyces griseus: nucleotide sequals As Reference number: S17775: MUID:91375432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB: Y00459; GB: S55493; NID: g1621271; PID: e275192; PID: 91621272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X54434
A;Note: the authors translated the initiation codon GTG for residue 1 as Val
C;Species: Streptomyces glaudescens
C;Date: 13-14n-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
C;Accession: S44230
R;Mayer, G.; Piepersberg, W.
Submitted to the EMBL Data Library, April 1994
A;Reference number: S44224
A;Reference number: S44224
A;Reference preliminary
A;Molecule type: DNA
A;Residues: 1-281 <MAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Streptomyces griseus
C;Date: 16-5ep-1992 #sequence_revision 16-Sep-1992 #text_change 20-Mar-1998
C;Accession: S17776
R;Mansouri, K.; Piepersberg, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein (insertion sequence ISH27-3) - Halobacterium halobium C;Species: Halobacterium halobium C;Species: Halobacterium halobium C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 30-Jun-1998
                                                                                                                                                                                                                                                                                                                                             Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 281;
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                          A;Cross-references: EMBL:X78974; NID:g475235; PID:g581673
C;Genetics:
A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                             1;
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17;
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                                                                                                                                                                                                                                                                                                                                                Score 35; DB 2
Pred. No. 17;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB;
Pred. No. 17;
2; Mismatches
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A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.3%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                Query Match 60.3%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conservative
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234 RIAARRIALR 243
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| ||:|:|
234 RLAARRLAMR 243
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A;Molecule type: DNA
A;Residues: 1-388 <PFE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RLAIRRIALR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RLAIRRIALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: strF
A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            strF protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
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O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
Do, R.se. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-276 «KAN»
A; Residues: 1-276 «KAN»
A; Resizes references: EMBL:D90901; GB:AB001339; NID:g1651897; PID:d1017629; PID:g1651970
A; Notes: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Keywords: transport protein
                                                                     ö
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                                                                                                                                                                                                                                                                                                    :Species: Macaca mulatta (rhesus macaque)
:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
:Accession: S29990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Aug-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:221819; NID:938568; PIDN:CAA79885.1; PID:938569
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Reywords: transmembrane protein
F;219-284/Domain: Immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABC-type transport protein slr0977 - Synechocystis sp. (strain PCC 6803)
N:Alternate names: protein slr0977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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A;Status: nucleic acid sequence not shown; translation not shown
                            Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 276;
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                        ore 36; DB 2;
ed. No. 12;
Mismatches 2
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17;
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14;
                                                                                                                                                                                                                                                                                                                                                            R;Bontrop, R.R.
submitted to the EMBL Data Library, February 1993
A;Reference number: S29990
A;Accession: S29990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35; DB 2
Pred. No. 17;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36;
Pred. No.
                            Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: S74322; MUID: 97061201
                                                                                                                                                                                                                                                                            histocompatibility antigen, HLA-F-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.18;
54.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.3%;
66.7%;
                        Query Match 62.1%;
Best Local Similarity 41.7%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 62.1
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 60.3
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                ||: ||::::|
259 YRVVARRLSIKY 270
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31 YTLAWRDIAVRY 42
                                                                                                                   1 YRLAIRRIALRY 12
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98 RVALRKLLLRY 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-348 <BON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: S74745
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Conserved hypothetical protein AF1684 - Archaeoglobus fulgidus
CiSpecies: Archaeoglobus filgidus
CiSpecies: Archaeoglobus
CiSpecies: Archaeoglobus
CiSpecies: Content R.B.; Guadkenbush, J.E.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
FRICAR R.D.; Guadkenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weldman, J.F.; McDonald, L.
Arthors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woose, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A; Reference number: A69250; MUID:98049343
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-459 <a href="https://dx.bc/">Akids</a>
A; Cross-references: GB:AE000987; GB:AE000782; NID:92689310; PIDN:AAB89565.1; PID:9264
C; Superfamily: hypothetical protein MJ0966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable fumarate reductase flavoprotein subunit APE0950 - Aeropyrum pernix (strain K C; Species: Aeropyrum pernix
C; Species: Aeropyrum pernix
C; Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C; Accession: F725691
R; Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tawawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res. 6 83-101, 1999
A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A; Reference number: A72450; MUID:99310339
A; Accession: F72691
A; Ascession: F72691
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-573 <RAM>
A; Residues: 1-573 <RAM>
A; Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAA79934.1; PID:d1043720; PID:g
A; Experimental source: strain K1
C; Genetics:
                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 53;
                                                                                                                                                                                                                                                                      Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.6%; Score 34; DB 2; Length 469; 58.3%; Pred. No. 44; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                        Indels
submitted to the EMBL Data Library, April 1994
A;Reference number: S44224
A;Accession: S44225
A;Moleoule type: DNA
A;Residues: 1-267 <MAY>
A;Cross: references: EMBL:X78972; NID:g475227; PID:g581604
A;Start codon: GTG
                                                                                                                                                                                                                                                                    Score 34; DB 2;
Pred. No. 26;
2; Mismatches
                                                                                                                                                                                                                                                                    58.6%;
70.0%;
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66.7%;
                                                                                                                                                                                                                                                                 Query Match 58.6
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 58.3
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            2 RLAIRRIALR 11
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                     hypothetical protein APE2034 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: D72507
C;Accession: D72507
C;Accession: D72507
B;Kawarabayasi, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Accession: D72507
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-178 <KAM>
A;Cross-references: DDBJ:AP000063; NID:95105654; PIDN:BAA81044.1; PID:d1044830; PID:9510
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C; Date: 13.Jan-1995 #sequence_revision 13.Jan-1995 #text_change 09-Sep-1997
C; Accession: S44224
A; Reference number: S44224
A; Stetus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                strf protein - Streptomyces bluensis (fragment)
C;Species: Streptomyces bluensis
C;Species: Streptomyces bluensis
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 10-Sep-1997
C;Accession: S44225
R;Mayer, G.; Piepersberg, W.
                                                                                                             Gaps
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                                                         Length 388
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A;Residues: 1-267 <MAY>
A;Cross-references: EMBb:X78973; NID:9475232; PID:9475234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
17;
                                                      Score 35; DB 2;
Pred. No. 23;
2; Mismatches
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Pred. No. 26;
2; Mismatches
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63.6%;
                                                      60.3%;
75.0%;
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Best Local Similarity 70.0%;
Matches 7; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Experimental source: strain K1
C, Genetics:
A, Gene: APE2034
                                                                                                          Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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                                                                               Best Local Similarity
Matches 6; Conserv
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154 YRLAVRRL 161
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                                                         Query Match
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C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 13-Aug-1999
C;Accession: H71504; 146047
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t
A;Reference number: A71570; MUID:99000809
                                                                                                                                                                                                                                                                                                       A. Molecule type: DNA
A. Residues: 1-141 <ARN>
A. Residues: 1-141 <ARN>
A. Residues: 1-141 <ARN>
A. Cross-references: GB. AE001323; GB. AE001273; NID: 93328931; PIDN: AAC68107.1; PID: 9332
A. Experimental source: serotype D. strain UW-3/CX
B. Gu, L.; Wenman, W.M.; Remacha, M.; Meuser, R.; Coffin, J.; Kaul, R.
J. Bacteriol. 177, 2594-2601, 1995
A. Title: Chlamydia trachomatis RNA polymerase alpha subunit: sequence and structural
A. Reference number: 140743; MUID: 95247702
A. Accession: 140747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 20-115, 'R',117-141 <GUL>
A;Cross-references: GB:L33834; NID:9620026; PIDN:AAA74990.1; PID:9620030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 2; Length 141;
Pred. No. 22;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 54.5
Shee 6; Conservative
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Job time: 22208 sec
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64 RLAVGRLMVRY 74
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                                                                                                                                                                                                                                                                                                                                                                                            R;Plamann, M.; Minke, P.F.; Tinsley, J.H.; Bruno, K.S.
J. Cell Biol. 127, 139-149, 1994
A;Title: Cytoplasmic dynein and actin-related protein Arpl are required for normal nucle
A;Reference number: A54802; MUID:95014704
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                                                                                                                                                                                                                                                            dynein heavy chain, cytosolic - Neurospora crassa
N:Contains: dynein ATPase (EC 3.6.1.33)
C:Species: Neurospora crassa
C:Date: 10-Sep.1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein YDR360w - yeast (Saccharomyces cerevisiae) .
C;Species: Saccharomyces cerevisiae
C;Date: 23-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 26-Aug-1999
C;Accession: S69745
Gaps
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A; Description: The sequence of S. cerevisiae cosmid 9476.
A; Reference number: S61146
A; Reference number: S61146
A; Accession: S69745
A; Molecule type: DNA
A; Residues: 1-128 < DUZ>
A; Cross references: EMBL:U28372; NID:g849170; PID:g2194159; MIPS:YDR360w
C; Genetics:
A; Map position: 4R
C; Superfamily: Saccharomyces hypothetical protein YDR360w
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Pred. No. 20;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
   Indels
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A; Molecule type: DNA
A; Residues: 1-4367 < PLA>
A; Cross-references: GB:L31504; NID:g473489; PID:g473490
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superfamily: dynein heavy chain, cytosolic

(Reywords: ATP; heterotetramer; hydrolase; microtubule

(1943-1950/Region: nucleotide-binding motif A (P-loop)

(1943-224)-224/Region: nucleotide-binding motif A (P-loop)

(1955-2612/Region: nucleotide-binding motif A (P-loop)

(1957-2954/Region: nucleotide-binding motif A (P-loop)
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Pred. No. 3.8e+02;
2; Mismatches 1;
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   Mismatches
5;
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Best Local Similarity 54.5%;
Matches 6; Conservative
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Best Local Similarity 66.7%;
Matches 6; Conservative
   Conservative
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C;Superfamily: dynein heav
C;Keywords: ATP; heterotet
F;1943-1950/Feejton: nucleo
F;2240-2247/Region: nucleo
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2859 AVRRIAMEY 2867
                                                                                                                320 AVREIAIRY 328
                                                         4 AIRRIALRY 12
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   Matches
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1 YRLAIRRIALR 11

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Gaps

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protein L17

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February 8, 2000, 01:26:02; Search time 68.63 Seconds (without alignments) 5.222 Million cell updates/sec

US-08-653-294-36 58 1 YRLAIRRIALRY 12 Title: Perfect score: Seguence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

82229 seqs, 29864866 residues Searched:

82228 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

SwissProt_38:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P33617 macaca m	P09397 streptomyce		260	-		-	P76585 escherichia							-	_	P05147 emericella			_		COX	bos tal	gallus	rattus			P34794 brassica na			vario	P49917 homo sapien	32843 sacch	o.
SUMMARIES	ID	- ₹	STRF_STRGR	DYHC_NEUCR	RL17_CHLTR	TSMT_MOUSE	BGL2_BACSU	PRC_ECOLI	YPHG_ECOLI	NH10_YEAST	HRMA_PSESY	SECY_BACSU	ACH6_CAEEL	PRXC_CURIN	YE7A_SCHPO	MDR3_CRIGR	RPOH_METJA	3DHQ_EMENI	YCD4_YEAST	DAPB_MYCTU	BIOB_MYCTU	DEGS_ECOLI	DNAJ_COXBU	ACH3_BOVIN	ACH3_CHICK	ACH3_RAT	ACH3_HUMAN	Y664_HAEIN	RUB2_BRANA	CRTI_CERNC		PRTP_VZVD		RN12_YEAST	PYR1_SQUAC
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σ¥	Query Match	α.	ö	ω.	56.9	ė.	ė.	ė.	٠.	υ.	Ŋ.	'n.	'n.	'n.	ď.	ď.	53.4	53.4	53.4	e,	53.4	e.	e,	ω.	53.4	m.	ς.	m	m	m	m	m	m	m	m
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	Result No.	٦	7	m	4	ហ	φ	7	æ	Ø	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58	30	31	32	33	34

Q03132 saccharopol P45444 emericella 034162 alcaligenes P07618 vaccinia vi P21083 vaccinia vi P33055 variola vi P13895 budgerigar Q92cv4 rickettsia P33392 desulfovibr P47248 mycoplasma Q47748 enterococcu
ERY2_SACER DYHC_EMENI HEMN_ALCEU VJO5_VACCY VJO5_VACCY VJO5_VARCY PLS_MEDV PTH_RICPR HMC5_DESVH DNJL_MYCGE
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3567 4344 491 134 133 145 126 310 323
53.4 52.6 51.7 51.7 51.7 51.7 51.7
30 31 30 30 30 30 30 30 30 30
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ALIGNMENTS

Length 348; DB 1; Score 36;

Query Match

62.18;

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         "Cytoplasmic dynein and actin-related protein Arpl are required for normal nuclear distribution in filamentous fungi.";

"Cytoplasmic dynein and actin-related protein Arpl are required for normal nuclear distribution in filamentous fungi.";

"Cell Biol. 127:139-149(1994).

-!- FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN ACTS AS MOTOR FOR THE INTRACELLULAR RETROGRADE MOTILITY OF VESICLES AND ORGANEILES ALONG MICROTUBLIES. REQUIRED TO MAINTAIN UNIFORM NUCLEAR DISTRIBUTION IN HYPHAE.

-!- SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF INTERMEDIATE AND LIGHT CHAINS.

-!- SUBCELLULAR LOCATION: CYTOPLASMIC.

-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                      EMBL; L31504; AAA64908.1; .. Motor protein; ATP-binding; Motor protein; Microtubules; Dynein; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01167; RIBOSOMAL_L17; 1. PFAM; PF01196; Ribosomal_L17; 1.
                                                                                                                                                                                                                                                                                                                                                                                   ATP
ATP
ATP
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01-FEB-1996 (Rel. 33, Last sequ
15-DEC-1998 (Rel. 37, Last anno
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66.7%;
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STRAIN-434/BU / SEROVAR L2;
MEDLINE; 95247702.
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Best Local Similarity 66.7
Matches 6; Conservative
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2859 AVRRIAMEY 2867
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ID RL17_CHLTR
AC P47760;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                      STRAIN=N2-3-11;
MEDILINE; 91375432.
MANSOURI K., PIEPERSBERG W.;
"Genetics of streptomycin production in Streptomyces griseus:
"Genetics of streptomycin production in Streptomyces griseus:
nucleotide sequence of five genes, strFGHIK, including a phosphatase
                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PATHWAY: STREPTOMYCIN BIOSYNTHESIS.
-!- SIMILARITY: LOW, TO THE AMINO-TERMINAL DOMAIN OF GLUCOSE-6-
               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Gen. Genet. 228:459-469(1991).
-!- FUNCTION: MAY BE INVOLVED IN THE FORMATION OF N-METHYL-L-GLUCOSAMINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 281;
6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Euascomycetes; Pyrenomycetes;
Sordariales; Sordariaceae; Neurospora,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            281 AA; 31726 MW; 75CEB24C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).
                                                                                                                                                                                   01-MAR-1989 (Rel. 10, Created)
01-AGC-1992 (Rel. 23, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
STREPTOMYCIN BIOSYNTHESIS PROTEIN STRF.
Pred. No. 5.2;
                                                                                                                                                      281 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35;
Pred. No. 6
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70.0%;
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 54.5%;
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Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 60.3
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHATE ISOMERASE.
                                                                                                                                                                                                                                                               Streptomyces griseus.
                                                                 |:|:|:|
RVALRKLLLRY 108
                                              2 RLAIRRIALRY 12
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234 RLAARRLAMR 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=74-OR23-1A;
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01-NOV-1995 (
01-NOV-1997 (
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ID STRE_STRGR
AC P09397;
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P45443;
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Length 4367;

(POTENTIAL). B81B5E92 CRC32;

(POTENTIAL) (POTENTIAL)

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                                                                             Gaps
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J. Bacteriol. 177:2584-2601(1995).
-!- SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOWAL PROTEINS.
                                                                             ö
Score 34; DB 1; Length 436
Pred. No. 2.1e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UL-FEB-1996 (Rel. 33, Last Sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
50S RIBOSOMAL PROTEIN L17.
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360 RIGLRRITSRY 370
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                                           SEQUENCE FROM N.A.
                                                                                                                               SEQUENCE FROM N.A.
 Sacillus subtilis.
                                                      STRAIN=168;
MEDLINE; 95219080.
                                                                                                                                                        MEDLINE; 97124189
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ID PRC_ECOLI
AC P23865;
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ACT_SITE
SEQUENCE
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                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                        Thesis (1992), University of Louisville, U.S.A.
-!-CATALTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DIMETHYL SULFIDE
S-ADENOSYL-L-HOMOCYSTEINE + TRIMETHYLSULFONIUM.
-!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS EC 2.1.1.1,
EC 2.1.1.28 AND EC 2.1.1.96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PROBABLE BETA-GLUCOSIDASE (RC 3.2.1.21) (GENTIOBIASE) (CELLOBIASE)
(RETA-D-GLUCOSIDE GLUCOHYDROLASE) (AMYGDALASE).
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                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                        Score 33; DB 1; Length 122;
Pred. No. 6.5;
; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
WARRER D.R., HOFFMAN J.L.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-ROV-1997 (Rel. 35, Last annotation update)
THIOETHER S-METHYLIRANSFERASE (EC 2.1.1.96) (TEMT)
Ribosomal protein.
SEQUENCE 122 AA; 13969 MW; B8C43F7D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 1;
Pred. No. 15;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31B87F7A CRC32;
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                                                                                                                                                                  264 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01100; NNWT PNWT_TEMT; 1.
PFAM; PF01234; NNWT_PNWT_TEMT; 1.
Transferase; Methyltransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29460 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M88694; AAA62365.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.9%;
                                        Query Match 56.9%;
Best Local Similarity 54.5%;
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:102963; TEMT
                                                                                      2 RLAIRRIALRY 12
                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase; Methy SEQUENCE 264 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 YRAALRRLA 185
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                                                                                                                                   TSMT_MOUSE
ID TSMT_MOUSE
AC P40936;
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ID BGLZ_BACSU
AC P42403;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 88298684.

WEDLINE; 88298684.

VOSMAN B., KUIKEN G., KODISTRA J., VENEMA G.;

VOSMAN B., KUIKEN G., MOLISTRA J., VENEMA G.;

17-kilodalton DNA-entry nuclease and the competence-specific 18-kilodalton protein.";

2. Bacteriol. 170:3703-3710(1988).

3. Bacteriol. 170:3703-3710(1988).

1- CATALYTIC ACTIVITY: HUPROLYSIS OF TERMINAL, NON-REDUCING BETA-D-GLUCOSE RESIDUES WITH RELEASE OF BETA-D-GLUCOSE.

1- SIMILARITY: BELONGS TO FAMILY 1 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 1.
PFAM; PF00232; Glyco_hydro_1; 1.
Hypothetical protein; Hydrolase; Glycosidase; Cellulose degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1991 (Rel. 20, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
TAIL-SPECIFIC PROTEASE PRECURSOR (EC 3.4.21.-) (PROTEASE RE) (PRC . PROTEIN).
                                                                                                                                                                                                           FUJISHIMA Y., YAMANE K.;
"A 10 kb nuclectide sequence at the 5' flanking region (32 degrees)
of srfAA of the Bacillus subtilis chromosome.";
Microbiology 14:127-279(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YAMANE K., KUMANO M., KURITA K.;
"The 25 degrees-36 degrees region of the Bacillus subtilis
chromosome: determination of the sequence of a 146 kb segment and
identification of 113 genes.";
Microbiology 142:3047-3056(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTON DONOR (POTENTIAL).
NUCLEOPHILE (BY SIMILARITY).
E92CD679 CRC32;
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 682 AA.
                                  Bacillus/Staphylococcus group; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D30762; BAA06429.1; -.
EMBL; D50453; BAA08975.1; -.
EMBL; M21672; -; NOT_ANNOTATED_CDS.
EMBL; 299105; CAR12135.1; -.
HSSP; P11546; IPBG.
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Best Local Similarity 54.5
Matches 6; Conservative
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SEQUENCE FROM N.A.
STRAIN-K12 / W3110;
MEDLINE; 91310589
HARA H., YAMAMOTO Y., HIGASHITANI A., SUZUKI H., NISHIMURA Y.;
"Cloning, mapping, and characterization of the Escherichia coli progene, which is involved in C-terminal processing of penicillin-binding protein 3.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 96161995.
KEILER K.C., SAUER R.T.;
"Sequence determinants of C-terminal substrate recognition by the Tsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protease.";
J. BALJ. Chem. 271:2589-2593(1996).
-i- FUNCTION: INVOLVED IN THE CLEAVAGE OF A C-TERMINAL PEPTIDE OF 11
-i- FUNCTION: INVOLVED THE PRECURSOR FORM OF PENICILLIN-BINDING PROTEIN 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 330-403 FROM N.A. MEDLINE; 93077473. SEOANE A., SABBAJ A., MCMURRY L.M., LEVY S.B.; SEOANE A., SABBAJ A., MCMURRY L.M., LEVY S.B.; Multiple antiblotic susceptibility associated with inactivation of the pro gene.; J. Bacteriol. 174:7844-7847(1992).
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STARAIN-KIZ / MG165;
MEDILINE: 9742617
BLATTNER: 9742617
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RILEY M., COLLADO-YIDES J., GLASNER F.D., RODE C.K., MXHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
MAU B., SHAO Y.;
                                                                                                                                                                                            MEDLINE; 92108041.
SILBER K.R., KRILER K.C., SAUER R.T.;
SILBER A.R., KRILER K.C., SAUER R.T.;
Typ: a tail-specific protease that selectively degrades proteins with nonpolar C termin!";
Proc. Natl. Acad. Sci. U.S.A. 89:295-299(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE; 99175453.
KUNTE H.J., CRANE R.A., CULHAM D.E., RICHMOND D., WOOD J.M.;
"Protein ProQ influences osmotic activation of compatible solute
transporter ProP in Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE: 97251358.

MEDLINE: 97251358.

ITOH T., AIBA H., BABA T., FUJITA K., HAYASHI K., INADA T.,
ISONO K., KASAI H., KIMURA S., KITAKAWA M., KITAGAWA M.,
MAKINO K., MIKITT., MIZOBUCHI K., MORI H., MORI T., MOTOMURA K.,
NAKADE S., NAKAWURA Y., NASHIMOYD H., NISHIO Y., OSHIMA T.,
SAITO N., SAMPEI G., SEKI Y., SIVASUNDARAM S., TAGAMI H.,
TAKEDA J., TAKEMOTO K., WADA C., YAWAMOTO Y., HORIUCHI T.;
TA 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
DNA RES. 3:379-392(1996).
            Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 96081954.
KELLER K.C., SAUER R.T.;
Tidentification of active site residues of the Tsp protease.";
"1. Biol. Chem. 270:28864-28868(1995).
                                                                                                                                                                                                                                                                                                                                                                     sequence of Escherichia coli K-12.";
                                                                                                                                                        Bacteriol. 173:4799-4813(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriol. 181:1537-1543(1999).
                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequenc
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-33 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBSTRATE SPECIFICITY.
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                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                  SEQUENCE FROM N.A.
                                   Escherichia.
OR TSP
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(PBP3). PROTEASE THAT SELECTIVELY DEGRADES PROTEINS WITH NONPOLAR CHERMALNAL. MAY BE INVOLVED IN PROTECTION OF THE BACTERIUM FROM THERMAL AND OSMOTIC STRESSES.
SUBCELLULAR LOCATION: ASSOCIATED WITH THE PERIPLASMIC SIDE OF THE CYTOPLASMIC MEMBRANE.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S41 (SERINE PROTEASE).
SIMILARITY: CONTAINS 1 PDZ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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SEQUENCE FROM N.A.
MEDLINE; 9742617
BLATTNER; 9742617
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAXHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 127.3 KD PROTEIN IN CSIE-GLYA INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 1; Length 682;
Pred. No. 44;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
TAIL-SPECIFIC PROTEASE.
PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine protease; Signal.
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3CF7B39A CRC32;
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M75634; AAA24699.1; -
AE000277; AAC74900.1; -
D90826; CAB21562.1; -
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76663 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D00674; BAA00577.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 56.9
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A42475; A42475.
ECOGENE; EG10760; PRC.
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682 AA;
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P76585;
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ACT_SITE
CONFLICT
SEQUENCE
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YPHG_ECOLI
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Nucleic Acids Res. 18:1647-1647(1990).
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Best Local Similarity
Matches 7; Conserv
                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                            STRAIN=PSS61;
MEDLINE; 94100578.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YRLAIRRIALRY
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   HEMA PROTEIN.
                                                 Pseudomonas.
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ID SECY_BACSU
AC P16336;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                               NHP10 PROTEIN.
NHP10 OR HMO2 OR YDL002C OR YD8119.05C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
MURPHY L., RICHARDS C., GENTLES S., HARRIS D., BARRELL B.G.
RAJANDREAM M.A.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-: SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-: SIMILARITY: CONTAINS 1 HMG BOX.
                                                                                                                Length 1124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 55.2%; Score 32; DB 1; Length 203; Similarity 45.5%; Pred. No. 18; 5; Conservative 4; Mismatches 2; Indels
                                                                                0A06B4C6 CRC32;
                                                                                                                Score 33; DB 1;
Pred. No. 76;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80A216B6 CRC32;
                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                            203 AA.
                                        EMBL: AE000341; AAC75602.1; -. ECOGENE: EG13468: yphG. Hypothetical protein. SEQUENCE 1124 AA; 127284 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HMG
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SGD: L0002765; NHPLO.
PFAM: PF00505; HMG_box: 1.
Nuclear protein; DNA_binding.
                                                                                                                 56.9%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z48008; CAA88059.1; -.
                                                                                                    Ouery Match
Best Local Similarity 87.5.
7; Conservative
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ID HRWA_PSESY STANDARD
AC Q08370,
DT 01.NOV-1995 (Rel. 32, C,
DT 01.NOV-1995 (Rel. 32, L,
DT 01.NOV-1995 (Rel. 32, L,
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                                                                                                                                                                                   412 YRLAIREI 419
                                                                                                                                                              1 YRLAIRRI 8
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Q03435;
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SEQUENCE
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NH10_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide sequence and properties of the hrmA locus associated with
the Pseudomonas syringae pv. syringae 61 hrp gene cluster.";
Mol. Plant Microbe Interact. 6:553-564(1993).
-I- FUNCTION: UNKNOWN. MAY SERVE A REGULATORY FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=168;
MEDLINE; 90251170.
SUH J.-W., BOYLAN S.A., THOMAS S.M., DOLAN K.M., OLIVER D.B.,
SUH J.-W., BOYLAN S.A., THOMAS S.M., DOLAN K.M., OLIVER D.B.,
SIGN J.-W., BOYLAN S.A., THOMAS S.M., DOLAN K.M., OLIVER D.B.,
"ISOLATION of a secy homologue from Bacillus subtilis: evidence for a common protein export pathway in eubacteria.";
Mol. Microbiol. 4:305-314(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                            STRAIN-PSS61;
HUANG H.C., HUTCHESON S.W., COLLMER A.;
HUARacterization of the hrp cluster from Pseudomonas syringae pv.
syringae 61 and InphoA tagging of exported or membrane-spanning Hrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YOSHIKAWA H., DOI R.H.;
"Sequence of the Bacillus subtilis spectinomycin resistance gene
Pseudomonas syringae (pv. syringae).
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
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Pred. No. 36;
1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypersensitive response.
SEQUENCE 375 AA; 41458 MW; 733EEB06 CRC32;
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01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PREPROTEIN TRANSLOCASE SECY SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                            401. Plant Microbe Interact. 4:469-476(1991).
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174 YRLSITRKTLSY 185
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STANDARD;

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ACH6_CAEEL
093149;
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                                                                                                                                                      -i- FUNCTION: INVOLVED IN PROTEIN EXPORT. INTERACTS WITH SECA AND SECE TO ALLOW THE TRANSLOCATION OF PROTEINS ACROSS THE PLASMA MEMBRANE, BY FORMIGE PART OF A CHANNEL.

-i- SUBUNIT: ONE OF SEVEN SECRETORY PROTEINS (SECA-F & SECY) THAT COMPRISE THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS.

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-i- SIMILARITY: BELONGS TO THE SECY/SEC61-ALPHA FAMILY.
                               NAKAMURA K., NAKAMURA A., TAKAMATSU H., YOSHIKAWA H., YAMANE K.; "Cloning and characterization of a Bacillus subtills gene homologous to E. coli secY."; Election of a Bacillus subtills gene homologous J. Biochem. 107:603-607(1990).
                                                                                     SEQUENCE FROM N.A. MEDLINE; 96186897. SUH J.W., BOYLAN S.A., OH S.H., PRICE C.W.; "Genetic and transcriptional organization of the Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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1C8A4316 CRC32;
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EMBL; M31102; AAB59118.1; -.
EMBL; D00619; BAA00495.1; ALT_INIT.
EMBL; L47971; AAB06819.1; -.
EMBL; 299104; CAB11912.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Translocation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47243 MW;
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PROSITE; PS00756; SECY_2; 1.
PFAM; PF00344; SECY; 1.
                                                                                                                                  spc-alpha region.";
Gene 169:17-23(1996)
                                                                                                                                                                                                                                                                                                                                                                                             PIR; S08629; BWBSSY
PIR; S12683; S12683
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431 AA;
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        SEQUENCE FROM N.A. MEDLINE; 90292990.
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACETYLCHOLINE RECEPTOR, BETA-TYPE SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRXC_CURIN STANDARD; PRT; 609 AA.
P49053;
01-FEB-1996 (Rel. 33, Casted)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
VANADIUM CHLOROPEROXIDASE (EC 1.11.1.10) (VCPO) (VANADIUM CHLORIDE CPO.
                                                                                        Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Y08637; CAA69927.1; -.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
PFAM; PF00065; neur_chan; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last senotation update)
ACETYLCHOLINE RECEPTOR, BETA-TYPE SUBUNIT ACR-3 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL. CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY.
102629B3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.2%; Score 32; 58.3%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56245 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 58.3.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 YQIKIRRKALFY 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440
46
151
487 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
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DISULFID
SEQUENCE
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TRANSMEM
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PRXC_CURIN
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Gaps

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Indels

Pred. No. 42; ; Mismatches

Query Match 55.2%; Score 32; Best Local Similarity 55.6%; Pred. No. 4 Matches 5; Conservative 4; Mismatch

|:|:||:| 237 AVRKIAIQY 245

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4 AIRRIALRY 12

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DB 1; Length 431;

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RESULT 15
MDR3_CRIGR
ID MDR3_CRIGR
AC P23174;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                          MEDELNE; 96133943.

MESSERSCHMIDT A., WEVER R.;

MACKER SCHMIDT A., WEVER R.;

MACKER SCHMIDT A., WEVER R.;

from the fungus Curvularia inaequalis.";

Proc. Natl. Acad. Sci. U. S.A. 93:392-396(1996).

-!- CATALYTIC ACTIVITY: 2 RH + 2 CHLORIDE + H(2)O(2) = 2 RCL + 2
          Eukaryota; Fungi; Ascomycota; Euascomycetes; Loculoascomycetes;
Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Curvularia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=972;
SKELTON J., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WOOD V.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO YEAST YGL144C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.2%; Score 32; DB 1; Length 609; 50.0%; Pred. No. 61; tive 2; Mismatches 4; Indels
                                                                    MUIJSERS A.O., MESSERSCHMIDT A., WEVER R.;
Muijsers A.O., MESSERSCHMIDT A., WEVER R.;
Primary structure and characterization of the vanadium chloroperoxidase from the fungus Curvularia inaequalis.";
Eur. J. Blochem. 229:566-574(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 454 454 P -> S (IN AA SEQUENCE).
609 AA; 67530 MW; 19112E80 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase; Peroxidase; Vanadium; 3D-structure.
ACT SITE 404 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 80.1 KD PROTEIN C4A8.10 IN CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             723 AA
                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE; 95262722.
                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
                                                                                                                                                                                                                                                                -:- SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X85369; CAA59686.1; -. PDB; 1VNC; 08-NOV-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                   -1- COFACTOR: VANADIUM
 Curvularia inaequalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304 YNQIVRRIAVTY 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
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YE7A_SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISCELLANBOUS: PGP ISOFORMS DIFFER IN THEIR DRUG TRANSPORT CAPABILITIES: PGP1 AND PGP2 CAN MEDIATE MDR, WHILE PGP3 APPARENTLY
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE: 92135896.

ENDICOTT J.A., SARANGI F., LING V.;

ENDICOTT J.A., SARANGI F., LING V.;

ENDICOTT J.A., SARANGI F., LING V.;

Gene family.";

DNA Seq. 2:89-101(1991).

-!- FUNCTION: ENERGY-DEPENDENT EFFLUX PUMP RESPONSIBLE FOR DECREASED DRUG ACCUMULATION IN MULTIDRUG-RESISTANT CELLS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS). MDR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Transmembrane; Transport; Duplication;
                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                 55.2%; Score 32; DB 1; Length 723; 54.5%; Pred. No. 74; ive 4; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1991 (Rel. 20, Created)
U-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
MULTIDRUG RESISTANCE PROTEIN 3 (P-GLYCOPROTEIN 3).
                                                                                                                                                     EMBL; 298762; CAB11480.1; -.
Hypothetical protein.
SEQUENCE 723 AA; 80090 MW; 159D795B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1281 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
CYTOPLASMIC
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POTENTIAL.
POTENTIAL.
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POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cricetulus griseus (Chinese hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M60042; AAA68885.1; -.
                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 54.5-
اتامم 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :||| |::|:|
647 HRLAWRKVAVR 657
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YRLAIRRIALR 11
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955 875 POTENTIAL.

938 958 POTENTIAL.

975 995 POTENTIAL.

996 1281 CYTOPLASMIC (POTENTIAL).

429 436 ATP (POTENTIAL).

1071 1078 ATP (POTENTIAL).

1281 AA; 140866 MW; 9FE9DF5C CRC32;
 TRANSMEM
TRANSMEM
DOMAIN
NP_BIND
NP_BIND
SEQUENCE
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o ; 0; Gaps Query Match
Best Local Similarity 70.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels

Oy 2 RLAIRRIALR 11 | | | | | | | | | Db 1184 RLAIRRALIR 1193

Search completed: February 8, 2000, 01:26:02 Job time: 1562 sec

Q924b6 escherichia P91068 caenorhabdi 045795 caenorhabdi Q9xil2 arabidopsis Q59958 streptococc Q49843 mycobacteri

067313 Q924B6 P91068 O45795 Q9XIL2

Q59958 Q49843

09yvn7 melanoplus 09yvn7 melanoplus 018455 homo sapien 09x174 squash yell 09x789 chlamydla pn 021162 caenorhabdl 060503 cricetulus 016763 caenorhabdl 09wzx9 thermotoga 029x28 arenoplus 023552 trypanosoma 023555 arabidopsis

099VN7 098VN7 098HV4 098Z38 022Z59 021Z62 060503 016763 098ZX9 099ZX9 026952 026952 049569

P95486 pseudomonas 007074 porphyromon 097211 leishmania 082630 arabidopsis 060313 homo sapien

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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WILD A.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Z18061; CAB02939.1; JoineD.
EMBL; Z78413; CAB01667.1; JoineD.
EMBL; Z181061; CAB01667.1; JoineD.
HSSP; P19491; IGR2.
PFAM; PF00060; I19_chan; 1.
SEQUENCE 795 AA; 89703 MW; DD722166 CRC32;
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O86347.
01-NOV-1998 (Trembirel. 08, Created)
01-NOV-1998 (Trembirel. 08, Last sequence update)
01-NOV-1999 (Trembirel. 12, Last annotation update)
HYPOTHETICAL 33.5 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.7%; Score 41; DB 5; 58.3%; Pred. No. 7.6; ive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q22063 PRELIMINARY;
Q22063; Q93489;
01-NOY-1996 (TrEMBLEL 01, C,
01-MAY-1999 (TREMBLEL 10, L,
01-NOY-1999 (TREMBLEL 12, L,
TOLC3.10 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 70.7
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
1 YRLAIRRIALRY 12
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YRTSLRRLATRY 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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086347
1D 08
AC 08
DT 01
DT 01
DE HY
GN RV
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Q22063
SO DRA READ OCT THE DRA ID DRA
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086347 mycobacteri
08583 sphingomona
09xb05 myxococcus
02694 trypanosoma
P7218 clostridium
02695 streptomyce
09x876 streptomyce
09x876 streptomyce
016382 caenorhabdi
09yaa5 aeropyrum p
053815 streptomyce
054257 streptomyce
054257 streptomyce
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O28589 archaeoglob
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O9xeg1 gossypium }
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                                                                                               8, 2000, 19:16:17; Search time 176.54 Seconds (without alignments) 4.713 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                               225878
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                225878 seqs, 69334122 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                          summaries

    protein search, using sw model

                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q54259
Q9X876
Q9YAA5
Q53815
Q53815
Q54257
Q45803
Q9XDG3
Q9YDG3
Q9YDG3
Q9YDG3
Q9XCG1
P87286
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Q9XB05
Q9Y213
Q26954
P72880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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O86347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_human:*
sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_organelle:*
sp_phage:*
                                                                                                                                                           US-08-653-294-36
58
1 YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_archea:*
sp_bacteria:*
sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Listing first 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
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                                                                                                    February
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Match I
                                                                                                                                                                           Perfect score:
Sequence:
                                                                                                                                                                                                                        Scoring table:
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Maximum DB :
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No.
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Created)
Last sequence update)
Last annotation update)

795 AA

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Gaps

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Indels

2;

Length 795

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01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last Sequence update)
01-MAY-1997 (TrEMBLrel. 03, Last annotation update)
cDU2, CDU1, TCDD, TCDE, TCDE, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium difficile.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genetic and functional analysis of genes required for the modification of the polyketide antibiotic TA of Myxococcus submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AJ132503; CAB46503.1; - 4CC64E85 CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 313;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 2;
Pred. No. 18;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 2;
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4F20347A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 AA.
                                                                                                                                     325 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  441 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ER-15;
PAITAN Y., ORR E., RON E.Z., ROSENBERG E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                          Created)
                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-VPI10463;
VON EICHEL-STREIBER C.;
Submitted (JAN-1997) to the EMBL, EMBL, X92982; CAA63559.1;
EMBL, X92982; CAA63559.1;
EMBL, X92982; CAA63558.1;
SEQUENCE 313 AA; 33380 MW; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.18;
41.78;
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58.3%;
                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, MEMBRANE ASSOCIATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12,
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Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 0
(TrEMBLrel. 0
(TrEMBLrel. 1
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                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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259 YRVVARRLSIKY 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                    Myxococcus xanthus.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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026954;
01-NOV-1996 (
01-NOV-1996 (
01-NOV-1999 (
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                                                                                                                                  Q9XB05
Q9XB05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P97213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT Q26954
ID Q26
AC Q26
DT 01-
DT 01-
                                                                 RESULT
09XB05
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P97213
                                                                                                                                                                          SON REPARED OF SON RE
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                                                                                                                                                                                        MEDLINE; 98295987.

COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D., GORDON S.V., EIGLAMEIER K., GAS S., BARRX III C.E., TERAIA F., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., DAVIES R., DEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLROYD S., HORNESY T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPHY L., OLIVER S., SEEGER K., SKELTON S., SQUARES S., SQUARES S., SQUARES S., SUBSTON J.E., TAYLOR K., WHITEHEAD S., BARRELL B.G.;

"DECIPIATION LABORATION S., SQUARES S., SQARES R., SULSTON J.E., TAYLOR K., WHITEHEAD S., BARRELL B.G.;

NORTHER S., SEEGER K., SKELTON S., SQUARES S., SQARES R., SULSTON J.E., MOULE S., SALS S., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Mycobacterium tuberculosis.
Bacteriä; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROMINE M.F., STILLWELL L.C., WONG K.-K., THURSTON S.J., SISK E.C., SENSEN C.W., GARSTERLAND T., SAFFER J.D., FREDRICKSON J.K.; "Complete sequence of a 184 kb catabolic plasmid from Sphingomonas surmaticivorans strain F199"; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF079317; AAD03868.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 63.8%; Score 37; DB 2; Length 243; Best Local Similarity 63.6%; Pred. No. 13; Matches 7; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the EMBL/GenBank/DDBJ databases.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL 26.5 KD PROTEIN.
Sphingomonas aromaticivorans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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PFAM; PF00175; oxidocad_fad; 1.
PFAM; PF00175; oxidocad_fad; 1.
SEQUENCE 309 AA; 33517 MW; B152B590 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Plasmid.
SEQUENCE 243 AA; 26455 MW; 40CDFBF4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB;
Pred. No. 4.5;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARKHILL J.;
Submitted (JUN-1998) to the
EMBL; ALO08967; CAA15591.1;
HSSP; P33164; 2PIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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65 YRIAIRRIA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YRLAIRRIA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-H37RV;
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MURPHY L., HARRIS D.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BEYER S., DISTLER J., PIEPERSBERG W.;
"The str gene cluster for the biosynthesis of 5'-hydroxystreptomycin in Streptomyces glaucescens Gla.0 (ETH 22794): new operons and evidence for pathway-specific regulation by StrR.";
Mol. Gen. Genet. 250:775-784(1996).
EMBL: X78944; CAASS72.1:
EMBL: AJ006985; CAA07379.1: -
SEQUENCE 281 AA; 31427 MW; 30CD0C63 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEGUENCE FROM N.A.
STRAIN-ARCI 19032 (GLA.O);
RETZLAFF L., MAYER G., BEYER S., AHLERT J., VERSECK S., DISTLER J.,
PIEPERSBEGG W.
                                                                                                                                                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Streptomycin Production in Streptomycetes: a Progress Report."; (In) Baltz R.H., Hegeman G.D., Skatrud P.L. (eds.); Industrial microorganisms. Basic and applied molecular genetics, pp.183-194, ASM Press, Herndon (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.3%; Score 35; DB 2; Length 281; 70.0%; Pred. No. 38; 1; Indels 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-A3(2);
BENTLEY S.D., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
                                                                                                                                                                                                                                                                             STRAIN-GLA 0;
MAYER G., PIEPERSBERG W.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
GLA O GENES STRB1, STRF, STRG, STRH, STRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN (FRAGMENT).
SCEIS.01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-ATCC 13032 (GLA.0);
PIEPERSBERG W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ATCC 13032 (GLA.0);
MEDLINE; 96204519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                         Streptomyces glaucescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:| ||:|||
234 RIAARRLALR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 RLAIRRIALR 11
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09x876
09x876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
Q9X876
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A REPAREMENT OF THE PROPERTY O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-PCC6603;
MEDLINE; 97061201.
KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYAJIWA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
                                                                                   Sukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                    MEDLINE; 98226175.
TIBBETTS R.S., JENSEN J.L., OLSON C.L., WANG F., ENGMAN D.M.;
The DnaJ family of protein chaperones in Trypanosoma cruzi.";
MOL. Biochem. Parasitol. 91:319-326(1998).
EMBL; L46819; AAC18897.1; -..
HSSP; P08622; 1XBL.
PROSITE; PSO0635; DNAJ_1; 1.
SPROUTE; PSO06226; DNAJ_1; 1.
SPROUTE 441 AA; 48819 MW; E6AD2FAZ CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Length 441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Cyanobacteria; Chrococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
ABC TRANSPORTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35; DB 2;
Pred. No. 37;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4DBF5330 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 5
Pred. No. 38;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       276 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 3:109-136(1996).
EMBL; D90901; BAA16896.1; -.
PFAM; PF01061; ABC2_membrane; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31542 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.1%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 63.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 60.3
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1997 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 RLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | ||:||:|
23 RTAYRRLALKY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 AA;
                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                      rypanosoma cruzi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | || | ||:||
31 YTLAWRDIAVRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-PCC6803;
TABATA S.;
                                                                                                                                                                   STRAIN-PBOL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P72880
P72880;
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Q54259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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Gaps

Last sequence update)
Last annotation update)

Created)

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STRAIN-K1;
MEDLINE: 99310339.
MEDLINE: 99310339.
JIN-NO K., TARAHASHI M., SEKINE M., BABA S., ANKAI A., KOSUGI H.,
JIN-NO K., TARAHASHI M., SEKINE M., BABA S., ANKAI A., KOSUGI H.,
HOSOYAMA A., FUKUI S., NACAI Y., NISHIJIMA K., NAKAZAWA H.,
TAKAMIYA M., MASUDA S., FUNAHASHI T., TANAKA T., KUDOH Y.,
YAMAZAKI J., KUSHIDA N., OGUCHI A., AOKI K., KUBOTA K., NAKAMURA Y.,
NOMURA N., SAKO Y., KIKUCHI H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19484 MW; FEA2CD00 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea; Crenarchaeota; Aeropyrum
                                                                                                                                                                                                                                                                                                                                                                                                                            178AA LONG HYPOTHETICAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AP000063; BAA81044.1;
SEQUENCE 178 AA; 19484 MY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 58.6
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
                                                                                                                                                                                                                                           PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
: ||||| | |
594 FSFAIRRIVLNY 605
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Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 RLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:| ||||: |
34 RMACRRIAIVY 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 RLAIRRIALR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aeropyrum pernix
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SEQUENCE
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Q53815;
                                                                                                                                                                                                                                                                                Q9YAA5;
                                                                                                                                                                                                                                       Q9YAA5
                                                                                                                                                        RESULT 11
099XA5
10 091XA5
10 091XA5
DT 01-NOV
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Q53815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STAR REPORTED AND SOUR SET AND 
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C. STRAIN-BRISTOL. N2;
MEDILINE; 94150718.

A WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
A BONTIELD J., BURTON J., CONNELL M., COPERT J., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DUTBIN R., FAVELLO A., FULTON L.,
CRAXTON M., DEAR S., DU Z., DUTBIN R., FAVELLO A., FULTON L.,
A JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATRELILE P.,
A JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATRELLE P.,
A RALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
A SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
THERRY-MEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
T. 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                genetic and physical map for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                             REDENBACH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J., KINASHI H., HOPWOOD D.A.;
"A set of ordered cosmids and a detailed genetic and physical mithe 8 Mb Streptomyces coelicolor A3(2) chromosome.";
MOI. Microbiol. 21:77-96(1996).
EMBL: ALO49707; CAB41270.1; -.
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EMBL; AF016442; AAB65917.1; -. SEQUENCE 725 AA; 84926 MW; A4847D75 CRC32;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JONES K., WOHLDMANN P.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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99;
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Pred. No. 99;
1; Mismatches
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Pred. No.
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58.3%;
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70.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                   STRAIN=A3(2);
MEDLINE; 97000351.
                                                                              FROM N.A.
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SEQUENCE
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Length 178;

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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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                                         2; Indels
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MAYER G., PIEPERBERG W.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; X78972; CAA55568.1;
                                                                                                                                                                                                                                                                     UL-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1996 (TrEMBLrel. 01, Last annotation update) grsp 5564 GENES STRB AND STRF (FRAGMENT).
Score 34; DB 1;
Pred. No. 37;
2; Mismatches
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29777 MW;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
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234 RVAARRLALR 243
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Search completed: February
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SEQUENCE
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MEDLINE: 94150718.
MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
MILSON R., AINSCOUGH R., COPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAM J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCHURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., WALERSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATENSTON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                     Streptomyces galbus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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MAYER G., PIEPERSBERG W.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; X78973; CASS5570.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
LLOYD C., WILKINSON J.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                      01-NOV-1996 (TIEMBLIEL. 01, Created)
01-NOV-1996 (TIEMBLIEL. 01, Last sequence update)
01-NOV-1996 (TIEMBLIEL. 01, Last annotation update)
DSM 40480 GENES STRB1 AND STRF (FRAGMENT).
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Last annotation update)
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Pred. No. 56;
                                                                                                                                                                                                                                    82D9D7A4 CRC32
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Pred. No. 73;
              267 AA
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                                                                                                                                                                                                                                    267 AA; 29909 MW;
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70.0%;
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EMBL: 282051; CABO4815.1; -.
PFAM: PF01461; 7tm_4; 1.
SEQUENCE 350 AA: 40291 MW;
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Similarity 75.0%;
6; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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              PRELIMINARY;
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Caenorhabditis elegans.
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Best Local Similarity
Matches 6; Conserv
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SEQUENCE FROM N.A.
VYSOTSKAIA V.S., SCHWARTZ J.R., YU G., TORIUMI M., LENZ C., LIU S.,
LI J., KREMEDTSKAIA I., LUROS J., GONZALEZ A., ALTAFI H., ARAUJO R.,
BUUTHLER E., CHAO Q., CONN L., CONMAY A.B., DUNN P., HANSEN N.,
HUIZAR L., KIM C., PALM C., ROWLEY D., SHINN P., WALKER M.,
DAVIS R.W., ECKER J.R., FEDERSPIEL N.A., THEOLOGIS A.;
"Arabidopsis thallana chromosome 1 BAC T2K10 sequence.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Wataryota, Viifolplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermarophyta, Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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                                                                              Last sequence update)
Last annotation update)
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Pred. No. 81;
1; Mismatches 1
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384 AA
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                                                    Created)
  PRT;
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                                              01-MAY-1999 (TEEMBLEEL 10, 01-MAY-1999 (TEEMBLEEL 12, TZK10.3 PROTEIN.
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Best Local Similarity 77.8%;
Matches 7; Conservative
PRELIMINARY;
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AYRRMALRY 50
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AF152405 Drosophila melanog
X99512 D.melanogaster PFTAI
AF152399 Drosophila melanog
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US AC017966 8849 bp DNA
INITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
pleces
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LOCUS
LOCUS
DEFINITION Three Drosophila melanogaster genes for transfer RNAs (Glu SPECINITION TO 1146
ACCESSION V00238 J01146
VERSION V00238.1 GI:8458
KEYWORDS transfer RNA; transfer RNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fruit fly.

Drosophia melanogaster

Bukaryota: Metazoa: Arthropoda: Tracheata; Hexapoda: Insecta;

Pterygota; Diptera: Brachycera; Muscomorpha: Ephydroidea;

Drosophilides: Drosophila.

I (bases I to 1650)

Hosbach, H.A., Silberklang, M. and McCarthy, B.J.

Evolution of a D. melanogaster glutamate tRNA gene cluster

Gell 21 (1), 169-178 (1980)
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Gaps: 0
Percent Identity: 66.667

    1050
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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3526
3617
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190 c 213 g 323 t
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/note="tRNA Glu"
/db_xref="FlyBase:FBgn0011851"
464. .535
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/note="transfer RNA:glu4:62Aa'
/allele=""
/db_xref="FlyBase:FBgn0011851"
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262. .333
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294.12
312.93
322.50
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/note="tRNA Glu"
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/note="tRNA Glu"
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112.28
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AC017966.1 GI:6553224
HTG; HTG2_PHASE2.
fruit fly.
Drosophila melanogaster
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38.00
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Ratio: 3.833
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                                                                                                                                              seq_name: gb_in1:DMRNA3
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   gb_in2:AF152405
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AF152406 Drosophila melanogast
AF152401 Drosophila melanogast
AF152401 Drosophila melanogast
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AF152403 Drosophila melanogast
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-WODEL=frame+_p2n.model -DEV-x1p
-WODEL=frame+_p2n.model -DEV-x1p
-WODEL=frame+_p2n.model -DEV-x1p
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-MODEL=frame+_0.000 -GOPPCL=0.000 -GOAPOP-4.500
-GOAPEXT=0.050 -XGAPOP=10.000 -XGAPOFXT=0.500 -FGAPOP-6.000
-GOAPEXT=7.000 -YGAPOP=10.000 -YGAPOFXT=0.500 -FGAPOP-6.000
-DELEXT=7.000 -START=1 -MATRIX-b10sum62 -TRANG-human40.cd1
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -ALIGN=15 -MODE-LOCAL
-OUTFMT-pfs -NORM-ext -MINLEN-0 -MAXLEN-1000000 -USER-US08653294
-NCPU=6 -ICPU=3 -NO_XLDXY -WAIT -THREADS=1
                                                                                                                                              About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
       out_format : pfs
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Database length: -1518192014
Search time (sec): 10176.920000
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Query length: 12
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9b_in1:DMRNA3
9b_htg7:AC010566
9b_htg4:AC0105647
9b_in2:AC005847
9b_ba1:WC00233
9b_ba1:WC0025
9b_ba2:AF026541
9b_ba2:AF026541
9b_htg7:AC013772
9b_htg7:AC013705
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gb_htg3:AC001249
gb_htg3:AC0011145
gb_htg2:AC004555
gb_htg1:CEY49A3
gb_bal:AR013582
gb_bal:AR003326
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gb_htg2:HSDJ655C5
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gb_ba2:AE000122
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gb_in2:AF152403
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gb_in2:AF152406
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gb_htg4:AC012150
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gb_in1:CEC15H11
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Direct Submission
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1 (bases 1 to 149314)

S Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K., Bodota, B., Bouck, J., Carter, M., Chacko, J., Chen, Z., Cox, C., Burrows, J., Carter, M., Ding, Y., Danah-Rashid, N., Dayda-Rocha, S., Durbin, K.J., Ferraguto, D., Ding, Y., Domah-Rashid, N., Gorrell, J., Forcum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J.H., Gorrell, J., Forcum-Tansey, J., Fartatz, P., Ganesh, R., Gorrell, J.H., Gorrell, J., Holloway, C., Horsak, H., Jackson, L.E., Jackson, L., Jia, Y., Jones, M., Holloway, C., Horsak, H., Jackson, L.E., Jackson, L., Lucter, R., Lichtarge, O., Liu, J., Liu, W., Logan, O., Lu, J., Lucter, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M., Morris, S., Ranish, S., Rakton, S., Rayton, B., Scher, L., Quiles, M., Reiter, D., Rives, M., Sparks, A., Stamps, A., Scherer, S., Shah, E., Shah, E., Shah, E., Shah, E., Shah, E., Shah, H., Simon, M., Sparks, A., Stamps, A., Scherer, S., Shah, E., Weinstock, G., Weinstock, C., Weinson, R., Volo, Wabbah, M., Watlington, S., Weinstock, G., Weinstock, I.R., Williamson, A., Worley, K., Wren, J., Williamson, A., Worley, K., Wen, J., Chan, J., A., Maringtock, G., Weinstock, C., Weinson, R., Volo, Wabbah, M., Weinstock, G., Wein
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                                                                                                                                           Sukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                  Pterygota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroddea; Drosophilidae; Drosophila.
1 (bases 1 to 8849)
Adams,M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
1735 c 1884 g 2626 t
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Ratio: 3.833 Gaps: 0
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HTG: HTGS_PHASE1.
fruit fly.
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Worley, K.C.
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Submitted (16-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Ruman Genetics, Baylor College of Medicine, One Baylor Plaza, Houstron, TX 77030, USA

Baylor Plaza, Houstron, TX 77030, USA

* NOTE: This is a 'working draft' sequence. It currently

* consists of 89 contigs. The true order of the pleces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
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Largen, V. G., Chew, M., Doyle, C. M., Farran, D. E.,

Kim, S. H., Lee, B., Lomotan, M. A., Mak, J., Mazda, P., Moshrefi, A. R.,

Kim, S. H., Lee, B., Lomotan, M. A., Mak, J., Mazda, P., Moshrefi, A. R.,

Moshrefi, M., Mixon, K., Pacleb, J. M., Park, S., Pfeiffer B., Punch, E.,

Snir, E., Twomey, B., Wan, K. H., Zhang, R., S., Pfeiffer B., Punch, E.,

Squencing of Drosophila chromosome 3L, region 61F3-62A2

AL Upublished (1997)

S Celniker, S. E., George, R. A., Galle, R. F., Hoskins, R. A.,

Syirskas, R. R., Harris, N. L., Agbayani, A., Arcaina, T. T., Baxter, E.,

Blazej, R. G., Chavez, C., Chew, M., Doyle, C. M., Farfan, D. E.,

Flanagan, J., Houston, K. A., Hummasti, S. R., Karra, K., Kearney, L.,

Rim, S. H., Lee, B., Lomotan, M. A., Mak, J., Mazda, P., Moshrefi, A. R.,

Kim, S. H., Lee, B., Lomotan, M. A., Mak, J., Marda, P., Moshrefi, R.,

Boliect Submission

Nicot Submission

Submitted (12-0CT-1998) Berkeley Drosophila Genome Project, MS

64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road,

Berkeley CA 94720

For further information about this sequence, including its location

and relationship to other sequences, please visit our sequence

archive Web site (http://www.fruitfly.org/sequence/) or send email

to bdgp@fruitfly.berkeley.ed, 73-50, 92-76.
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     Blazej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E.,
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/db_xref="taxon:7227"
/chromosome="3L"
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LOCUS M.CB2533 40245 bp DNA
DEFINITION Mycobacterium leprae cosmid B2533.
VERSION AL035310 GI:4200258
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US-08-653-294-36 x AC005847/rev
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        seq_documentation_block:
        DNA
        INV
        22-OCT-1998

        LOCUS
        ACO05847
        268369 bp
        DNA
        Sequence (PIS DS03179 (D226), DS06357

        DEFINITION
        Drosophila melanogaster DNA sequence (PIS DS03179 (D226), DS06357
        COMPLET (D231), DS06962 (D232), and DS07291 (D240)), Sequence (D230), DS06962 (D231), DS06962 (D231), DS06962 (D231), ACO05847 (D240131 ACO04436 ACO04438 ACO04488 ACO04489

        ACCESSION
        ACO05847.1 GI:3779012

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1 (Jases 1 to 268369)
Celniker, S. E., George, R. A., Galle, R. F., Hoskins, R. A., Svirskas, R. R., Harris, N. L., Agbayani, A., Arcaina, T., Baxter, E.,
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/clone="RPC198-2701"
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Percent Similarity: 100.000
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US-08-653-294-36 x AC010564
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                                  72324
73760
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27-AUG-1999

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misc_feature
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Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. All CDS over 100 codons have been analysed. Gene prediction is based on positional base preference in codons sepecially where there is an increase in the observed/expected third position G + C. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally we choose the most upstream initiation codon). If this cannot be identified we choose the most upstream initiation codon.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                  Eiglmeier,K., Honore,N., Woods,S.A., Caudron,B. and Cole,S.T.
Use of an ordered cosmid library to deduce the genomic organization
of Mycobacterium leprae
Mol. Microbiol. 7 (2), 197-206 (1993)
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/note="MLCB2533.01c, ansP, probable L-asparagine permease,
partial CDS, len: >366 aa; highly similar to many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Details of M. leprae sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Sanger Centre is funded to complete the sequence of M. leprae by the Heiser Program for Research in Leprosy and Tuberculosis of The New York Community Trust.

Work in Paris is supported by the Heiser Trust, the Association Française Raoul Follereau and the Groupement de Recherches et des
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (URL, http://www.sanger.ac.uk/Projects/)
CDS are numbered using the following system eg MLCB33.01c. ML (M. leprae), cB33 (cosmid name), .01 (first CDS), c (complementary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (26-JAN-1998) Mycobacterium leprae sequencing project,
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CBIO 1SA E-mail: barrell(sanger.ac.uk Cosmids supplied by Dr.
Stewart T. Cole, [3] Unite de Genetique Moleculaire Bacterienne,
Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15,
France Requests for cosmids should be sent to Karin Eiglmeier

    (bases I to 40245)
    James, K.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.

                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium
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pseudogene; RLEP; sec-independent.
Mycobacterium leprae.
Mycobacterium leprae
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complement(1. .1099)
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Hamlin, N. and Churcher, C.M.
Unpublished
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MEDLINE
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//doce="MACDE233.02c, ansP2, probable L-asparagine permease, len: 505 as; highly similar to many anino-acid permease e.g. ANSP_SALTY (EMBL:004851) S.typhlmurium AnsP. L-asparagine permease (L-asparagine transport protein) (497 aa), fasta scores:opt: 1891 z-score: 2218.9 E(): 0, 58.9% identity in 477 aa overlap. Equivalent to M.tuberculosis Rv2127 (MTCV261.26, 83.7% identity in 485 ac overlap). Also similar to M.tuberculosis permease Rv0346c (MTCV13E10.06c, 69.8% identity in 473 aa overlap). Probable integral membrane protein, contains PS00218 Amino acid permeases signature. Pfam match to entry PF00324 aa_permeases. amino acid permease. Annotated as ORF TR:049802, designated lysp in M.leprae cosmid EMBL:U00017"
                           S.typhimurium AnsP. L.asparagine permease (L-asparagine transport protein) (497 aa), fasta scores; opt: 1508 2-score: 1696.8 E(): 0, 61.2% identity in 366 aa overlap. Equivalent to M.tuberculosis Rv2127, ansP (MYCZ61.26, M.tuberculosis permease Rv0346c, aroP2 (MYCZ1810.06c, M.tuberculosis permease Rv0346c, aroP2 and permeases a overlap). Probable integral membrane protein, contains PS00218 Amino acid permeases aginature. Pfam match to entry PF00324 aa_permeases, amino acid permease Annotated as ORF TR:049801, designated aroP2 in M.leprae cosmid EMBL:000017
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GTGLFLGAGGRLARAGPGLFLVYAVCGVFVFLILRALGELVLHFPSSGSFVSYAREFF
GTGAAVVGWLYFLDWAATAIVDTTAIATYTHRWT IFTALPQWTLALLALAVULWML
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VAPLIVVSSGVWFAYAAVELVGTAAGFTVEPKKIMPRAINSVIARIAIFYVGSVILLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="matlaespepksgasragvigeeagyhkgikprolomigiggai
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geraayvygwlyfldwawtalvdttalatylhrwtiftalpgwtlallalavvlvwnl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISVEWFGELEFWAALIKVCALMAFLVVGTIFLGGRYPVDGHNTGLSLWTSHGGLFPTG
VAQLIVVSSGVWFAYAAVELVGTAAGETVEPKKIMPRAINSVIARIAIFYVGSVILLA
LLLPYSAFKASESPFVTFFSKVGFYGAGDLMNIVVLTAALSSLNAGLYATGRVWHSIA
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INGSGPKFTARMSKNGVPYGGILLAAVICLCGVALNAFNPGQAFEIVLSVAALGIIAG
MGTIVLCQLRLHKMAKAGIMRRPRFRMPLAPYSGYLTLAFLFAVLVVMAFDKPIGTWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Pfam match to entry PF00324 aa_permeases, Amino acid permease, score 245.80, E-value 6e-70"
amino-acid permeases e.g. ANSP_SALTY (EMBL:U04851)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative L-asparagine permease"
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complement(2. .991)
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complement(833. .925)
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VASLIVIVPALIAGWYSIRKRVMTIARERMGYTGPFPAIANPPVQPSERSHSQNP"

complement(1354. .2691)
/gene="ansP2"
/note="Ffam match to entry PF00324 aa_permeases, Amino
acid permease, score 501.80, E-value 5.1e-147"

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/product="52126_C2_220"
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LLISLAAIVVTTIFGFIWYSHSIFGLESLGFWLRRPYCSLPOSARADISPDGGCRLLA
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NIAGILITYGRIKSWRRGLIFAMFVFAAVFTPGSDPFSWTALGAALTVLLELAIQLVRL
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SRMFERDKNELRDLGIPLEVGKVSALDPSEGYRINRDAYALPPVELTPDEAAAVAVAT
QLWESQELITATQGALLKLRAAGVDIDPLDTPVVIASSSGVSSLRGSEDFLSILLSAI
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QVQAPEALAYRVRNAAVAALESYQVTAQA"
complement(1701. .2444)
                                                                                                                                                           Submitted (01-NOV-1993) Department of Genetics, Harvard Medical School, 200 Longwood Avenue, Boston MA 02115
3 (bases 1 to 42157)
                                                                                                                                                                                                                                                                                             Submitted (01-MAR-1994) Department of Genetics, Harvard Medical School, 200 Longwood Avenue, Boston MA 02115
On Mar 31, 1994 this sequence version replaced gi:414223.
This sequence data was produced by the Genome Sequencing Center located at Collaborative Research Incorporated (1365 Main St., Waltham MA, 02159). 617-487-7979). Please contact Doug Smith (smith@cr.cric.com). The annotation should be considered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary and incomplete.

Location/Qualifiers
1. 42157
Corganism="Mycobacterium leprae"
/db_xref="taxon:1769"
complement(133. 1086)
/note="match to yigu and yigv E.coli; B2126_C1_183"
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complement(1132. .1398)
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     1 (pases 1 co serving smith, D.R. Unpublished 2 (bases 1 to 42157) Robison, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
  (bases 1 to 42157)
                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                             Robison, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                            REFERENCE
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                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                      complement(2903. 3856)
/gene="MLCB2533.03c", hypothetical protein, len: 317 aa;
/gene="MLCB2533.03c, hypothetical protein, len: 317 aa;
/note="MLCB2533.03c, hypothetical protein Rv2125
similar to M.tuberculosis hypothetical protein Rv2125
(MTCY261.21) (EMBL:207559) (292 aa), fasta scores; opt:
1648 2-score: 2382.2 E(): 0, 84.1% identity in 290 aa
overlap. Also some similarity to M.leprae hypothetical
protein TR:Q49847 (29.7% identity in 279 aa overlap).
Annotated as OMF TR:Q4977, hypothetical protein in
M.leprae cosmid EMBL:U00017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="STREMBL:049797"
Atanslation="MPPHRAYRHASSALKPYADSYTLRDGGPDRGALPELHNTVVV
Artanslation="MPPHRAYRHASSALKPYADSYTLRDGGPDRGALPELHNTVVV
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HYSHPPNPKATVALLRRVEDVLDVBYPLADLPTQAEDWEGALTEIAABDELAEY
SLEGRGDAEYDVDALGKIDGDALAAEFERYLRRRRPGFGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mote="MLCB533.04, metH, probable 5-methyltetrahydrofolate-homocysteine methyltransferase, 5-methyltetrahydrofolate-homocysteine methyltransferase, 1en: 1183 aa; similar to many members of vitamin-Bl2 dependent methionine synthase family e.g. METH ECOLI (EMBL:X16584) E.coli metH (1226 aa), fasta scores; opt: 1617 z-score: 1000.7 E(): 0, 31.6% identity in 1228 aa overlap. Equivalent to M. tuberculosis Rv2124c (MTCY261:20c, 88.7% identity in 1183 aa overlap). Annotated as METH_MYCLE, designated metH2 in M.leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1994
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Mycobacterium leprae
Bacteria: Firmicutes: Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium.
                                                                                                                                                                                       /note-"PS00218 Amino acid permeases signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
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                                                                                                        /note="conflict: C is CT in EMBL:ML017"
complement(2500. .2592)
1668. .2835
/note="1168 bp perfect direct repeat"
2104
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Gaps: 0
Percent Identity: 75.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TyrArgLeuAlaIleArgArgIleAlaLeuArgTyr 12
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Mycobacterium leprae cosmid B2126.
U00017
                                                                                                                                                                                                                    complement(2903. .3856)
/gene="MLCB2533.03c"
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                                                                               /gene="ansP2'
                                                                                                                                                                    /gene="ansP2
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/gene="metH"
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/gene="metH"
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4.400
83.333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-36 x MLCB2533
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LOCUS U00017
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                                                     misc_feature
                                                                                                                                    misc_feature
  repeat_unit
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VERSION
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KEYWORDS
SOURCE
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RAGEWYLEDLLYDAEQRLADEGIGGDIYLFRNNTDSAGNSYGCHENYLIYRAEFSRI
SDVLLPFLYTRQLIGGAGWLYGPRAAFTGLSQRAEHIWGGSATTRSRPIINTNDE
PHADAEKYRELLYYTGSONWCETTWLKYGTRALMEMYEGYPFROFSLDNFIRAIR
EVSHDITGRRPVRLAGGRQASALDIOREYYTRAFEHLQTREPNYQFEQVVDLWGFSAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="wiresepdrlptnlafpgisvingssfydllrrqapellpyslgg
GQSGGGQQLSHGTTIVVLKYPGGVVIAGDRRSTQGNMIAGRDVRKVYITDDYTATGIA
GYDANAVERLEARLYAVELEHYEKLEGVPLTFAGKVNRLAIMYBSNLTAAWQGLLALPLL
AGYDIAPDPQSAGRIVSFDAAGGWNIEEEGYQSVGSGSIFAKSSIKKLYSQVSDDS
ALRVAIEALYDAADDDSATGGPDLVRGIYPTAVTIGAEGAAEVTESRIAELAREIIES
RSRAYTLGSFGGSEK"
                         VAPIGPAGAVTVPDGVDLRRIVSDAVAEVSTGATARVWVVDGRATALRHAGRPAGVRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MKIADANVLLYSGNTSSEHTGHPCAGSTVRLSCADRIGEGWVPL
LVFVRPATKMGLVLRTMSSEDAIGQVADWLTGPSAVLMCLTVRHAAFLVKILV"
complement(6822. .7115)
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NPSRSLQKISELYDRVGFAAAGKFNEFDNLRRGGIQFADTRGYAYDRRDVTGRQLANV
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GSRQAVQFPYRPSRAEPYTMRNVEPWGVITENSCWYLVGHDCDRNATRTFRLSRIGSE
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RRAFRRIIGSGLEALLREKDSKGSKGAQNPKGARDSKNSKSYGESTD"
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RTRWDYEVESPLRDARGFDLSRSAGPPPVVDADEVGAANMILTNGARLYVDHAHPEYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(9142. .10686)
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CDS

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TLKRGIINTRDEPHADADRYRRLHVIVGDANLAETSTYLKLGTTALVLDLIEEGPVHG
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14353. .14763
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AAASWDSVIFDLGGDSLVRIPTLEPLRGSKAHVGALLDSVDSAAELVEQLTTKPVDPG
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complement(13640. .13921)
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complete cds; and CeoC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis CeoB (ceoB) gene, (ceoC) gene, partial cds.
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Gaps: 0
Percent Identity: 75.000
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                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="RLEP"
complement(11986. .12465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis. Mycobacterium tuberculosis
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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4.400
83.333
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US-08-653-294-36 x U00017/rev
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                                                                                                                                                                                                                                                                                                                                                                    repeat_region
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Defails of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C.

CAUTION: In some cases we may not have predicted the correct intitation codon. Where possible we choose an initiation codon (atg, gt, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein Rv2680"
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PRAHQLELRASWTATTPDLGAHVQAFCDVLEHAAGLPPAGVTDLGSRSRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome
Trust Genome Campus, Hinxton, Cambridge CB10 15A Unite de Genetique
Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux,
75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
On Jun 27, 1998 this sequence version replaced gi:2181970.
                                                                                                                                                          Cole,S.T., Brosch,R., Parkhill,J., Garnier,T., Churcher,C.,
Harris,D., Gordon,S.V., Eiglmeier K., Gas,S., Barry III,C.E.,
Tekatala,F., Backonk,K., Basham,D., Brown,D., Chillingworth,T.,
Connor,R., Davies,R., Devlin,K., Feltwell,T., Gentles,S.,
Hamlin,N., Holroyd,S., Hornsby,T., Jagels,K., Krogh,A., McLean,J.,
Moule,S., Murphy,L., Oliver,S., Osborne,J., Quail,M.A.,
Rajandream,M.A., Rogers,J., Rutter,S., Seeger,K., Skelton,S.,
Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="Rv2680"
102. -3Rv2680"
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similar to M. leprae protein U1764v. FASTA scores;
sptr|050005|05005 U1764v (213 aa) opt: 1136 z-score:
12311 E(): 0;83.9% identity in 193 aa overlap. TBparse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="fragment designated v010. Does not represent a
                                                                                                                                                                                                                                                                                                                                                                                                                          Deciphering the biology of Mycobacterium tuberculosis from the
                                                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Erratum:[[published erratum appears in Nature 1998 Nov 12:396(6707):190]]
2 (bases 1 to 38631)
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/organism="Mycobacterium tuberculosis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete genome sequence
Nature 393 (6685), 537-544 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref-"taxon:1773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
     Mycobacterium tuberculosis. Mycobacterium tuberculosis
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102. .734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="H37Rv"
                                                                                                                                     (bases 1 to 38631)
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  SOURCE
ORGANISM
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AUTHORS
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAC69359.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAC69360.1"
Ab_xxef="0G1:258255"
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                                                                                                                                                                                                                                      Submitted (23-SEP-1997) Molecular Microbiology and Immunology, Johns Hopkins University, 615 N. Wolfe Street, Baltimore, MD 21205, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
LOCUS MTCY05A6 38631 bp DNA BCT 17-JUN-1998
DEFINITION Wycobacterium tuberculosis H37Rv complete genome; segment 120/162.
ACCESSION 296072 AL123456
VERSION 296072.1 GI:3261793
1 (bases 1 to 1692)
Chen,P. and Bishai,W.R.
Novel selection for isoniazid (INH) resistance genes supports a
role for NAD+-binding proteins in mycobacterial INH resistance
Infect. Immun. 66 (11), 5099-5106 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="TrkA homolog; complements the INH-sensitive phenotype of oxyR deletion mutant of E. coli" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="TrkA homolog; complements the INH-sensitive phenotype of oxyR deletion mutant of E. coli"

    1692
/organism="Mycobacterium tuberculosis"
/strain="H37Rv"

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Gaps: 0
Percent Identity: 75.000
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                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'product~"CeoB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="CeoC"
                                                                                                                                                                2 (bases 1 to 1692)
Chen, P. and Bishai, W.R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            681. .1364
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681. .1364
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1361. .>1692
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US-08-653-294-36 x AF026541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
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DEFINITION
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KEYWORDS
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                          AUTHORS
TITLE
                                                                                                                                        MEDLINE
REFERENCE
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gene

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/dell...5900
/gene="arsh"
/gene="arsh"
/gene="arsh"
/note="Rv2684, (MTCY05A6.05), len: 429. Function: arsh,
corresponds to antigen 45 of M. leprae, a transmenbrane
protein related to arsenical pumps. FASTA best: Ad45_MYCLE
P46838 46 kd membrane protein (429 aa) opt: 2060; E(): 0;
MTCY05A6.06, (428 aa) E(): 0; 76.6% identity in 427 aa
overlap. TBparse score is 0.891"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation-"mkvnidptaptfatyrrdmraegmaedypvysidsdaldaarmi
AEHRLPGLLVTAGAGKQYAVLPASGVVRFIVPRYVQDDPLLAGVLNESTADRCAERLS
GKKVRDVLPDHLVEVPPANADDTIIEVAAVMARLRSPLLAVVKDGSLLGVVTASRLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Mote-"RAZ685, (MTCY05A6.06), len: 428. arsB, Function: unknown membrane protein very similar to M. leprae antigen 45(P46838) and MTCY05A6.05; related to arsenical pumps. PASTA best: AG45_MYCLE P46838 46 kd membrane protein (429 and opt: 2041; E(): 0; 74,08 identity in 427 as overlap. Highlysimilar to MTCY05A6.05; E(): 0; 76.6% identity in 427 as overlap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seg_documentation_block:
LOCUS AC013772 142796 bp DNA HTG 09-DEC-1999
DEFINITION Homo sapiens clone RP11-7024, WORKING DRAFT SEQUENCE, 6 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5968. 5973
/note="possible RBS, GGAGGA, for Rv2685"
5980. 7266
/gene="arsB"
5980. 7266
/gene="arsB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3APISFWEFTRKGAVVTAVSIALAAIYLWLRYFVLLH"
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Gaps: 0
Percent Identity: 75.000
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/db_xref="SPTREMBL:007187"
'db_xref="SPTREMBL:007185"
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AC013772.2 GI:6553994
HTG: HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=]
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US-08-653-294-36 x MTCY05A6
                                                                                            AALKT"
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                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="SPTEMBL:007183"
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LTKGHGAADWSKRPQDPSCLABVGMRPPALVDTELAGRLAGFDRVLAAWGERLELGLG
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PPPGRWYRKPAAARLDAARALTBVSGRRORRSAAWAALAARESPDPPEIAEPANGP
PPPGRWYRKPAAARLDAARALTBVSGRRORRSAAGGGDGS"
COMPLEMENT (2049. .3965)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"dxs"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESEHDWVESSHASAALSYADGLAKAFELTGHRNRHVYAVVGDGALTGGMCWEALINNIA
ASRREVIIVVNDNGRSYAPTIGGVADHLATLKLQPAYEQALETGRDLVRAVPLVGGLW
FELHSVKAGIKDSLSPQLEFDLGLKYVGPVDGHDERAVEVALRSARRFGAPVIVHV
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                                                                                                                                                                                                               Anote-"Rv2681, (MTCY05A6.02), len: 438. Function: unknown twery similar to hypothetical W. leprae protein U17640. FASTA best: G699161 U17640 (429 aa) opt: 2146. E(): 0; 77.4% identity in 416 aa overlap. TBparse score is 0.915"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAFDQIMMDVALHKLPVTMVLDRAGITGSDGASHNGMWDLSMLGIVPGIRVAAPRDAT
RLREELGEALDVDDGPTALRFPKGDVGEDISALERRGGVDVLAAPADGLNHDVLLVAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAFAPMALAVAKRLHNQGIGVTVIDPRWVLPVSDGVRELAVQHKLLVTLEDNGVNGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Yagene"RV2683" (MTCY05A6.04), len: 165. Function: unknown /note="Rv2683, (MTCY05A6.04), len: 165. Function: unknown but highly similar to M. leprae protein U1764Q. FASTA best: 6699165 U1764Q. F184 an) opt: 750; E(): 0; 73.8% identityin 164 aa overlap. TBparse score is 0.926"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4099. .4102
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4109. .4606
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4109. .4606
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                                                                                                                                                                 736. .2052
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                                                                                         /clone="Y05A6"
                                                                                                                   736. .2052
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source
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DNA HTG 03-NOV-1999
*** SEQUENCING IN PROGRESS ***, in ordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence was identified as CDM:10214117 by the submitter. For further information on this sequence you may e-mail to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fruit fly.

Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 56237)

Adams, M. and Venter, J.C.

Direct Submission

Submitted (03-NOV-1999) Celera Genomics, 45 West Gude Drive,

Rockville, ND, USA
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This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
                            /clone_lib="RPCI-11 Human Male BAC"
47989 a 24580 c 24540 g 45686 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 142796
                                                                                                                                                                                                                         Percent Identity: 66.667
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/db_xref-"taxon:7227"
1 12291 c 11944 g 15645 t
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Gaps: 0
Percent Identity: 72.727
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/clone-"RP11-7024"
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AC013205
AC013205.1 GI:6223127
HTG: HTGS_PHASE2.
fruit fly.
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Locus MTV002 56414 bp
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US-08-653-294-36 x AC013772/rev
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US-08-653-294-36 x AC013205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_htg5:AC013205
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Locus Ac013205
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TITLE
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                                                                                                                                                                                                                                              Uppublished

Saldwin, J., Barna, N., Backerly, R., Boguslawkiy, L., Boukhgalter, B.,

Baldwin, J., Barna, N., Beckerly, R., Boguslawkiy, L., Boukhgalter, B.,

Baldwin, J., Barna, N., Beckerly, R., Boguslawkiy, L., Boukhgalter, B.,

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,

Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,

Ferreira, P., Fitzhqy, W., Forrest, C., Funke, R., Gage, D.,

Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Hotton, L.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

McEwan, P., McGurk, A., McKeran, K., Macdaughlin, J., Meldrim, J.,

Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,

Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,

Rocerof, R., Pollara, V., Kiley, R. Roy, A., Santos, R., Severy, P.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Naman, D., Ye, W.J., Zimmer, A. and Zody, M.

Direct Submission

Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome

Roce 10, 1999 this sequence version replaced gi:6425750.

All repeats were identified using RepeatMasker:

Sant, A.F.A. & Green, P., (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center: Whitehead Institute/ MIT Center for Genome Research
                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 14279)
1 shares, E. Linton, L., Nusbaum, C. and Lander, E. Homo sapiess, clone RP11-7024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
Web Site: http://www-seq.wl.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Conter project name: L2959
Center clone name: 7_0_24
Center clone name: 7_0_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2142: contig of 2142 bp in length gap of unknown length 4834: contig of 2632 bp in length gap of unknown length gap of unknown length gap of unknown length 55157: contig of 15946 bp in length gap of unknown length gap of unknown length gap of unknown length gap of unknown length
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1. .142796

    142796
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/db_xref="taxon:9606"

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                                   Homo sapiens
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/db_xref="SPTREMBL:033281"
/transl_table=11
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(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed(expected third position G + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gt, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon. If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge Ealt 15A Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                        Cole,S.T., Brosch,R.,
Harris,D., Garnier,T., Churcher,C.,
Harris,D., Gordon,S.V., Eiglmeler,K., Gas,S., Barry III,C.E.,
Harris,D., Gordon,S.V., Eiglmeler,K., Gas,S., Barry III,C.E.,
Connor,R., Badcock,K., Basham,D., Chillingworth,T.,
Hamlin,N., Holroyd,S., Hornsby,T., Jagels,K., Krogh,A., McLean,J.,
Moule,S., Murphy,L., Oliver,S., Osborne,J., Quail,M.A.,
Rajandream,M.A., Rogers,J., Rutter,S., Seeger,K., Skelton,S.,
Barrell,B.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <1. >56414
/note="fragment designated v002. Does not represent a
physical clone"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Details of M. tuberculosis sequencing at the Sanger Centre are
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                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacterlaceae;
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Parkhill.J.

    . 56414
/organism="Mycobacterium tuberculosis"

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/strain="H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete genome sequence
Nature 393 (6685), 537-544 (1998)
98295987
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/clone="Y154"
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AL008967 AL123456
AL008967.1 GI:3261491
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Cole, S.T., Brosch, R.,
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/gene="Rv2737c, (MTV002.02c), len: 790 aa. rech, /note="Rv2737c, (MTV002.02c), len: 790 aa. rech, /note="Rv2737c, (MTV002.02c), len: 790 aa. rech, /note="Rv2737c, (MTV002.02c), reca protein (790 aa). Contains self-splicing protein element (intein) from 2294 to 969 (c), similar to intein II from TR:E332317 from TREME:V13030) DNA-directedDNA polymerase (EC 2.7.7.7) from Thermococcus sp. (1829 aa), fasta socres; opt: 81 z-score: 235.2 E(): 6e-06, 24.6%identity in 183 aa overlap. Contains PSO0017 ATP/GTP-blindingsite motif A (P-loop), PSO0121 rech shanture, and PSO0088IProtein splicing signature. See Davis et al, (1992) cell71(2):201-210"
                                                                                                                                        /translation-"mtvscpppstsereeqaralclrlitarsftraelagqlarrgy
bedignruchanglyddfdfaegwygsrranaakskralaaelhkgydddytty
vlggidagaergraeklyrarlrrevliddgtdearvsrrlvamlarrgyggilacev
viaelaaerbrry
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AGELKKGDRYAQPRRPDGFOSDAPIPADHARLIGYLGGGGGWGWGGFFPINETNVQR
ALIDDVTRIAATLGGAAHPOGRISLAIAHRPGERNGYADLCQQAGIYGKLAWBRIIPN
WFFEPDIAADIVGNLLFGLFESDGWVSREQTGALRVGYTTTSEQLAHQIHWLLLRFGV
GSTYRDXDPPTGRRPSTGARRAIGSKROYFEVRISGDNOWTAFRESVPWAMGPRGAALIQ
AIPRATGGRRRGSQATYLAAEMTDAVLNYLDBRGYTAQBAANIGVASGDPRGGRKQV
LGASRLRRDRVQALADALDDKFLHDMLAEELRYSVIREVLFTRRARTFDLEVEELHTL
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GDSHVGLQARLMSQALRKMTGALNNSGTTAIFINQLRDKIGVMFGSPETTTGGRALKF
YASVRMDVRRVETLKDGINAVGNRTRVKVVKNKCLAEGTRIFDPVTGTTHRIEDVVDG
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QGKENARNFLVENADVADEIEKKIKEKLGIGAVVTDDPSNDGVLPAPVDF"
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SIALDVALGIGGLPRGRVIEIYGPESSGKTTVALHAVANAQAAGGVAAFIDAEHALDF
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N-terminus is highly similar to the N-terminus of the
Upstream ORFWTV002.07c (78.4% identity in 37 aa overlap),
also similarto ALOSO958 (52448_5 Streptomyces coelicolor
cosmid 4H8 (64aa) opt: 185 z-score: 283.5 E(): 2.9e-08,
39.7% identityin 63 aa overlap"
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/note="PS00017 ATP/GTP-binding site motif A (P-loop)"
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/note="possible RBS upstream of Rv2737c"
complement(3247. .3453)
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/protein_id="caa15534.1"
/db_xref="G1:2624260"
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/protefl_id-"CAA1553.1"
/db_xref-"G1:2624258"
/db_xref-"SWISS-PROT:P26345"
                                                                                                            /db_xref="SPTREMBL:033280"
/product="recx"
/protein_id="CAA15532.1"
/db_xref="GI:2624257"
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/gene="Rv2738c"
/note="Rv2738c, (MTV002.
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/gene="recA"
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US-08-653-294-36 x AC017383
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Ratio:
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/protein_id="Cas15536.1"
/db_xref="GI:2624262"
/db_xref="SPTREMBL:033283"
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/translation="MAELTETSPETPETTEAIRAVEAFLNALQNEDFDTVDAALGDDL
/YENVGFSR.RGGRATATLLERMOGNVGFEVKIHRIGADGAAVLTEETDALIIGPLRV
OFWVCGVFEVDDGRITLWRDYFDVYDMFKGLLRGLVALVVPSLKATL"
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LOCUS AC017383 115873 bp DNA
DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                           /translation-"mrvavvacpdpghsfpalalcorfraadptptletgvewleaar
Aagidaveldglaatdrdldagarihrraaqmavlnvprlralepelvvsdvitacgg
Maaellgipwvelnphplxlpskglppigsglaagtgirgrlrdatmraltgrswrag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRQRAAAVRVEIGLPARDPGPLRRLIATLPALEVPRPDWPAEAVVVGPLHFEPTDRVLA
PAGTGPVVVVVAPSTRALTGTAGLTEVALOSLTGEGTVPGSGRLVVSRLSGADLLVPPPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Rv2741, (MTV002.06), len: 525 aa; Member of M
tuberculosis PE_ PGRS subfamily, similar to many eg.
                                                                                                                                                                                                                                                                                                     /codon_start=1
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Gaps: 0
Percent Identity: 88.889
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complement(3464. .4630)
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US-08-653-294-36 x MTV002/rev
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Percent Similarity: 100.000
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Ratio:
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SOURCE THIS TITLE THE ALLEGGE ENGODESTICE TRACHESTS: HORADOGS: INSCRIBE MEDICAL MEDICA
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us-08-653-294-36.rge

COMMENT

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unknown length
of 1609 bp in length
unknown length
of 1436 bp in length
unknown length
of 1417 bp in length
unknown length
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unknown length
unknown length
of 1991 bp in length
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of 1187 bp in length
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of 1767 bp in length
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of 2101 bp in length
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of 1623 bp in length
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of 1542 bp in l
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of 984 bp in le
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of 3316 b
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of 1337 b
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of 1468 b
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of 3388 b
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of 2637 b
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of 1619 h
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of 1893 h
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of 1405 h
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58824
60375
63760
                                                          Direct Submission

Submitted (28-APR-1999) Drosophila Genome Center, Lawrence Berkeley

Laboratory, MS 64-121, Berkeley, CA 94720, USA

Laboratory, MS 64-121, Berkeley, CA 94720, USA

On Aug 2, 1999 this sequence version replaced gi:5629944.

For further information about this sequence, Including its location
and relationship to other sequences, please visit our sequence
archive Web site (http://www.fruitfly.org/sequence/) or send email
to bdgggefruitfly.berkeley.edu. All contigs in this submission meet
the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 94 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
Rubin,G.M.
                                                                                                                                                                                                                                                                                                                                       f unknown length
g of 1029 bp in length
f unknown length
g of 1091 bp in length
f unknown length
of 1218 bp in length
g of 1218 bp in length
f unknown length
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t unknown length
g of 1011 bp in length
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of 1310 bp in length
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of 1037 bp in length
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unknown length
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of 733 bp in length
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of 701 bp in length
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of 622 bp in length
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unknown length
of 1093 bp in length
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20938
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22268
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22872
                                                                         TITLE
JOURNAL
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Submitted (15-JUL-1998) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://fruitfly.berkeley.edu/sequence/) or send library locations: 75-21, 43-37, 68-85.
Location/Qualifiers
Svirskas,R.R., Harris,N.L., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Chavez,C., Chew,M., Doyle,C.M., Farfan,D.E., Flanagan,J., Houston,R.A., Hummasti,S.R., Karra,K., Kearney,L., Kim,S.H., Lee,B., Lomoten,M.A., Mak,J., Mazda,P., Mok,M.S., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Punch,E., Snir,E., Twomey,B., Wan,K.H., Whitelaw,R.R., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS AC007352 183365 bp DNA HTG 02-AUG-1999
DEFINITION Drosophila melanogaster chromosome 2 clone BACR19116 (D626) RPCI-98
19.J.16 map 47A-47B strain y; cn bw sp, *** SEQUENCING IN PROGRESS
ACCESSION AC007352
VERSION AC007352.5 GI:5670591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DS03499 (P217) is a bridge, sequence extending from 83,000 to bp 111,462, and DS08132 (D174) extends from bp 102,799 to bp 173,970.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 183365)

Celniker, S. E., Agbayani, A., Arcaina, T. T., Baxter, E., Blazej, R.G.,

Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,

Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,

Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,

Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P.,

Moshrefi, A. R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,

Pfelifer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="Pls DS01995 (D179), DS03499 (D217), and DS08132 (D174)"
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/organism="Drosophila melanogaster"
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Gaps: 0
Percent Identity: 72.727
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US-08-653-294-36 x AC005286
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1 (Dases 1 to 17370)

Svirskas, R.R., Harris, N.L., Agbayani, A., Arcaha, T.T., Baxter, E., Blazej, R.G., Chav, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, R.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Mok, M.S., Moshrefi, A.R., Noshrefi, M., Nixon, R., Pacleb, J.M., Park, S., Pefelffer, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Whitelaw, K.R., Yee, A., Zhang, R., Zieran, L.L. and Kimmel, B.

Sequencing of Drosophila chromosome 2R, region 56F7-56F9 Unpublished (1997)

E. (Dases I to 173970)

Celniker, S.E., George, R.A., Galle, R.F., Hoskins, R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Subclones in sac from Pl clones DS01995 (D179), DS03499 (D217), and DS08132 (D174)) DNA.
Drosophila melanogaster
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Gaps: 0
Percent Identity: 66.667
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SOURCE
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us-08-653-294-36.rge

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172452 TATTTGCTAGCTGCGCGCGCGTGGCTTGTCGTTAC 172487
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Submitted (22-APR-1999) Drosophila Genome Center, Lawrence Berkeley, Laboratory, MS 64-1999) Drosophila Genome Center, Lawrence Berkeley, Laboratory, MS 64-191, Berkeley, CA 94720, DSA
Laboratory, MS 64-191, Berkeley, CA 94720, DSA
To And 27, 1999 this sequence version replaced gii:629943.
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.
* NOTE: This is a "working draft' sequence. It currently consists of 30 contigs. The true order of the pleces
* is not known and their order in this sequence record is
                                                                        Celniker S.E., Agbayani, A., Arcaina, T.T., Baxter.E., Blazej, R.G., Butenfif, C., Champe, M., Chev, M., Ciesiolka, L., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Maxda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Petifer, B., Poon, L., Sequeira, A., Sethi, H., Shir, E., Stylskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and Rubin,G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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unknown length
of 1469 bp in length
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unknown length
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                                        TITLE
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AUTHORS
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to: 183365

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/clone="BACR19J16 (D626) RPCI-98 19.J.16"
/clone_llb="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC llbrary, partial EcoRI in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2321 others
                                                           gap of unknown length contig of 613 bp in length contig of 513 bp in length gap of unknown length gap of unknown length contig of 718 bp in length gap of unknown length contig of 707 bp in length gap of unknown length contig of 525 bp in length gap of unknown length gap of unknown length contig of 714 bp in length gap of unknown length gap of unknown length contig of 693 bp in length.
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of 634 bp in length
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/organism="Drosophila melanogaster"
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Percent Identity: 66.667
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/db_xref="taxon:7227"
/chromosome="2"
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183365:
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Human pl6p27 fusion protein
Human pl6p27 fusion protein
CDK inhibitory fusion prote
Human pl6(GS)p27 fusion pro
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A computer readable medium has been developed which has recorded on it
982 nucleotide sequences isolated from the Enterococcus faecalis genome.
712938 to X13919 represent these nucleotide sequences which are primary
nucleotide sequences, also known as contigs. The computer-based system
can identify fragments of the Enterococcus faecalis genome with
commercial importance. The products can be used to detect the presence
of Enterococcus faecalis in samples. They can also be used for
diagnosing Enterococcal infection in an animal and monitoring
progression of disease, and for identifying agents which can be used to
modulate the growth or pathogenicity of Enterococcus faecalis, or
another related organism, in vivo or in vitro. In particular the
can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                  Entercoccus faecalis; contig; SEQ ID NO:420.

Entercoccus faecalis; contig; detection; Entercoccus infection;
Waccine; attenuation; computer readable medium; ds.
Entercoccus faecalis.
W09850555-A2.

N09850555-A2.

N09850555-A2.

N09850555-A2.

N1-1998; U08985.

N2-NOV-1998; U08985.

N2-NOV-1997; US-066009.

NR 14-NOV-1997; US-066009.

NR 16-MAY-1997; US-066009.

NR 199-045171/04.

NR WPI: 99-045171/04.

NR WPI: 99-045171/04.
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Gaps: 0
Percent Identity: 63.636
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                                                                                                                                                                                       seq_documentation_block:
ID X13357 standard; DNA; 4114 BP.
AC X13357;
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US-08-653-294-36 x X13357
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Ratio:
  N_Geneseq_36:X26224
N_Geneseq_36:X26235
N_Geneseq_36:T74052
N_Geneseq_36:X26223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                               FIFEWERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               414 | Enterococcus faecalis genome c

414 | Enterococcus faecalis genome c

861 | Bacterial antibiotic resitance

1400 | Sequence encoding Serratia pho

382 | Human gene signature HUMGSO857

731 | PR-1 like gene Stratia pho

24025 | Mutated BRCAl genomic sequenc

24025 | Mutated BRCAl genomic sequenc

24026 | Mutated BRCAl genomic sequenc

24021 | Mutated BRCAl genomic sequenc

24026 | Mutated BRCAl genomic sequenc
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                                                                                                                                                                                    Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-MODEL=frame+_p2n.model -DEV=xlp
-MCPGIL_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.2
-DF=N_Geneseq_36 -QFMT=fastap -SUFFT=rng -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000
-GAPEXT=4.000 -MINMATCH=0.100 -VGAPOP=10.000 -VGAPEXT=0.500
-GAPOP=4.500 -GGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN-0
-MAXLEN-1000000 -USER-US08653294 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
                                                                                                              About: Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  582
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OM of: US-08-653-294-36 to: N_Geneseq_36:*
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Database sequences: 311585
Database length: 125096042
Search time (sec): 873.190000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search information block:
Query: US-08-653-294-36
Query length: 12
                                                       Date: Feb 8, 2000 7:32
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N_Geneseq_36:X13357
N_Geneseq_36:Q12225
N_Geneseq_36:T28565
N_Geneseq_36:R60877
N_Geneseq_36:R60873
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N_Geneseq_36:117516
N_Geneseq_36:117516
N_Geneseq_36:117519
N_Geneseq_36:117519
N_Geneseq_36:117521
N_Geneseq_36:117521
N_Geneseq_36:117521
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N_Geneseq_36:044280
N_Geneseq_36:T17455
N_Geneseq_36:T17515
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N_Geneseq_36:T17520
N_Geneseq_36:T17525
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N_Geneseq_36:T17513
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N_Geneseq_36:T17526
N_Geneseq_36:T17527
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N_Geneseq_36:T17530
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N_Geneseq_36:Q60295
N_Geneseq_36:X26229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N_Geneseq_36:V73802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N_Geneseq_36:T16336
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N_Geneseq_36:T74053
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  DACON 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PERSONANTIAL CONTROLL OF MEMBRANE PROTECTION - BY division of protein fine cartridge genes corresp. to helix structure polypeptide(s) bisclosure: Fig 1: 17pp; Japanese.

A gene cassette is prepd. by division of the OR membrane protein encoding helix structure polypeptides. Restriction sites are indicated. A base sequence contg. such a sequence downstream to the tryptophan regulating gene darived from the E. coli tryptophan operon, the trpic or the trpE polypeptide translation regulating base sequence, and the N-terminal Met of the trpic (or trpE) or trpE polypeptide, respectively, is introduced in an expression vector for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacterial antibiotic resitance gene, aacC2, probe.
Detection; probe; amplification primer; bacterial pathogen; pneumonia; Bscherichia coll; Klebsiella pneumoniae; Pseudomonas aeruginosa; Proteus mirabilis; Streptococus pneumoniae; Staphylococcus aureus; Staphylococcus apidermidis; Enterococcus faecalis; respiratory tract; Staphylococcus saprophyticus; Streptococcus progenes; urinary tract; Haemophilus influenzae; Moraxella catarrhalis; septicaemia; meningitis; infection; intra-abdominal infection; skin infection; meningitis; bacterial resistance; beta-lactam antibiotic; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: Q12225 from: 1 to: 1371
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/*tag= a
//label= sph1
/note= "restriction enzyme site"
592. .597
                                                                                                                                                                                                                                                                                                                    note= "restriction enzyme site"
                                                                                        /*tag= b
/label= MluI
/note= "restriction enzyme site"
884. .889
                                                                                                                                                                                                                           'note* "restriction enzyme site"
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/label= BamHI
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ID T28565 standard; DNA; 861 BP.
                                                                                                                                                                                                                                                                       /*tag= d
/label= NheI
                                                                                                                                                                                   /*tag= c
/label= NdeI
                                                                                                                                                                                                                                                  .069. .1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-36 x Q12225/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 38.00
Ratio: 3.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                               27-MAY-1991.
06-OCT-1989; 260261.
06-OCT-1989; JP-260261.
(HTA ) HTACHI KK.
WPI: 91-197925/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: N_Geneseq_36:T28565
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                                                                   misc_feature
                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
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Bergeron MG, Ouellette M, Roy PH;

Mary 96-179953/18.

WHI; 96-179953/18.

WHI; 96-179953/18.

WHI; 96-179953/18.

Well of for the detection of bacterial species using probes and primers - allows detection and quantification of antibiotic cesistant bacteria in patients, the environment and food claim 82; Page 142-143; 216pp; Bnglish.

The sequences given in 728660-76 represent fragments derived from bacterial antibiotic resistance genes which were used as probes in the method of the invention comprises using probes and/or amplification primers which are specific, ubiquitous and sensitive for amplification primers which are specific, ubiquitous and sensitive for determining the presence and/or amount of nucleic acid comprises a selected target region hybridisable with the probes or primers and detecting the presence and/or amount of the bacterial species.

Comprises a selected target region hybridisable with the probes or primers and detecting the presence and/or amount of the bacterial species.

Comprises a selected bacterial species. This method may be used to detect commonly encountered bacterial pathogens, e.g. Escherichials oll, and/or amount of the bacterial species. This method may be used to streptococcus pneumoniae, Staphylococcus aureus, Staphylococcus sprophylicus, Streptococcus sprogenes, Haemophilus influenzae and Moraxalla catarrhalis. Streptococcus pyogenes, Haemophilus influenzae and Moraxalla catarrhalis. These bacterial species are associated with approx. 90% of urinary tract infections and with a high percentage of other severe infections. The analytic method may also be used to evaluate a bacterial resistance to beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-OCT-1991 (first entry)
Sequence encoding Serratia phospholipase and promoter.
Phospholipids; fatty acids; pNU121; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 37.00 Length: 12
Ratio: 3.700 Gaps: 0
Percent Similarity: 83.333 Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TyrArgLeuAlaIleArgArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag- a
216. .1175
/*tag- b
/note- "Claim 23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: T28565 from: 1
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ID N60877 standard; DNA; 1400 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 A;
                                                                     (ROYP/) ROY P H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: N_Geneseq_36:N60877
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/*tag=
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DK-005000.
DK-006060.
WO-DK0051.
DK-000097.
12-SEP-1994; US-304732.
(BERG/) BERGERON M G.
(OUEL/) OUELLETTE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-36 x T28565
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09-MAY-1985; DK-0051.

10-MAY-1985; DK-00506

09-MAY-1986; WO-DK005

09-JAN-1987; DK-00095

(BENA.) BENZON A AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
Quality:
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A single-stranded DNA (or its complementary strand or the corresp.

double-stranded DNA) which comprises one of the 7837 "GS" sequences
given in T19001-T56837 and which is able to hybridise to part of
human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
sequences were obtained from 3'-directed cDNA libraries prepared
from various human tissues; synthesis of cDNA was initiated from the
3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
untranslated sequence; sunique to a particular mRNA species, almost
all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
is constructed so as to reflect accurately the relative abundance of
different mRNAs in the particular tissue from which it was derived.
The appearance frequency of a given GS in a cDNA library can be
determined (esp. using primers and probes derived from the GS
sequences) as a means of diagnosing abnormal cell function or for
recognising different cell types.
                                                                                                                                                Disclosure; Fig 9; 66pp; English.

The gene product may be expressed by an E.coli host transformed with a plasmid encoding the phospholipase gene esp. under control of a Serratia regulatory sequence. The phospholipase product may be used to hydrolyse fatty acids from phospholipids and lipids. Sequence 1400 BP; 283 A; 420 C; 453 G; 244 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss. WO9514772-A1.
                                                                                    Producing bacterial enzyme esp. nuclease - using hybrid plasmid which contains DNA from Serratia spp. encoding extracellular
                                                                                                                                                                                                                                                                                                                                                          Quality: 37.00 Length: 11
Ratio: 3.364 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 54.545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 2058-2059; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1323 TGGCGCGTGGCGATACGCAGGGTATCCATGCGC 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: N60877 from: 1 to: 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TyrArgLeuAlaIleArgArgIleAlaLeuArg 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T26331 standard; cDNA to mRNA; 382 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-1996 (first entry)
Human gene signature HUMGS08571.
(MOLI/) MOLIN S.
Molin S. Givskov M, Riise E;
WPI: 86-318851/48.
P-PSDB: P61318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: N_Geneseq_36:T26331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matsubara K, Okubo K;
WPI; 95-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-36 x N60877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1
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12

Length:

36.00

Quality:

alignment_scores:

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New DNA contg. plant systemic acquired resistance genes - and transgenic plants contg. them, impart disease and pest resistance, a lso Arabidopsis gene promoter to control DNA transcription claim 21: Page 70: 85pp; English.

Claim 21: Page 70: 85pp; English.

Claim 21: Page 70: 85pp; English.

Chis sequence represents the DNA sequence of a maize PR-1 like gene, and sequence was isolated by screening a Bri-induced cDNA clibrary of maize. This sequence, Q99800-Q99803 and Q99805 are claimaged in recombinant/chimaeric DNA molecules of the invention. These sequences were isolated by differential screening of a cDNA library, consequences were isolated by differential screening of a cDNA library, consequences were isolated by differential screening of a cDNA library, consequence of cyclohexamide. The genes are used in the creation of transgenic plants. All of these sequences confer anti-pathogenic corporaties to transgenic plants. Transgenic expression of 2 or more of the recombinant molecules of the invention that encode anti-pathogenic corporations provides a synergistic increase in plant protection, and may calso offer protection against a wider range of pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR-1 like gene PR-1mz.
SAR; tobacco; protein-synthesis independent gene; cyclohexamide;
systemic acquired reistance response; anti-pathogen; plant protection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 9
Gaps: 0
Percent Identity: 77.778
       Gaps: 0
Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ryals JA, Uknes SJ, Ward ER;
                                                                                                                                                                                                                                                                                                                                          36 TACAGGGGTGAACTACCGGGGCTGGCCCTCAGATAT 71
                                                                                                                                                                                                                                                                                                    1 TyrArgLeuAlaIleArgArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to reverse of: Q99804 from: 1
                                                                                                                                                                                                                               to: 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: T26331 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID Q44280 standard; DNA; 1092
AC Q44280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-36 x Q99804/rev
4.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: N_Geneseq_36:099804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JAN-1995; IB0002.
13-JAN-1994; US-181271.
(CIBA ) CIBA GEIGY AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.00
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                                                                                                                       alignment_block:
US-08-653-294-36 x T26331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alexander DC, Ryal
WPI; 95-263872/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
           Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     maize; PR-1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9519443-A2.
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2789. .3328
//tag= m
//tag= n
                                                                                                               *tag= 'f'
note= "indefinite interval within intron 2"
141
                                                                                                                                                                                                                                        2261. .2677
/*tag- 1
/*tag- 1
/*note= "intron 3"
2569. .2581
/*note= "indefinite interval within intron 3"
678. .2788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79598. .3610

74tag- q

70te- "indefinite interval within intron 5"

653
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5538
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note= "site of 1 nucleotide deletion"
1076. 4088
/*tag= v
note= "indefinite interval within intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4391. .4392
//tag= y
//ote= known polymorphic site"
//tag= z
//tag= z
 **tag= c
note= "known polymorphic site"
[513. 1611
                                                                                                                                                                                                                                                                                                                                                                            *tag= 1
note= "known polymorphic site"
789. 3328
                                                                                                                                                                         g
"known polymorphic site"
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note= "known polymorphic site"
814. .3902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= t
/note= "intron 6"
1223
                                                                                    *tag= e
note= "intron 2"
925. .1937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag= p
note= "intron 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= o
/note= "exon 5"
3407. 3813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= w
/note= "exon 7"
1365. .6571
                                           /*tag= d
/note= "exon 2"
1612. .2206
                                                                                                                                                                                                                   *tag= h
note= "exon 3"
                                                                                                                                                                                                                                                                                                                                                  *tag= k
note= "exon 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag= s
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                                                                                                                                                                                                    . 2260
                                                                                                                                                                         *tag=
                                                                                                                 misc_feature
                                                                                                                                                           misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutation
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                                                                        intron
                                                                                                                                                                                                                                                  intron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Off-OCT-1996 (first entry)
Mutated BRCAl genomic sequence from sample set MSKCC family 19921.
Cancer therapy, breast and ovarian cancer predisposing gene; immunogen; antibody production; germline alteration; probe; lesion neoplasia; human; gene therapy; protein replacement therapy; protein mimetic; BRCAl; ds. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                         3401. The genes were designated lipD (Q44280) and limD (Q44281) and they code for a lipses and a lipses modulator protein, respectively. Due to the extreme GC content of the DNA, the sequence was difficult to determine (hence the "others" in the sequence). The limD start codon is positioned 3 bp downstream of the lipD stop codon. LipD and LimD were found to be homologous to LipA and LimA, respectively. In denaturation/renaturation experiments, LimA chaperone protein was
                                                                                                                                                                                                                                                                                                                                                              Prepn. of active lipase in high quantities - by subjecting to denaturation and restructuring in presence of chaperone molecule Example 10; Page 43; 78pp; English.
09-DEC-1993 (first entry)
Pseudomonas cepacia DSM 3401 lipD gene.
Lipase; LipD; lipase modulator; limD; chaperone molecule;
lipolysis; detergent; ss.
Pseudomonas cepacia.
                                                                                                                                                                                                                                                                                                           Joergensen ST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to reverse of: Q44280 from: 1
                                                                                                                                                                                                                                                                          80-DEC-1991; WO-DK0402.
NOVO ) NOVO-NORDISK AS.
Suckley CM, Diderichsen BK, Hobson A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         353 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   960 CTGGCCGTACAGCGCGCTGCACTTCGATAC 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LeuAlalleArgArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Oualifiers
256. .355
/*tag= a
.note= "axon 1"
356. .1512
/*tag= b
.note= "intron 1"
                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID T17455 standard; cDNA; 24025 BP.
AC T17455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uble to produce active LipD.
                                                                                                  /*tag= a
480
/*tag= b
481
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712. .714
/*tag= d
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US-08-653-294-36 x Q44280/rev
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4.000
90.000
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                                                                                                                                                                                                                                                                                                                       McConnell DJ;
WPI; 93-227318/28.
P-PSDB; R39396.
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Quality:
Ratio:
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			£											interval within intron 10"			.	=	=						=				Ł	
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.6677 ab		<u>.</u>	polymorphic		polymorphic		*o+io oideromation	7. J. W. L. P. W. L.	. .6	ai "known polymorphic site"	•		10"	ite inte			polymorphic	polymorphic	polymorphic		polymorphic	polymorphic	polymorphic	•	"known polymorphic	polymorphic	polymorphic	polymorphic	ax "known polymorphic	
.6677 ab	"exon 8". 9163	"intron	ad "known	ae	"known 9209	af "exon 9"	ag "Ynoun	10530	"intron				"intron .11396	al "indefir			an "known	ao "known	ap "known	aq	"known	ar "known	as "known	at		au "known p	av "known F	aw "known p	ax "known p	
6572.	/note= 6678	/"tag= /note= 6823	/*tag= /note=	9106 /*tag=		/*tag= /note=	/*tag=	9210.	/note= 9376	/*tag= /note=	10331. /*tag=	/note- 10608.	/ ray / /note= 11384.	/*tag= /note=	11598. /*tag=	11908	/*tag= /note= 11994	/*tag= /note=	/*tag= /note=	13004 /*tag=	/note- 13009	/*tag= /note= 13048	/*tag=	13238 /*tag=	/note= 13448	/*tag= /note= 13539	/*tag= /note= 13951	/*tag= /note=	/*tag= /note=	14046
		eature		eature			earnie		eature				eature			eature	pature		מסר	eature	eature	4		eature	eature	eature	eature	;	eature	eature
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OCT-1996 (first entry)

ted BRCA1 genomic sequence from PM15.

ser therapy; breast and ovarian cancer predisposing gene; immunogen;

lbody production; germline alteration; probe; lesion neoplasia; human;

therapy; protein replacement therapy; protein mimetic; BRCA1; ds.

sapiens.
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15425. 15511
/*tag= bf
/*tag= exon 12"
/*tag= bg
/*tag= bg
/*tag= bh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 24025
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Gaps: 0
Percent Identity: 63.636
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14874
/*tag- ba
/note- "known polymorphic site"
14891
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.15424
bd
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[6127. .16565
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"known polymorphic site"
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/*tag- b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag- bk
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16243
/*tag- bl
                                                                                                                                                                                               "intron 11"
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15 standard; cDNA; 24025 BP.
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:3-294-36 x T17455/rev
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14966
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/note="
15024...
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15284
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6678. 9163
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6823
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9106
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9206
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10607. 11996
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10607. 31995
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11833. 31995
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*tag- al
note- "exon 11"
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1405- ax
/note- 'known polymorphic site'
/*tag- ay
/note- 'known polymorphic site'
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//note-."known polymorphic site"
13950
/*tag- av
/note- "known polymorphic site"
14040
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note- "known polymorphic site"
1993
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ote- "known polymorphic site"
1538
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note- "known polymorphic site"
2951
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note= "known polymorphic site"
3003
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"known polymorphic site"
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3047
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note= "known polymorphic site"
3237
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note- "known polymorphic site"
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note=
3008
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1612. .2206
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//ote= "intron 2"
1925. .1937
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//ote= "indefinite interval within intron 2"
2141
                                                                                                                                                                                           misc_feature
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interval within the intron"
3814. .3902
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3903. .47.
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10608. .11597
/*tag= n at 11383-11396 represent an indefinite
Interval within the intron"
11598. .15023
- v
15024. .15424
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note= "n at 17290-17302 represent an indefinite
nteral within the intron"
.7536. .17726
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"n at 18299-18312 represent an indefinite
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interval within the intron"
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6678. 9163
"n at 1925-1937 represent an indefinite I within the intron"
                                                                                                                                                                                                                                                                                                                                                                                             3903. .4224
/*tag= m
/*teg= n at 4076-4088 represent an indefinite
Interval within the intron"
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4365. .6571
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9208. .10530
/*tag= 10531
/*tag= 10531
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15512. .15952
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       seq_documentation_block:

AC T18325,
AC T18325,
DT 05-JUN-1996 (first entry)
DT 05-JUN-1996 (first entry)
B BRCA1, human breast and ovarian cancer predisposing gene.
KW BRCA1; breast cancer; ovary cancer; predisposing gene;
KW susceptibility gene; diagnosis; prognosis; gene therapy; ds.
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3.600 Gaps: 0
90.909 Percent Identity: 63.636
 14873
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14890
/*tag- ba
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14965
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note= "known polymorphic site"
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.15510
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16369. .16381
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1. :55

1. :55

1. :55

56. :155

/*tag- c

1533 .1611

/*tag- 2

/*tag- 2

/*tag- 2

/*tag- 2
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15283
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/note= "known polymc
15424. 15510
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US-08-653-294-36 x T17515/rev
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Quality:
Ratio:
Percent Similarity:
     misc_feature
                                                         misc_feature
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																,	11 0 636			24026						predisposing gene; immunogen; probe; lesion neoplasia; human;	CEIN MIMELIC; BRCAI; GS.				
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	misc_feature	FT misc_feature FT FT	misc_feature	misc_feature	misc_feature		misc_feature	misc_feature	miso feature	0 Table 1 Tabl	misc_feature	misc_feature		FT misc_feature	misc_feature	alignment_scores:	Quality: Ratio: Percent Similarity:		×;	യ	2 ArgLeuAlaile 	seq_name: N_Geneseq_36:T17512	seq_documentation_blo				OS Homo sapiens. FH Kev	exon	intron		FT MISC_ICACUIC
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al within the intron" .18787	41 19298 aq	• 🖫 :	. ah . 20190		.20267 aj	.21094 ak	/note= "n at 20/6/-20/79 represent an indefinite interval within the intron" 2010s 2113s			within the intron"	an .22233				aq "n at 22567-22579 represent an indefinite al within the intron"	. 22906	ar .23287 as	"n at 23050-23062 represent an indefinite al within the intron"		. 23098 au	"n at 23580-23592 represent an indefinite al within the intron" .24026	av .	aw "polymorphic site"	ax		ay "polymorphic site"	az "polymorphic site"	ba		bb "polymorphic site"	bc "polymorphic site"
interval 184171		/note= "r interval 192991		/note= interva	20191. /*tag-	20268. /*tag-	/note= interva 21095		/*tag=	interval 215842	/*tag= 21668.	/*tag= /note=	interval 22234	/*tag= 22289.	/*tag= /note= interva	228332	/*tag= a 229072 /*tag= a	/note= interva		3349. *tag=	/note= "n interval 236992	/*tag= 2725				/*tag= /note= 4392	/*tag- /note-	6823 /*tag=		/*tag= /note= 0207	I 1

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misc feature		misc_feature	exon		misc_reature	intron	misc_feature		exon	intron	misc_feature	exon		misc_feature	misc_feature		misc_teature	misc_feature	mico fonturo	ייידאר_זפטרתיפ	misc_feature	misc_feature	•	misc_feature	misc_feature	9	misc_reature	misc_feature	misc feature		misc_feature	misc_feature
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d exon 2		"intron	f "indefinite	p.	"Known 2260	- "exon 3	"intron	.2581 . j	. "indefi .2788	exon 4	r 1 r known	.3328 y= m g= "intron	3075 g= n		J= 0	3813 3= p	3610	g= q e= "indefinite	J= r		E 4	g= t e= "intron	4088 9- u	- 4	9= v e= "exon 7		. ₹.	"known	0 6	2	.6677	aa "exon 9163 ab
/*tag= d /note= "e	•		. pu ()	2141 /*tag=	/note= 2207	/".cay= /note= 2261	/*tag=	2569/*tag=	/note= 2678.	/*tag= /note= 2725	/*tag= /note=	/*tag= /*ote=	3063/*tag=	/note- 3329.	/*tag= /note=	3407 /*tac	3598	/not	3653 /*tag= /pote=	3814.	/note= 3903.	/*tag= /note=	4076. /*tag=	/note=	/*tag= /note=	4365. /*tag=	4391.	/rtag= /note=	/*tag= /note=	6538 /*tag=	/note= 6572	/*tag= /note= 6678

us-08-653-294-36.rng

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note= "exon 4"
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note= "indefinite interval within intron 2"
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"indefinite interval within intron 4"
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note= "indefinite interval within intron 5"
653
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538
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note= "known polymorphic site"
602. .4614
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"known polymorphic site"
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/note= "intron 3"
2569. .2581
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/note= "exon 8"
6678. .9163
/*tag- ab
/note- "intron 8"
                                               "tag= e
note= "intron 2"
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note= "intron 5"
598. .3610
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.2677
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* "exon 2" .2206
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note= '
329. .3
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note=
407
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Mutated BRCA1 genomic sequence from PM05.
Cancer therapy, breast and ovarian cancer predisposing gene; immunogen, antibody production; germline alteration; probe; lesion neoplasia; human; gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.
Homo saplens.
                                                                                                                                                                                                                                               to A mutation at known polymorphic site"
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"indefinite interval within intron 12"
.16126
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Percent Identity: 63.636
                                                                                     bb
"known polymorphic site"
.15424
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16370. .16382
/*tag= bl
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.15659
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/*tag= a
/note= 'exon 1"
356. 1512
/*tag= b
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ID T17513 standard; cDNA; 24026 BP.
AC T17513;
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3.600
90.909
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US-08-653-294-36 x T17512/rev
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14891
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note=
5647.
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note=
5953.
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Mutated BRCA1 genomic sequence from PM11.

Mutated BRCA1 genomic sequence from PM11.

Cancer therapy; breast and ovarian cancer predisposing gene; immunogen; antibody production; germline alteration; probe; lesion neoplasia; human; gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.
                                                                                                                                                                                                                               bg
"indefinite interval within intron 12"
.16126
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 11
Gaps: 0
Percent Identity: 63.636
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fnote= "known polymorphic site"
1513. 1611
*tag- d
/note- "exon 2"
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"known polymorphic site"
.15424
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"known polymorphic site"
.16565
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//note- "known polymorphic site"
//4tag- bl
 ba
"known polymorphic site"
                                                                                                                            "known polymorphic site".
15511
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256. .355
/*tag= ax
/note= "exon 1"
356. .1512
/*tag= b
/note= "intron 1"
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ID T17514 standard; cDNa; 24026 BP.

AC T17514;

DT 04-0CT-1996 (first entry)

DE Mutated BRAN1 genomic sequence from
KW cancer therapy; breast and ovarian
KW antibody production.
                                                                                                                                                                                        *tag= bf
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5647. .15659
                                                                                       "intron 11"
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15512. .15952
/*tag= bf
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6243
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US-08-653-294-36 x I17513/rev
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3.600
90.909
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5284
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15425.
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    Quality:
    Ratio:
    Percent Similarity:
                          misc_feature
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/note= "known polymorphic site"
/note= "known polymorphic site"
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/note= "exon 9"
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// Atag= ac
// Atag= "known polymorphic site"
9106
                                                                                                                         *tag= af
note= "known polymorphic site"
210. .10530
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"known polymorphic site"
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note= "known polymorphic site"
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note= '
0531.
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*tag=
note= '
1384. .
*tag=
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10te=
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to: 24026

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FT	E E E		· Fr	FE	FI	FF	F F F	16	F	FF	FT	FI	EE	FT	FI	F F 1	FF	1 E	FT	FF	FT	FT	FT	L L L L	FI	E E	FF	FF	- E- E	1 E E	144	FT	FI
	1937 f		/*tag= for // // // // // // // // // // // // //		22612677 /*tag= 1	/note= "intron 3" 25692581	/*tag= j /octe= "indefinite interval within intron 3" /778 -7188	/tag= k	_	# m	/*tag= m /note= "intron 4"	.3075 n	<pre>/note= "indefinite interval within intron 4" 33293406</pre>	/*tag= o /note= "exon 5"	3813 P	/note= "intron 5" 3598. 3610	<pre>/*tag= q /*cote= "indefinite interval within intron 5" .ce></pre>	/*tag= r	٠ m.	/*tag= s /note= "exon 6"	.4224 t	/note= "intron 6" 40764088	<pre>/*tag= u /note= "indefinite interval within intron 6"</pre>	42254364 /*trag= v //notes= excn 7"	.6571	/note= "intron 7" 43914392		46024614 /*tag= y /*tag= y	זוותפוזוורפ דוורפוימו אורווו דוורוסו	/ tag = 2 /note="known polymorphic site" 6577	// / / / / / / / / / / / / / / / / / /	9163 ab	/note= "intron 8" 6823
FT intron FT FT	r misc_feature	FT misc_feature	FT FT FT exon		r intron	r r misc_feature	FT FT BT AYON		r misc_feature	r I intron		r misc_feature r	r F exon		r intron r	r misc_feature		r misc_ieacuie	r F exon		FT intron FT	FT FT misc_feature	FT	FT exon FT FT	FT intron	FT misc_feature		FT misc_teature FT	FT misc_feature		FT GAOL	FT intron	FT FT misc_feature

us-08-653-294-36.rng

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598. 3610
note- "indefinite interval within intron 5"
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538
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note= "indefinite interval within intron 3"
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note= "488
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ID 117516 standard; cDNA; 24026 BP.

AC 117516;

DT 04-OCT-1996 (first entry)

E Mutated BRCAl genomic sequence from PM16.

KW Cancer therapy; breast and ovarian cancer predisposing gene; immunogen;

KW gene therapy; protein replacement therapy; protein mimetic; BRCAl; ds.

CS PMOS sapiens.

CS PMOS sapiens.
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note= "indefinite interval within intron 12"
5953. .16126
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                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
Quality: 36.00 Length: 11
Ratio: 3.600 Gaps: 0
Percent Similarity: 90.909 Percent Identity: 63.636
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.15424
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US-08-653-294-36 x T17514/rev
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5425.
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misc_feature
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1598. .15023
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 "known polymorphic site"
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.10530
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"known polymorphic site"
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"known polymorphic site"
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note= "known polymorphic site"
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/note= "known po]
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2952
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3009
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4041
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                                                                                                           intron
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                                            exon
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Percent Identity: 63.636
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note- "known polymorphic site"
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                                             bd
"known polymorphic site"
.15511
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/note- "known polymorphic site"
16370, 16382
/*tag- bl
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note= "known polymorphic site"
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                                                                                                      "intron 12"
.15659
                                                                                                                                                                                                     "intron 13"
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.15952
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3.600
90.909
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note=
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Quality:
Ratio:
Percent Similarity:
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16370. 16382
/*tag* bl
bb
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.15424
                                                           bd
"known polymorphic site"
.15511
                               *tag= bc
note= "intron 11"
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.15659
                                                                                                "exon 12"
                                                                                                                                                                                      "exon 13"
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                      intron
                                                                                                            intron
                                                                               exon
                                                                                                                                                                      exon
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alignment_block: US-08-653-294-36 x T17517/rev

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AQ057253 CIT-HSP-2343E21.TF
AQ114390 CIT-HSP-2377N1.TF C
AQ870816 nbeb0041C06f CUGI R
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1. 724

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/lab_host="E. Coli XL2 Blue MRF'"
/note="Vector: pBlueScript II (SK-); Site_1: EcoRV; C. parvum (IOWA isolate) genomic DNA was hydrodynamically sheared to produce fragments having a tight size distribution between 2-4 kb by Dr. Yvonne Thorstenson of the Stanford DNA Sequencing and Technology Center
                                                                                                                                                                                           AQ851612 724 bp DNA GSS 18-OCT-1999 CpG1352B CpIOWAgDNA1 Cryptosporidium parvum genomic similar to SKB1 homologue (negative regulator of mitosis) (regulator of Shk1, a p21(Cdc42/Rac)-activated kinase (PAK)), genomic survey sequence. AQ851612. GI:6063307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dex 0811, San Francisco, CA 94143-0811, USA
Tel: 415 206 8846
Fax: 415 206 3353
Email: malaria@itsa.ucsf.edu
For Annotation Data see http://medsfgh.ucsf.edu/id/CpTags/home.html
Class: shotgun.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Cryptosporidium parvum.
Cryptosporidium parvum.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.

1 (bases 1 to 724)
Strong,W.B. and Nelson,R.G.
Cryptosporidium parvum GSS project
Cryptosporidium parvum GSS project
Onpublished (1997)
On Sep 10, 1998 this sequence version replaced g1:3553959.
Contact: Nelson, R. G.
Contact: Nelson, R. G.
Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of California, San
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AQ840156 nbxb0052C09f CUGI Rice
AQ327491 nbxb0041M03r CUGI Rice
AY132998 AV132998 Mus musculus
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AQ075626 CIT-HSP-2354C2.TR CIT-
AQ044478 CIT-HSP-323B113.TF CIT
AI110273 BSBMMFSZ44D198F BEUGIE
AQ869567 nbeb0035D05f CUGI Rice
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AI107515 GH05237.5prime GH Dros
AI135307 GH12986.5prime GH Dros
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-MODEL-frame+-pln.model -DEV=xlp
-MODEL-frame+-pln.model -DEV=xlp
-G-/cgnl_1/USFTO_spool/US08633294/runat_04022000_160700_15770/app_query.fasta.2
-G-/cgnl_1/USFTO_spool/US08633294/runat_04050-GAPEXT=4.000
-DB=SST -OFMT=fastap -SUFFIX=FST -GAPOP=6.000
-GAPEXT=7.000 -CAGAPOP=10.000 -CAGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPEDP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cd1
-LIST=A5 -DOCALIGN=200 -THR_SCORE=pct -ALIGN=15 -MODE-LOCAL
-OUTFMT=pfs -NORM=AXT -MINLEN-0 -MAXLEN-1000000 -USER-US08653294
-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1
                                                                                                             About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Ouery length: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ846844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_est6:N76762
gb_est1:Z30048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gssb_db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :8ss6_dp
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DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE JOURNAL MEDLINE COMMENT

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Indubilished (1997)
On Jun 22, 1998 this sequence version replaced gi:3247088.
Contact: Robert Strausberg, Ph.D.
Tal: (301) 496-11550
Email: Robert_Strausbergenh.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Gistribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/Librar at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Organ: Xidney; Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-1325831, 1471368-1472903 and Fatima Bonaldo. "Subtraction by Bento Scares and M. Fatima Bonaldo."
                                                                                                                                                                 A1949481 547 bp mRNA EST 06-SEP-1999 wq10g04.xl NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2470902 3',
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 547) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:2470902"
/clone_lib="NCI_CGAP_Kid12"
/tissue_type="2 pooled tumors (clear cell type)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 12
Gaps: 0
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 TACCCACTAGCCCTGAAAAGGGTAAAACTTCGATAT 254
1 TyrArgLeuAlaIleArgArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -40UP from Gibco
High quality sequence stop: 454.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B"
                                                                                                                                                                                                                                                                     AI949481.1 GI:5741713
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C
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                                                                                            seq_name: gb_est37:A1949481
                                                                                                                                                                                                                       mRNA sequence.
A1949481
                                                                                                                                               seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                      human.
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                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H72837 504 bp mRNA EST 27-0CT-1995 ys06c01.s1 Soares fetal liver spleen lNFLS Homo sapiens cDNA clone IMAGE:213984 3', mRNA sequence.
                                                                                                                                                                                                                                                                                       Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 504)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,M., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Materston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
Insert Size: 528
High quality sequence stops: 380
Source: IMAGE Consortium, LLNL
This clone is available royaity free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 528
Std Error: 0.00
Seq primer: promega -21ml.3
High quality sequence stop: 380.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On May 8, 1995 this sequence version replaced gi:799648. Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:213984"
/clone_lib="Soares fetal liver spleen lNFLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 12
Gaps: 0
Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="GDB:3779288"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="male"
                                                                                                                                                                                        H72837.1 GI:1044653
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US-08-653-294-36 x H72837/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.000
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                                                                     seq_documentation_block:
LOCUS H72837
                       seq_name: gb_est5:H72837
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Percent Similarity:
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                                                                                                                                                                                                                                                 human.
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source

FEATURES

212 t

to: 504

to reverse of: H72837 from: 1

Align seg 1/1

BASE COUNT

ORIGIN

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T 3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into RNA browided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
LOCUS AQ137850 461 bp DNA GSS 24-SEP-1998
LOCUS AQ137850 WF CIT Approved Human Genomic Sperm Library D Homo saptens: genomic clone plate=3058 Col-18 Row=F, genomic survey
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fat: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:697495
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 352.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 461)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman, Reller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 10 Gaps: 0 Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 CTCGCGGTGCGTAGGGTCAGGCTGAGGTAT 214
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AQ137850
AQ137850.1 GI:3528503
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116 c
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US-08-653-294-36 x AA983105
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Percent Similarity:
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ORIGIN
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                       FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS AA993105 429 bp mRNA EST 27-MAY-1998
DEFINITION ua35b12.r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone
IMAGE:1348703 5', mRNA sequence.
ACCESSION AA983105.1 GI:3160383
                                        seq_documentation_block:
LOCUS L33574 325 bp mRNA EST 08-OCT-1996
DEFINITION BNAESTF350 Mustard flower buds Brassica rapa cDNA clone F0350, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 429)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                               1 (bases 1 to 325)
Lim,C.O., Kim,H.Y., Kim,M.G., Lee,S.I., Chung,W.S., Park,S.H., Hwang,I. and Cho,M.J.
Expressed sequence tags of Chinese cabbage flower bud cDNA
Plant Physiol. 111 (2), 577-588 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Apr 13, 1998 this sequence version replaced g1:2958638.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps: 0
Percent Identity: 63.636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Mustard flower buds"
/note="Devel_stage = flower bud
115 c 58 g 82 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Lim,C.O., Hwang,I. and Cho,M.J.
Email: pmbbrc@nongae.gsnu.ac.kr.
Location/Qualifiers
1. .325
/organism="Brassica rapa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="pekinensis"
/db_xref="taxon:3711"
/clone="F0350"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to reverse of: L33574
                                                                                                              sequence.
L33574
L33574.1 GI:508041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-36 x L33574/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio: 3.545
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_est21:AA983105
                                                                                                                                                                                                   Brassica rapa.
                                                                                                                                                                                                                          Brassica rapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
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      seq_name: gb_est1:L33574
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Quality:
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                                                                                                                                                    VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
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BASE COUNT ORIGIN

REFERENCE AUTHORS

MEDLINE JOURNAL

COMMENT

TITLE

FEATURES

ACCESSION

Holzman, T., Adams, M.D. and

ORGANISM

REFERENCE AUTHORS

KEYWORDS SOURCE

TITLE JOURNAL COMMENT

and

us-08-653-294-36.rst

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seq_name: gb_gss8:AQ075747
                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_est20:D25244
                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
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      ORIGIN
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakame@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonacaeee; Chlamydomonas.
I (bases 1 to 529)
Asamizu, E., Nakamura, Y., Sato, S., Fukuzawa, H. and Tabata, S.
A Large Scale Structural Analysis of cDNAs in a Unicellular Green
Alga, Chlamydomonas reinhardtii. I. Generation of 3451
Don-redundant Expressed Sequence Tags
DNA Res. (1999) In press
On May 18, 1998 this sequence version replaced gi:3137395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="CL56h04_r"
/clone_lb="Chlamydomonas reinhardtii C9"
/dev_stage="photoautotrophic growth"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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/db_xref="taxon:9606"
/clone="plate=3058 Col=18 Row=F"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
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LOCUS AV396088 529 bp mRNA EST 09-DEC-1999
DEFINITION AV396088 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii
CDNA clone CL56h04_r, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                           /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Co11 DH10B"
High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallacedu.washington.edu
Sequence Tagged Connector
Plate: 3058 row: F column: 18
Class: BAC end8
High quality sequence stop: 461.

    529
/organism="Chlamydomonas reinhardtii"

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Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 CATCGACTCACTATAAGGCGAATTCTGGCCAGGTAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
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/db_xref="taxon:3055"
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3.900
83.333
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US-08-653-294-36 x AQ137850
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Ratio:
Percent Similarity:
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Ikeda,J.
Isolation and characterization of 21 novel expressed DNA sequences
Isolation and characterization of human chromosome 4p
Genomics 22 (2), 302-312 (1994)
95104839
                                                                                                                                                                                                                                                                                                                                                                    D25244 572 bp mRNA EST 12-MAR-1998 HUMRES417B Clontech catalog #CLHL1076b Homo sapiens cDNA clone PES4-17, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Mammalla, Butheria, Prinates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 572)
1 (bases 1 to 573)
1 (shida,Y., Hadano,S., Nagayama,T., Tomiyasu,H., Wakasa,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on May 9, 1995 this sequence version replaced gi:804176.
Contact: Yoshikazu Ishidaa
Ikeda GenosPHERE project/ERATO/JRDC
Tokal University School of Medicine
Bohseidai, Isehara, Kanagawa 259-1193, Japan
Emall: shinjienga.med.u-tokai.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="RES4-17".
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/tissue_type="caudate".
/dev_stage="20-year-old adult" 18 other:
Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio: 3.900 Gaps: 0 Percent Similarity: 83.333 Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   572
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="4p15-4p16.1"
                                                                                                                                                                                                                                                 2 ArgleuAlalleArgArglleAlaLeuArg 11
                                                                                                                                                                      Align seg 1/1 to reverse of: AV396088
                                                                                                 alignment_block:
US-08-653-294-36 x AV396088/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                           D25244
D25244.1 GI:434739
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US-08-653-294-36 x D25244/rev
  Quality: 39.00
Ratio: 3.900
Percent Similarity: 100.000
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University
Unpublished (1999)
On Dec 20, 1995 this sequence version replaced gi:113566.
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 227
Fax: 650 723 8221
Email: walbot@stanford.edu
Plate: 618055 row: E column: 09.
 {\tt Walbot,V.}\\ {\tt Maize\ ESTs\ from\ various\ cDNA\ libraries\ sequenced\ at\ Stanford}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B74688.1 GI:2770375
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Ratio: 3.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AI943775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-36 x AI943775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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COMMENT
AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                  L Unpublished (1998)
Other_GSSs: CIT-HSP-2354G2.TF
Contact: Mark Adams
Contact: Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: medadams@tigr.org
Email: medadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                 Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
epophyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
Poaceae; Zea.
1 (bases 1 to 408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI943775 408 bp mRNA EST 09-AUG-1999
618045E09.x1 618 - Inbred Tassel CDNA Library Zea mays CDNA, mRNA
                                                                                                                                          Eukaryota. Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 360)

Adans, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
AQ075747 360 bp DNA GSS 20-AUG-1998
CIT-HSP-2354G2.TR CIT-HSP Homo sapiens genomic clone 2354G2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 others
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Gaps: 0
Percent Identity: 72.727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo saplens"
/db_xref="taxon:9606"
/clone="2354G2"
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/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                   genomic survey sequence.
AQ075747
AQ075747.1 GI:3437403
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US-08-653-294-36 x AQ075747/rev
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LOCUS AI943775
                                                                                                                                    Homo saptens
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Ratio:
Percent Similarity:
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Zea mays
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LOCUS
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Human:

Butherials

Butherials

Butherials

Butherials

Butherials

Butherials

Butherials

Butherials

I (bases) to 440)

I (bases) to 440)

Solden, K., Berry, K., Garnger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Building

Building

L pandom BAC End Sequence Database for Sequence-Ready Map

Building

L phopublished (1997)

Other_GSSs: CIT-HSP-2034E11.TP

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200

Email: maddams@tigr.org

Clones are available from Research Genetics (Info@resgen.com). BAC end Search/bac_end_search.html
/organism="Zea mays"
/cultivar="Ohio43"
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/lab_host="XxOLR"
/note="Organ: tassel; Vector: pAD-GAL4-2.1 (Hybrizap);
Inbred tassel library from Schmidt lab"
120 c 136 g 72 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 10
Gaps: 0
Percent Identity: 70.000
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1 others

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us-08-653-294-36.rst

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to reverse of: AA802286 from: 1
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US-08-653-294-36 x AA802286/rev
 81
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US-08-653-294-36 x AQ122064
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 455)
Mahalras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A0122064 455 bp DNA GSS 22-SEP-1998 HS_3077_B2_C10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3077 Col=20 Row=F, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone=lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                 1. .440
/organism="Homo saplens"
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/clone="2034511"
/clone="2034511"
/sax="Male"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
Vol Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
                                                                                                                                                                                                                                                                                                                            38.00 Length: 12
4.222 Gaps: 0
75.000 Percent Identity: 66.667
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Plate: 3077 row: F column: 20
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AQ122064.1 GI:3499230
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 Seq primer: M13-21
Class: BAC ends.
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LOCUS A0122064
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/note-"Organ: ovary; Vector: BlueScript SK; Site_1: EcoRI; Site_2: XhOI; Constructed using Stratagene ZAP-cDNA Synthesis Kit. Oligo dT-primed and directionally cloned at EcoRI and XhOI in BlueScript SK(+/-)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Drosophila melanogaster"
/db_xref="teaxon:7227"
/clone="GW0411"
/clone_llb="GW Drosophila melanogaster ovary BlueScript"
                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS AA802286 561 bp mRNA EST 25-NOV-1998
DEFINITION GM04141.5prime GM Drosophila melanogaster ovary BlueScript
Drosophila melanogaster cDNA clone GM04141 5prime, mRNA sequence.
ACCESSION AA802286
VERSION AA802286
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/lab_host="SOLR"
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|Gaps: 0
|Percent Identity: 80.000
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Gaps: 0
Percent Identity: 58.333
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                                                                               Quality: 38.00
Ratio: 3.800
Percent Similarity: 100.000
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to: 561

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LOCUS AI405570 572 bp mRNA EST 08-FEB-1999
DEFINITION GH25611.5prime GH Drosophila melanogaster head pOT2 Drosophila ACCESSION AI405570 GI:4248657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block: 573 bp mRNA EST 08-FEB-1999 LOCUS A1402268.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster coNA clone GH22268 5prime, mRNA sequence.
                                                                                                                                                                                                                fruit fly.

Drosophila melanogaster

Bukaryota; Metrazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryota; Metrazoa; Arthropoda; Tracheata; Brachycera;

Bressourpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 572)

1 (bases 1 to 572)

Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C.,

Brokstein, P., Lewis, S. and Rubin, G.M.

BOGP/HHMI Drosophila EST Project

Unpublished (1997)

On May 7, 1998 this sequence version replaced g1:3118953.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence AC005707; hit genomic sequence AC006089
Plate: 256 row: A column: 11
High quality sequence stop: 450.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps: 0
Percent Identity: 58.333
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                                                                                                                                                                                                                                                                                                                                                                                                                           G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
                 Align seg 1/1 to reverse of: AI405570 from: 1
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US-08-653-294-36 x AI405570/rev
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us-08-653-294-37.rag

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

February 8, 2000, 04:05:45; Search time 133.56 Seconds (without alignments) 1.773 Million cell updates/sec

US-08-653-294-37 51 1 RVDLRTLRGY 10

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

188963 seqs, 23686106 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

summaries Post-processing: Minimum Match 0% Listing first 45

A_Geneseq_36:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

Sign		Description	2	T-cell modulating	Human HLA-A2-(62-8	-	.1 61-84	61-84 1m	e fr	HLA-A2 CTL modulat	60-84.	Chimeric HLA-A2.1/	HLA epitope. HIV G	Peptide fragment o	HLA-Bw46 CTL modul	HLA-Bw46.60-84. Co	HLA-alpha-1. Use o	CP-1.	HLA-C exon Cb-2. H	O	Peptide fragment o	modulatin	. domain o	of cell	MHC class I-derive	Peptide fragment o	T-cell modulating	Human MHC 1 alpha	A. mediterranei ri	H2Kb 75-83 1mmunog	Human MHC 1 alpha	modu	Glucose transport		Н	מ
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SUM			P80911	51	R71439	144	R84876	84875	11222	33074	R95420	58385	44112	41206	33072	95418	71629	12465	12466	07033	11211	07521	90513	38111	59618	11210	07516	71431	52846	34869	R71430)7524	942	7	142	142
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Gaps

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Length 274; 1; Indels

DB 1;

Score 45; DB Pred. No. 0.1; 0; Mismatches

88.2%; 90.0%;

Query Match
Best Local Similarity 90.0
Matches 9; Conservative

1 RVDLRTLRGY 10

à g W07517 standard; peptide; 10 AA.
W07517 standard; peptide; 10 AA.
04-AUG-1997 (first entry)
T-cell modulating peptide #6.
T-cell modulator; autoimmune disease; tissue destruction; alphal-domain; mammal; major histocompatability complex; MRC class I; antigen; perforin; insulin-dependent diabetes mellitus; multiple sclerosis; inflammation; rheumatoid arthritis; psoriasis; pemphigus vulgaris; Sjogren's disease; thyroid disease; Hashimoto's thyroiditis; myasthenia gravis; granzyme; autologous target cell; cytokine release; T cell activation; therapy.

Human MHC 1 alpha MHC peptide repeat MHC peptide repeat Glucose transport Peptide membrane b Human MHC 1 alpha Human MHC 1 alpha MHC Class I-derive MHC I peptide DK-(Human MHC 1 alpha MHC Peptide DK-(Human MHC 1 alpha MHC Peptide having	NTS				onstitute the aipna-i, ile	alpha-1, alpha-2 and alpha-3.											ä	used for modulating cytotoxic T-lymphocyte activity in e.g.		a total of 23 HLA-A, B, C sequences.	protein sequences in the three extrecellular domains (alpha-1,	aipna-2 and aipna-3) are snown. Ine example concerned the effect of peptides from different HLA-A2 epitopes on cytolysis of target cells by		
ww407479000	ALIGNMENTS			ا ب	olec jolec	ains	S	9	nor far	region"	region"					Ü	mooo.	oudu.	ž.	from	ext	tope c	•	
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177 177 177 177 177 177 177 177 177 177			protein;	(first entry)	a class I HLA molecule	epitopes; extracellular domains plens.	Location/Qualifiers	I90	91180	note-"alpha	181272 /note="alpha-3	; }		46.			₽.	cyto	100	ce 1	s in	ent	different specificities	
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% % % % % % % % % % % % % % % % % % %		11 1	P80911:	18-SEP-1990	alpha-3 regions	HLA-A2 Homo sa	Key	region	region		region	WO8805784-A	11-AUG-1988.	30-JAN-	(STRD) Leland Stanford	Krensky AM, Parham P, WPI: 88-235147/33.	New peptide corresp.	used it	transplants of auto-immune diseases Example 9: Fig 4: 60pp: English.	The concensus sequence is derived from a	The pro	arpna-2 and arpna-3) are peptides from different H	CTL of	Sednence
		RESULT P80911	a S	占	38	N S	H.H.	H E	FI	FT	H H		5 2 5 6			PI DR	E.	E E	P. S.	ខ	ខ្ល	38	88	Š

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7 RVDLGTLRGY 16
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                                                                                                                                                                                              Witi, 90-30a Hulvill.

Treatment of auto-immune disease by admin. of peptide(s) corresp. to major histocompatibility complex antigens - esp. for delaying onset of cilinical symptoms of insulin dependent diabetes by modulating T cell madiated attack on target cells

Claim 7: Page 20; 24pp; English.

Worst Start Start Sepresent T-cell modulating peptides that can be used in the method of the invention. These sequences are based on a portion of the major histocompatability complex (MFC) class I antigen (see WOYSIO). The method is for affecting the course of an autoimmune disease involving T-cell mediated destruction of tissue in mammals. These involving T-cell mediated destruction of tissue in mammals. These course of specially to treat insulin-dependent diabetes mellitus, preferably being administered during the pre-clinical stage to delay onset of the disease. Other diseases that can be treated are multius, preferably being administered during the pre-clinical stage to delay onset of the peptides modulate T-cell mediated attack on autologous gravis, etc. The peptides modulate T-cell mediated attack on autologous cytokines, perforins, granzymes etc. associated with T cell activation. Sequence 10 AA;
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R71439-R71443 are human major histocompatibility complex class 1 (MHC 1) alpha 1 domain and HLA derived peptides and fusion peptides. They were used to modulate interactions between MHC 1/HLA and cell surface receptors. Via competitive inhibition the peptides diminish the receptors response, this feature may be useful for the treatment of neoplasias, lupus erythematosus and arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human HIA-A2-(62-85) antigen derived peptide.
Human HIA-A2-(62-85) antigen derived peptide; cell receptor;
interaction modulation; arthritis; neoplasias; lupus erythematosus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 1; Length 10;
Pred. No. 0.0047;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R71439 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                        14-NOV-1996.
05-APR-1996; U04710.
12-MAY-1995; US-440504.
(SANG-) SANGSTAT MEDICAL CORP.
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90.0%;
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12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA.
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                  Buelow R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT TREESULT TREES
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A claimed cell-mediated fimune (CMI)-specific immunogenic compsn. comprises a conjugate of a primary antigen bearing a primary epitope, with an immunomodulatory peptide (IP), i.e. the present peptide. The Promprises an allopeptide molety of at least 5 anino acids, whose sequence corresponds to a polymorphic region of a MHC encoded polymorphic Class I or II antigen. The compsn. can be used to ellcit a CMI-specific response which is prophylactic, or therapeutic for, e.g. microbial and viral infections, parasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          surface receptors. Via competitive inhibition the peptides diminish the receptors response, this feature may be useful for the treatment of neoplasias, lupus erythematosus and arthritis.

Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; Page 45; 103pp; English. R71439-R7143 are human major histocompatibility complex class 1 R71439-R7143 are human major derived peptides and fusion peptides. (MMC 1) alpha 1 domain and HLA derived peptides and fusion peptides. They were used to modulate interactions between MMC 1/HLA and cell
                                                                           Human MHC 1 and HLA fusion peptide Dk-(69-76)HLA-A2-(77-85).
Major histocompatibility complex class 1; MHC 1; ceel receptor; alpha 1 domain; fusion peptide Dk-(69-76)HLA-A2-(77-85); interaction modulation; arthritis; neoplasias; lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MaY-1996 (first entry)
HIA AW68.1 61-84 immunogenic peptide.
Antigen; epitope; cell mediated; immune specific; cancer;
Infection; infestation; mucin-1; MUC-1; tumour; HLA AW68.1 61-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New cell-mediated immune-specific immunogenic compsns. - used in prophylaxis and treatment of cancer, microbial infections, viral infections and parasitic infestations

Example 1; Page 62; 141pp; English.
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                                                                                                                                                                                                                                                                                                                                    Goldstein A, Goodenow RS, Olsson L;
WPI: 95-098577713.
Regulating cell surface receptor response - by modulating
Interaction between MHC class I antigen and the cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressing tumour cel
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Pred. No. 0.0083;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Koganty RR, Longenecker BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R84876 standard; peptide; 24 AA.
R71441 standard; peptide; 17 AA R71441;
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90.0%;
                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 86.3
Best Local Similarity 90.0
Matches 9; Conservative
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12-APR-1994; US-229606.
(BIOM-) BIOMIRA INC.
                                                                                                                                                                                                                                                                                                              (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                           12-AUG-1994; U09189.
12-AUG-1993; US-105416.
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WPI; 95-373528/48.
                                                                                                                                                                                  Homo sapiens.
WO9505189-A.
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Gaps

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Score 44; DB 1; Length 17; Pred. No. 0.0083; 0; Mismatches 1; Indels

86.3%; 90.0%;

Query Match 86.3 Best Local Similarity 90.0 Matches 9; Conservative

1 RVDLRTLRGY 10

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Example 13; Page 32; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HIA-A2. These sequences can be used to extend the period of The peptides are administered to a patient from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLA-A2 CTL modulating peptide (A2.1.60-84). Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-A2.
New peptide(s) based on Class I HLA antigen domains - used for modulating cytocoxic T-lymphocyte activity towards targets brample 13: Page 39; 61pp: English.

The peptide is used to modulate cytocoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL infection. The peptide can also be used for identifying CTLs activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removang subsets of CTLs from a T-cell composition. This peptide is derived from the HLA-A2.1 antigen and corresponds to the amino acid positions 60-84 of that antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clayberger C, Krensky AM, Parham P;
WPI; 95-538882/46.
Extension of acceptance period of transplants from MHC unmatched
donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                              86.3%; Score 44; DB 1; Length 25; llarity 90.0%; Pred. No. 0.013; Conservative 0; Mismatches 1; Indels
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Pred. No. 0.013;
); Mismatches
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05-APR-1995; U04349.
05-APR-1994; UG-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R83074 standard; peptide; 25 AA.
R83074;
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R95420;
12-NOV-1996 (first entry)
HLA-A2.1.60-84.
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90.0%;
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 9; Conserv
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AC R9
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Ding L, Koganty RR, Longenecker BM, Reddish MA;

WPI: 95-373528/48.

WPI: 95-373528/48.

The We cell-mediated immune-specific immunogenic compsns. - used in prophylaxis and treatment of cancer, microbial infections, viral infections and parasitic infectations.

Example 1: Page 62: 141pp; English.

Scample 1: Page 62: 141pp; English.

A claimed cell-mediated fumune (CMI) *specific immunogenic compsn.

Comprises a conjugate of a primary antigen bearing a primary epitope, with an immunomodulatory peptide (IP), i.e. the present peptide.

Comprises an allopeptide moiety of at least 5 amino acids, whose sequence corresponds to a polymorphic region of a MHC encoded polymorphic class I or II antigen. The compsn. can be conceded polymorphic class I or II antigen. The compsn can be therefore the present class is microbial and viral infections, parasitic infestations and cancer, partic. MUC-1 expressing tumour cells when the present peptide is the IP, and a MUC-1 epitope is the
                                                                                                                                      Gaps
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Peptide fragment of HLA-A2.1 antigen.
Human leukocyte antigen. HLA; peptide; transplantation; neoplasia;
parasitic disease; oyfotoxic T lymphocyte; modulation.
                                                                                                                                                                                                                                                                                                                                                                             30-MAY-1996 (first entry)
HLA A2.1 61-84 immunogenic peptide.
Antigen: epitope; cell mediated; immune specific; cancer;
infection; infestation; mucin-1; MUC-1; tumour; HLA A2.1 61-84;
immunogenic peptide.
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                                                                                          Length 24;
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                                                                                        Score 44; DB 1;
Pred. No. 0.012;
); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R41222 standard; peptide; 25 AA
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90.0%;
                                                                                        86.3%;
                                                                                        Query Match 86.3
Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-001-1995.
12-APR-1995; U04540.
12-APR-1994; US-229606.
(BIOM-) BIOMIRA INC.
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                1 RVDLRTLRGY 10
                                                                                                                                                                                                     1 RVDLRTLRGY 10
    primary epitope.
Sequence 24 AA;
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WO9317699-A.
                                                                                                                                                                                                                                                                                                                                                            R84875;
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Length 25; 1; Indels

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While Still 1940a. The companies of the modern of cris.

Tompsons. comprising lymphoid surface membrane proteins - which may may compans. Comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of Cris.

Example 7 9: 29pp. English.

Example 9: 29pp. English.

Example 7 160-84. These sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein p74 from a T-cell surface membrane protein p74 confidence of the special protein p74 confidence of the passed through an affinity column containing a covalently bound HIA-B2702 paliadromic peptide.

Compositions comprising the extracellular fragment of p74 combined with the extracellular fragment of p74 condidate compounds can be screened for their effect on the cytolytic activity of treatment of for their effect on the cytolytic activity of determining the mount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74 in an amount sufficient to compete cuit the p74 for the binding of the p74 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
HLA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; T-cell lysate; membrane proteih; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytocxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric HLA-A2.1/beta-2_microglobulin protein.
Antigen: major histocompatibility complex; MfG; lymphocyte; detection; immobilisation; cytotoxic T-cell; tumour; leukaemia; lymphoma; viral infection; chimeric; beta-2 microglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 0.013;
0; Mismatches 1; Indels
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313. .412
/note="from human beta-2 microglobulin"
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21-MAY-1995; US-551925.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
(INRM ) INST PASTEUR.
Abastado J, Kourilsky P, Langlade-Demoyen P, Lone Y; WPI; 98-018653/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .302
/note= "from HLA-A2.1 protein"
                                                                                                                18-MAY-1995.
10-NOY-1994, U12985.
10-NOY-1993, US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.3%;
90.0%;
                                                                                                                                                                                                Krensky AM;
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14-OCT-1998 (first entry)
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                WO9513288-A1.
                                                                                                                                                                                              Clayberger C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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W68385
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Percetion, purification and elimination of antigen-specific lymphocytes - for producing cytotoxic T cells for immuno-therapy of ancers and viral infection.

Example 2: Fig 10: 222pp; French.

Example 2: Fig 10: 222pp; French.

Coetween antigen-specific lymphocytes comprises forming a complex complex of antigen-specific lymphocytes comprises forming a complex complemently produced major histocompatibility complex (MHC) molecules, immobilising the complex and binding samples containing the antigen-specific lymphocytes. Expression of the MHC molecule in a cell is detected by antibodies against the MHC molecule or by an antibody to a chimeric MHC-marker protein, e.g. an MHC/Deta-2-microglobulin chimeric comprises the first 3 domains of the HLA-A2.1 heavy chain linked to human beta-2 microglobulin via a flexible linker. The method is also used to beta-2 microglobulin via a flexible linker. The method is also used to specific killing of tumour cells (solid tumours, leukaemia or lymphoma) by injection into a human or animal, but also for treating viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The patent claims epitopes of the HIV gp160 protein which are immunologically homologous to at least one epitope of the HLA immunologically homologous to at least one epitope of the HLA.

The patent family, preferably the HLA class 1 protein heavy chains. The present sequence is a region of the heavy chain alpha-1 domain, cw4 allele, to which the epitopes are homologous. In particular, the epitopes are homologous to the sequences TQKKRQAQ and NLRKLRGYY.

The identification of HLV gp160 epitopes homologous to HLA epitopes can be used to develop agents for vaccines and immunodiagnosis of HLY infection. The HLY phomologous HLA regions are able to induce anti-HLA autoantibodies and act as superantigens during the infection course, leading to a gradual and selective loss of certain T receptor families.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIA epitope.
Epitope: immuno-homologue; HLA; heavy chain; alpha-1 domain; allele;
cw4; superantigen; immunodiagnostic; AIDS; HIV; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI: 93-386478/48.
HIV GP160 epitope(s) immunologically homologous to HLA -develop agents for immuno-diagnosis and vaccines for HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAY-1993; ITO049.
11-MAY-1992; IT-RM0350.
(SANR-) FOND CENT SAN ROMANELLO DEL MONTE TABOR.
(SUPE-) INST SUPERIORE DI SANITA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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/label- epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.3%;
90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RVDLRTLRGY 10
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N-PSDB; V30457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection
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25-FEP-1993: U01758.
26-FEP-1993: U01758.
27-FEP-1993: U01758.
28-FEP-1993: US-844716.
29-MAR-1992: US-844716.
21 Clayberger CA, Krensky AM;
21 Clayberger CA, Krensky AM;
21 Clayberger CA, Krensky AM;
22 Clayberger CA, Krensky AM;
23 (1914) 24.
26 Talm 91 Page 53; 61pp; English.
27 Todulating cytcoxic T-lymphocyte activity towards targets
28 Claim 91 Page 53; 61pp; English.
28 Claim 91 Page 53; 61pp; English.
29 Claim 91 Page 53; 61pp; English.
20 Claim 91 Page 53; 61pp; English.
20 Claim 91 Page 53; 61pp; English.
21 Claim 91 Page 53; 61pp; English.
22 Claim 91 Page 53; 61pp; English.
23 Claim 91 Page 53; 61pp; English.
24 Claim 92 Page 53; 61pp; English.
25 Claim 92 Page 53; 61pp; English.
26 Claim 92 Page 53; 61pp;
27 Claim 92 Page 53; 61pp;
28 Claim 92 Page 53; 61pp;
29 Claim 92 Page 53; 61pp;
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21 Claim 92 Page 53; 61pp;
22 Claim 92 Page 53; 61pp;
23 Claim 92 Page 53; 61pp;
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25 Claim 92 Page 53; 61pp;
26 Claim 92 Page 53; 61pp;
27 Claim 92 Page 53; 61pp;
28 Claim 92 Page 53; 61pp;
29 Claim 92 Page 53; 61pp;
20 Claim 92 Page 54; 61pp;
20 Claim 92 Page 54;
20 Claim 92 Page 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLA-Bw46 CTL modulating peptide (Bw46.60-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-Bw46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 13; Page 32; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequent corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HLA-BW46. These sequences can be used to extend the period of
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                   15-MAR-1994 (first entry)
Peptide fragment of Class I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic T lymphocyte; modulation.
No9317699-A.
16-con-10-1
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recipient
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Score 40; DB 1; Length 22;
Pred. No. 0.071;
1; Mismatches 1; Indels
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Pred. No. 0.081;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Extension of acceptance period of transplants from MHC donor hosts - using Class I B75-84 MHC antigen of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R83072 standard; peptide; 25 AA.
78.4%;
80.0%;
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80.0%;
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Best Local Similarity 80.0.
                      Best_Local Similarity 80.0 Matches 8; Conservative
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                                                                                  1 RVDLRTLRGY 10
                                                                                                            12 RVNLRKLRGY 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
WO9526979-A1.
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    Query Match
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R41206
ID R4:
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While String lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example Page 9, 29pp. English.

Example Page 9, 20pp. English.

Example P
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acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIA-Bw46.60-64
HIA: PAY: alphal-helix; human-leucocyte-associated antigen; inhibitor;
HIA: PAY: alphal-helix; human-leucocyte-associated antigen; Hsc70; APC;
T-cell 1, sate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CIL; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 0.081;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ä
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80.0%;
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80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
Thes 8; Conserve
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                                                                                                                                                                                                                                                                                                                     25 AA;
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Disclosure; Page 7; 26pp; English.
Antibodies able to detect both epitopes of HIV gp160 and epitopes of beta-2-microglobulin free Class I HLA free heavy chains are pref.
prepd. using gp120-C5 and HLA alpha-1 peptides (R71628-29) which respectively include peptides HIV-26 and HLA-22.
                                                                            HIV; gp120; HLA; beta-2-microglobulin; HLA; passive immunization human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of antibodies reactive with HIV and HLA molecules - for detection of HIV infection and for providing passive immunity against HIV infection.
                                                                                                                                                                                                                                                                                                                     16-SEP-1994; ITO146.
10-SEP-1993; IT-RM0613.
SANR-) FOND CENT SAN RAFFAELE DEL MONTE TABOR.
                                                                                                                                                                                          Location/Qualifiers
16. .37
/label- HLA-22
                            R71629 standard; peptide; 45 AA.
                                                R71629;
21-SEP-1995 (first entry)
HLA-alpha-1.
                                                                                                                                                                                                                                                                                                                                                                                                                         95-123513/16.
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16-MAR-1995.
                                                                                                                                                                                                                         peptide
R71629
ID R7
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1 RVDLRTLRGY 10 ||:|| ||||| 27 RVNLRKLRGY 36

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Gaps

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Query Match 78.4%; Score 40; DB 1; Length 45; Best Local Similarity 80.0%; Pred. No. 0.15; Matches 8; Conservative 1; Mismatches 1; Indels

Search completed: February 8, 2000, 04:05:45 Job time: 9362 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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February 7, 2000, 18:04:42; Search time 111.22 Seconds (without alignments) 4.241 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-08-653-294-37 51 1 RVDLRTLRGY 10 Title: Perfect score: Sequence:

Scoring table:

142080 segs, 47169319 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

142080

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

pirl:* pir2:* pir3:* PIR_62:* 1: pirl: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ription	MHC class I histoc	H-2K	.A(u)	RT1.A(u) alpha cha		class I histocompa	class I	las	class I histocompa	histoc	class I	class I	class I	class I	MHC class I histoc	cell su	lass	ss I hist	class I	MHC class I histoc	ss I hist	las	н	s I hist	MHC class I histoc	class I	ss I hist	class I	class I	MHC class I protei
	QI	A35090	154459	S52367	160331	G02922	S18197	161867	B27638	JH0538	I54548	HLHU28	HLHUAW	нгниев	HLHU10	S06424	170694	I36965	S18198	148160	A45845	S03535	HLHUA2	JH0534	JH0536	137477	137482	~	JL0135	763	I84432
	DB	5	7	7	~	7	~	7	~	7	~	٦	۲	Н	Н	~	7	~	~	~	~	ď	П	~	~	~	~	(1	~	~	7
	Length	371	243	344	344	353	354	359	361	362	365	270	273	273	275	332	337	357	357	361	362	364	365	365	365	365	365	365	365	365	365
onerv	Match	100.0	\sim	90.2	90.2			•		90.2	90.2	86.3		86.3		86.3	86.3	86.3		86.3						86.3	٠	ů.	86.3	86.3	86.3
	Score	51	46	46		46	46	46		46	46	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44
Result	NO.		7	ж	4	2	G	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30

A11.2 - human HIA-AW33.1, HIA-AW	MHC class I histoc	MHC class I protei	HLA-Aw34.2 antiden	gene HLA-A-0203 pr	MHC HLA-A2.4a cha1	MHC class I histoc	gene HLA-A-0205 pr	gene HLA-A-6802 pr	MHC class I histoc	HLA-A30.3 precurso	MHC class I histoc	HLA-A*0210 - human
183063	172170	136961	137483	I38443	161857	I37542	I38442	138441	I38519	156039	138610	137470
365 2	365 2	365 2	365 2	365 2	365 2	365 2	365 2	365 2	365 2	365 2	365 2	365 2
86.3	86.3	86.3	86.3	86.3	86.3	86.3	86.3	. 86.3	86.3	86.3	86.3	86.3
4 4	44	4 4	4	44	44	44	44	44	44	44	44	44
31	M	3.4 4.5	36	37	38	36	40	41	42	43	44	. 45

ALIGNMENTS

	AESULT 1	
	A35090	
	MHC class I histocompatibility antigen RT1.A(a) (strain DA) - rat	
	C; Species: Rattus norvegicus (Norway rat)	
٠	C;Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 23-Ju1-1999	
	C;Accession: A35090	
	R;Rada, C.; Lorenzi, R.; Powis, S.J.; van den Bogaerde, J.; Parham, P.; Howard, J.C.	
	Proc. Natl. Acad. Sci. U.S.A. 87, 2167-2171, 1990	
	A; Title: Concerted evolution of class I genes in the major histocompatibility complex	
	A; Reference number: A35090; MUID:90192768	
	A; Accession: A35090	
	A; Status: preliminary	
	A; Molecule type: mRNA	
	A; Residues: 1-371 <rad></rad>	
	A; Cross-references: GB:M31018; NID:q1877415; PIDN:AAB49324.1; PID:q1877416	
	C; Superfamily: class I histocompatibility antigen; immunoglobulin homology	
	F:220-285/Domain: immunoglobulin homology <imm></imm>	

Gaps ö Length 371; Query Match 100.0%; Score 51; DB 2; Length 37 Best Local Similarity 100.0%; Pred. No. 0.0065; Matches 10; Conservative 0; Mismatches 0; Indels

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1 RVDLRTLRGY 10 a à

C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 02-Aug-1996
C; Accession: 154459
Musculus S; Davis, A.C.; Goodenow, R.S.
Immunogenetics 29, 355-357, 1988
A; Title: Sequence analysis of the C3H H-2K1-k gene: Relationship to the H-2 loci. A; Reference number: 154459, MulD: 89233303
A; Reference number: 154459
A; Accession: 154459
A; Accession: 154459
A; Accession: 154459
A; Molecule type: DNA
A; Residues: 1-243 <RES>
A; Residues: 1-243 <RES>
A; Residues: 1-243 <RES>
A; Cross-references: GB:M27134; NID:g199435; PID:g387456
C; Genetics: A; Ill2/1 MHC H-2K1-k - mouse

Gaps ö Query Match 90.2%; Score 46; DB 2; Length 243; Best Local Similarity 90.0%; Pred. No. 0.045; Matches 9; Conservative 1; Mismatches 0; Indels

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1 RVDLRTLRGY 10

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Class I histocompatibility antigen Gogo-A3 alpha chain - gorilla (fragment)
C; Species: Gorilla gorilla (gorilla)
C; Species: Gorilla gorilla (gorilla)
C; Species: Gorilla gorilla (gorilla)
C; Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Accession: S16197
R; Watkins, D.I.; Chen, Z.W.; Garber, T.L.; Hughes, A.L.; Letvin, N.L.
Immunogenetics 34, 185-191, 1991
A; Title: Segmental exchange between MHC class I genes in a higher primate: recombinat A; Reference number: S18197; MUID:91372865
A; Accession: S18197
A; Molecule type: nucleic acid
A; Residues: 1-354 <WAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross references: EMBL:X54375; NID:922889; PIDN:CAA38250.1; PID:922890 C; Superfamily: class I histocompatibility antigen; immunoglobulin homology F; 212-277/Domain: immunoglobulin homology <IMM>
                                    I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M30681; NID:9342845; PIDN:AAA88836.1; PID:9342846
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-359 <RES>
                                                                                              DB 2;
0.067;
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Pred. No. 0.068;
1; Mismatches
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Pred. No. 0.067;
0; Mismatches
                                                                                              Score 46; DB
Pred. No. 0.06
1; Mismatches
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90.0%;
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90.0%;
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Best Local Similarity 90.0.
                                                                                            Query Match 90.2
Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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91 RVNLRTLRGY 100
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91 RVDLETLRGY 100
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                A;Gene: Lero-G
C;Superfamily: class
  C; Genetics:
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C;Species: Leontopithecus rosalia (golden lion tamarin)
C;Date: 04 Sep-1997 *sequence_revision 04-Sep-1997 *text_change 23-Jul-1999
C;Accession: G02922
R;Cadavid, L.F.; Shufflebotham, C.; Ruiz, F.J.; Yeager, M.; Hughes, A.L.; Watkins, asubmitted to the EMBL Data Library, May 1996
A;Reference number: H01971
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A; Cross-references: EMBL:U59642; NID:g1389930; PIDN:AAB97485.1; PID:g1389931
                                                                                              RT1.A(u) protein alpha chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Feb-1997
                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-34 4.010.
A;Cross-references: EMBL:X82106; NID:91228090; PID:91228091
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: RT1.A(u)
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                   C; Accession: $52367
R; Joly, E.; Clarkson, C.; Howard, J.C.; Butcher, G.W. submitted to the EMBL Data Library, October 1994
A; Description: Isolation of a functional cDNA encoding the A; Reference number: $52367
A; Accession: $52367
                                                                                                                                                                                                                                                                                                                                                                                                              Score 46; DB 2;
Pred. No. 0.065;
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90.0%; Pred. No. 0.065;
ive 1; Mismatches
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
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90.0%;
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Best Local Similarity 90.00
Dest Local 9; Conservative
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96 RVNLRTLRGY 105
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Best Local Similarity
Matches 9; Conserv
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75 RVNLRTLRGY 84
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A/Gene: GDB:HLA-A
A/Cross-references: GDB:119310; OMIM:142800
A/Map position: 6p21.3-6p21.3
C/Superfamily: class I histocompatibility antigen; immunoglobulin homology
C/Seywords: duplication; glycoprotein; heterodimer; membrane protein; transplantation
F;1-90/Domain: alpha-1 <EX1>
F;91-182/Domain: alpha-2 <EX2>
F;91-182/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Homo sapiens (man)
C; Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 02-Sep-1997
C; Accession: A02187
C; Accession: A02187
E; Lopez de Castro, J.A.; Strominger, J.L.; Strong, D.M.; Orr, H.T.
Proc. Natl. Acad. Sci. U.S.A. 79, 3813-3817, 1982
A; Title: Structure of crossreactive human histocompatibility antigens HLA-A28 and HLA A; Accession: A02187
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C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     class I histocompatibility antigen HLA-A28 alpha chain - human (fragment)
                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: 1-365 <RES>
A;Residues: 1-365 <RES>
A;Cross-references: EMEL:X82669; NID:9642266; PIDN:CAA57986.1; PID:91000514
C;Genetics:
A;Gene: RT1.Alu
A;Introns: 22/1; 112/1; 204/1; 296/1; 339/1; 349/1; 365/1
C;Superfamilly: class I histocompatibility antigen; immunoglobulin homology
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RhBO J. 4, 2849-2854, 1985
A;Title: Exon shuffiling in vivo can generate novel HLA class I molecules.
A;Reference number: A91021; MUID:86055720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F)196-261/Domain: immunoglobulin nomology \text{IP}.196-261/Domain: immunoglobulin nomology \text{Immunoglobulin status experimental F}.86/Binding site: carbohydrate (Asn) (covalent) #status experimental F}.101-164,203-259/Pisulfide bonds: #status predicted
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Pred. No. 0.13;
0; Mismatches 1; Indels
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Pred. No. 0.069;
1; Mismatches (
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A;Gene: GDB:HLA-A
A;Cross-references: GDB:119310; OMIM:142800
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 90.2%;
Best Local Similarity 90.0%;
Matches 9; Conservative
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Best Local Similarity 90.0%;
Matches 9; Conservative
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A; Introns: 89/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RVDLRTLRGY 10
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A; Residues: 1-273 <HOL>
           A; Accession: I54548
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                                                                                                       A:Title: Molecular cloning of bovine class I MHC cDNA.
A:Title: Molecular cloning of bovine class I MHC cDNA.
A:Reference number: A32826; MUID:88258075
A;Reference number: A32826; MUID:88258075
C;Reference number: A32826; MUID:88268075
C;Reference number: A32826, MUID:88268075
C;Re
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C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Seywords: transmembrane protein
F:1-74/Domain: signal sequence #status predicted <SIG>
F:25-362/Product: class I histocompatibility antigen heavy chain, Gogo-Oko #status predi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A;Title: Gorilla class I major histocompatibility complex alleles: comparison to human
A;Feference number: JH0534; MUID:92078860
A;Accession: JH0538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenetics 41, 332, 1995
A;Title: Genomic organization and sequence of the rat major histocompatibility complex A;Reference number: 154548; MUID:95237905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                class I histocompatibility antigen Gogo-Oko heavy chain precursor - lowland gorilla C;Species: Gorilla gorilla (lowland gorilla)
C;Date: 30-Jun.1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: JH0538
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C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 16-Feb-1997 C;Accession: B27638 R;Ennis, P.D.; Jackson, A.P.; Parham, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            major histocompatibility complex class I - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
C;Accession: IS4448
R;Walter, L; Tiemann, C; Heine, L.; Gunther, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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A;Cross-references: EMBL:X60692; NID:g22908; PIDN:CAA43100.1; PID:g22909
A;Experimental source: EBV-transformed B cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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F:207-298/Domain: alpha-3 <AL2>
F:207-285/Domain: alpha-3 (AL3)
F:229-362/Domain: intracellular #status predicted <INT>
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90.0%; Pred. No. 0.069;
ive 0; Mismatches
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Pred. No. 0.068;
0; Mismatches
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Best Local Similarity 90.0
المالية 9; Conservative
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RVDLETLRGY 108
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Matches 9; Conserv
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J. Biol. Chem. 260, 13414-13423, 1985
J. Biol. Chem. 260, 13414-13423, 1985
A:Title: Comparison of HLA class I gene sequences. Derivation of locus-specific oligonud A:Reference number: A92500; MUID:86033791
A;Accession: B24512
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A;Cross-references: GDB:119310; OMIM:142800
A;Map position: 6p21.3-6p21.3
G;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Superfamily: heterodimer; transmembrane protein; transplantation antigen
F;130-195/Domain: immunoglobulin homology <IMM>
F;20/Binding site: carbohydrate (Asn) (covalent) #status predicted
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology C; Keywords: glycoproteth; heterodiamer: transmembrane protein; transplantation antigen F: 155-260/Domain: immunoglobulin homology < LMM> F: 85/Binding site: carbobydrate (Asn) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: class I histocompatibility antigen; immunoglobulin homology servands: glycoprotein; heterodimer; transmembrane protein; transplantation antigen 195-260/Domain: immunoglobulin homology CIMAP. 885/Binding site: carbohydrate (Asn) (coovalent) #status predicted
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Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Sep-1997
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C;Date: 31-Dec-1988 *sequence_revision 31-Dec-1988 *text_change 22-Jun-1999
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R:HOlmes, N.; Parham, P.
A.Title: Exon shuffiling in vivo can generate novel HLA class I molecules.
A:Reference number: A91021; MUID:86055720
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X;Residues: 1-275 <DAV>
A;Cross-references: GB:M11887; NID:g184157; PIDN:AAA52656.1; PID:g184158
C;Genetics:
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                                                                                                                                                      Length 273;
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0.13;
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0.13;
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Pred. No. 0.13;
0; Mismatches
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A;Cross-references: GDB:119310; OMIM:142800
A;Map position: 6p21.3-6p21.3
                                                                                                                                                      86.3%;
90.0%;
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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Residues: 1-273 <HOL>
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Length 275;

DB 1;

Score 44;

86.3%;

Query Match

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Nationate names: MHC Chia chain
C; Species: Pan troglodytes (chimpanzee)
C; Jactes 19 Mar-1997 #sequence_revision 19-mar-1997 #text_change 23-Jul-1999
C; Jactes 19 Mar-1997 #sequence_revision 19-mar-1997 #text_change 23-Jul-1999
C; Jaccession: S06424; I36599
R; Lawlor, D.A.; Ward, F.E.; Ennis, P.D.; Jackson, A.P.; Parham, P.
Nature 335, 268-271, 1988
A; Title: HiA-A and B polymorphisms predate the divergence of humans and chimpanzees.
A; Reference number: S06424; MUID:88319000
A; Reference number: S06424; MUID:88319000
A; Reference number: J322 CLMAP
B; Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
J; Immunol. 142, 3937-3950, 1989
A; Title: Diversity and diversification of HiA-A, B, C alleles.
A; Reference number: I36956; MUID:89235215
A; Accession: I36959
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A; Residues: 1-332 < RES>
A; Cross-references: GB:M24047; NID:g176818; PIDN:AAA35426.1; PID:g55
A; Cross-references: GB:M24047; NID:g176818; PIDN:AAA35426.1; PID:g55
C; Superfamily: class I histocompatibility antigen; immunoglobulin hor C; Keywords: glycoprotein; membrane protein
F;1-24/Domain: alpha-1 #status predicted < EX1>
F;25-114/Domain: alpha-1 #status predicted < EX2>
F;25-126/Domain: alpha-1 #status predicted < EX2>
F;250-285/Domain: immunoglobulin homology < IMM>
F;307-331/Domain: transmembrane #status predicted < TMM>
F;110/Bilding site: carbohydrate (Asn) (covalent) #status predicted
F;125-188,227-283/Disulfide bonds: #status predicted
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Job time: 22208 sec
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RVDLGTLRGY 108
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Matches 9; Conserv
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1 RVDLRTLRGY 10
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                            82229 segs, 29864866 residues
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HA19_CANFA
1A01_PANTR
1A01_PONPY
1A02_HUMAN
1A03_GORGO
1A03_PANTR
1A11_HUMAN
1A11_HUMAN
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HLAE_HUMAN
HLAE_PONPY
1OKO_GORGO
HA1B_BOVIN
1A69_HUMAN
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1A33_HUMAN
1A34_HUMAN
1A66_HUMAN
1A68_HUMAN
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1A03_HUMAN
HA1A_BOVIN
1CXX_HUMAN
1B44_HUMAN
1A01_SAGOE
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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CYTOPLASMIC.
POTENTIAL.
POTENTIAL.
; 4E8C6EFB CRC32;

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                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIA class I gene.";
J. Immunol. 140:4024-4030(1988).
[2]
SEQUENCE FROM N.A. (E*0102).
MEDLINE: 88285691.
MCDLINE: B.H., GERAGHIY D.E., SHIMIZU Y., DEMARS R., ORR H.T.;
"HIA-E. A novel HiAA class I gene expressed in resting T lymphocytes.";
J. Immunol. 141:897-904(1988).
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 98325367.
O'CALLAGHAN C.A., TORNO J., WILLCOX B.E., BRAUD V.M., JAKOBSEN B.K., CALLAGHAN C.A., TORNO J., WILLCOX B.E., BRAUD V.M., JAKOBSEN B.K., STUGART D.I., WCMICHAEL A.J., BELL J.I., JONES E.Y.;
"Structural features impose tight peptide binding specificity in the nonclassical MHC molecule HLA-E.";
MOI. Cell I:531-541(1998).
-!- FUNCTION: PREFERABLY BINDS TO A PEPTIDE DERIVED FROM THE SIGNAL SEQUENCE OF MOST HLA-A, -B, -C AND -G MOLECULES.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN E E*0101/E*0102.
EXTRACELLULAR ALPHA -1.
EXTRACELLULAR ALPHA -3.
EXTRACELLULAR ALPHA -3.
                                                                                                                                                                                                                                01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN E E*0101/E*0102
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 88229102.
MIZUNO S., TRAPANI J.A., KOLLER B.H., DUPONT B., YANG S.Y.;
"Isolation and nucleotide sequence of a cDNA clone encoding a novel
                                        ö
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
   100.0%; Score 51; DB 1; Length 371; 100.0%; Pred. No. 0.002;
                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 22-295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A32272; A32272.
PIR; A28834; A28834.
HSSP; P03899; IHSA.
MIM; 143010; -
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; ig; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
SIGNAL 1 2 358 HLA CLASS I HISTC
                                                                                                                                                                                                   358 AA.
                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M20022; AAA52655.1; -. EMBL; M21533; AAA59835.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (E*0101).
Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                           HLA-E OR HLAE OR HLA-6.2.
                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                               99 RVDLRTLRGY 108
                                                                           1 RVDLRTLRGY 10
                                                                                                                                                                                                 HLAE_HUMAN
P13747;
                                                                                                                                                                RESULT 2
HLAE_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                              ö
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MARDELINE, 92020194.

LAWLOR D.A., WARREN E., WARD F.E., PARHAM P.;

"Comparison of class I MHC alleles in humans and apes.";

Immunol. Rev. 113:147-185(1990).

-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASS I HISTOCOMPATIBILITY ANTIGEN
                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                           01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, E-1 ALPHA CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                     Pongo pygmaeus (Orangutan).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                    Score 46; DB 1; Length 358;
Pred. No. 0.023;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E-1 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                          BY SIMILARITY.
S -> L (IN E*0102).
/FIId=VAR_004394.
CONNECTING PEPTIDE
                                                                                            G -> R (IN E*0102)
/FTId=VAR_004395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                       CYTOPLASMIC TAIL.
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55E15638 CRC32;
                                                                                                                                                                                                                                                                                     359 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00200; IG_MHC; 1.
PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
NON_TER
SIGNAL
SIGNAL
SIGNAL
                                                                                                                   40130 MW;
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HSSP; P03989; 1HSA.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                      90.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40409
                                                                                                                                                    Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                       STANDARD;
305
329
3329
3358
107
107
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96 RVNLRTLRGY 105
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221
104
359 AA;
                                                                                                                   358 AA;
                                                                                                                                                                                                    1 RVDLRTLRGY 10
296
330
122
122
107
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                                                                                                                                                                                                                                                                                     HLAE_PONPY
P16212;
                                                                                                                                                                                                                                                                                                                                                           (FRAGMENT).
                                  DISULFID
DISULFID
CARBOHYD
VARIANT
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DISULFID
CARBOHYD
SEQUENCE
DOMAIN
TRANSMEM
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DOMAIN
                                                                                                                     SEQUENCE
                                                                                             VARIANT
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                        DOMAIN
                                                                                                                                                                                                                                                                RESULT 3
HLAE_PONPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC.
SIGNIFICANT WITH IMMUNOGLOBULIN C-REGION
DOMAINS AND BETA-2-MICROGLOBULIN.
                                                        01-07N-1990 (Rel. 13, Created)
01-07N-1990 (Rel. 13, Last sequence update)
01-07N-1990 (Rel. 13, Last annotation update)
BOLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN BL3-7 PRECURSOR.
BOS taurus (BOVINE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BOLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                          [1] SEQUENCE FROM N.A. MEDLINE; 88258075.
ENNIS P.D., JACKSON A.P., PARHAM P.;
ENNIS P.D., JACKSON A.P., PARHAM P.;
Molecular clonhing of bovine class I MHC cDNA.";
J. Immunol. 141:642-651(1988).
-i. FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1469_HUWAN STANDARD; PRT; 273 AA.
P10316;
01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, AW-69(A-28) ALPHA CHAIN
                                                                                                                                                                                                                                                                                                     THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.2%; Score 46; DB 1; Length 364; 90.0%; Pred. No. 0.023; 1:ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALPHA CHAIN BL3-7.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A27F581C CRC32;
                               364 AA.
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BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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                               PRT;
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HSSP; P30460; 1AGB.
PROSITE; PS00290; IG_MHC; 1.
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                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1117
2209
3301
331
364
301
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364
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Matches 9; Conser
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                                                                                                                                                                         Bovinae; Bos
                              HA1B_BOVIN
P13753;
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DOMAIN
SIMILAR
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DISULFID
DISULFID
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
1A69_HUMAN
ID : 1A69_HU
AC P10316;
DT 01-MAR-
DT 15-JUL-
DE HLA CLA
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RESULT 5
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                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-OKO ALPHA CHAIN PRECURSOR.
GOTILLA GOTILLA GOTILLA (Lowland gotilla)
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
CLASS I HISTOCOMPATIBILITY ANTIGEN,
GOGO-CNO ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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                              Length 359;
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                                                            0; Indels
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                          Score 46; DB 1;
Pred. No. 0.023;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X60692; CAA43100.1; -.
PIR; JH0538; JH0538.
HSSP; P30460; LAGB.
PROSITE; P500290; IG_MHC; 1.
PFAM; PF00129; MC_1; 1.
PFAM; PF00129; MC_2; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
SIGNAL BY SIMILARITY.
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                                                                                                                                                                                                       362 AA
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Pred. No. 0.02:
0; Mismatches
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llarity 90.0%;
Conservative 0
                            90.2%;
90.0%;
             Ouery Match
Best Local Similarity 90.0
نمرو 9; Conservative
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                                                                                                                                                                                                       STANDARD;
                                                                                                           MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110
362 AA;
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RVDLETLRGY 108
                                                                                          1 RVDLRTLRGY 10
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                       10KO_GORGO
P30388;
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DOMAIN
DISULFID
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CARBOHYD
SEQUENCE
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DOMAIN DOMAIN DOMAIN DOMAIN

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CHAIN

us-08-653-294-37.rsp

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HA19_CANFA
P18466;
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TRANSMEM
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SEQUENCE
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DAVIDSON W.F., KRESS M., KHOURY G., JAY G.;
"Comparison of HLA class I gene sequences. Derivation of locus-specific oligonucleotide probes specific for HLA-A, HLA-B, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                              SEQUENCE FROM N.A. (A*6901). , MEDLINE; 86055720.  
MEDLINE; 86055720.  
"Exon shuffling in vivo can generate novel HLA class I molecules.";  
"Exon shuffling in vivo can generate novel HLA class I molecules.";  
EMBO J. 4:3849-2854(1985).  
-:- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
THE IMMUNE SYSTEM..
                                                                                                                                                                 POLYMORPHISM: THE ONLY ALLELE OF AW-69 KNOWN IS A*6901 WHICH IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-NV-1997 (Rel. 35, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-10 ALPHA CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                            -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB 1; Length 273; Pred. No. 0.044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEBFB366 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                      EMBL; X03158; -; NOT_ANNOTATED_CDS.
EMBL; X03159; -; NOT_ANNOTATED_CDS.
PIR; B24671; HLHU69.
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90.0%;
                                                                                                                                                                                                                                                                                                                                              PS00290; IG_MHC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 86.3
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                    85
163
258
273
                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
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MIM; 142800; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RVDLRTLRGY 10
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                                                                                                                                                                               SHOWN HERE.
          HLA-A OR HLAA.
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P10313;
 (FRAGMENT)
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SEQUENCE
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01-NOY-1990 (Rel. 16, Last sequence update)
115-JUL-1999 (Rel. 38, Last annotation update)
DLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A9/A9 ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 90316611.
MEDLINE; 90316611.
"Nucleotide sequence of a dog class I cDNA clone.";
Immunogenetics 31:400-404(1990).
-:- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
HLA-C genes.";
J. Biol. Chem. 260:13414-13423(1985).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
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                                                                                      THE IMMUNE SYSTEM.
SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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Eutheria; Carnivora; Fissipedia; Canidae; Canis
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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Pred. No. 0.045;
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8B232F3C CRC32;
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90.0%;
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HSSP; P01892; 1HHH.
MIM; 142800; -
PROSITE; PS00290; IG_MHC; 1.
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PFAM; PF00129; MHC_I; 1.
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                                                                                                                                                 MICROGLOBULIN).
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Best Local Similarity
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LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
"Gorilla class I major histocompatibility complex alleles: comparison to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
-: FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1401_GORGO STANDARD; PRT; 365 AA.
P30375;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last annotation update)
01-APR-1993 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                               DLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A9/A9 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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PIR; JH0534; JH0534.
HSSP; PO1891; ZHA.
PROSITE; PS00209; IG_MHC; 1.
PFAM; PF00129; MHC_I; 1.
PFAM; PF00129; MHC_I; 1.
AMC I; Transmembrane; Glycoprotein; Signal.
SIGNAL BY SIMILARITY.
CHAIN 25 365 CLASS I HISTOCOMPATIBILITY ANTIGEN,
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BY SIMILARITY.
BY SIMILARITY.
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D5250E8D CRC32;
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PFAM; PF00129; MHC_I; 1.
MHC I: Transmembrane; Glycoprotein; Signal.
SIGNAL 1.
or send an email to license@isb-sib.ch)
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                                              EMBL; M32283; AAA30865.1; -.
                                                                                                                       PS00290; IG_MHC; 1
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Best Local Similarity 90.0-
                                                                        PIR; A45845; A45845.
HSSP; P03989; 1HSA.
PROSITE; PS00290; IG_
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115
208
300
330
125
228
110
362 AA;
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DOMAIN
TRANSMEM
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DISULFID
DISULFID
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SEQUENCE
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-3.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 ALPHA CHAIN PRECURSOR.
Pan troglodytes (Chimpanaee).
Eukaryota: Metazoa; Chimpanate; Craniata; Vertebrata; Mammalia;
Eutheria: Primatee; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 90201944.
LAMLOR D.A., WARREN E., WARD F.E., PARHAM P.;
"Comparison of class I MHC alleles in humans and apes.";
Immunol. Rev. 113:147-185(1990).
-:- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
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GOGO-A0101 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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BY SIMILARITY.
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; 6EC5FF0E CRC32;
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BY SIMILARITY.
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7, 40682CC4 CRC32;
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PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
SIGNAL
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PROSITE; PS00290; IG_MHC; 1.
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Best Local Similarity 90.0
Matches 9; Conservative
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308
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345
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P16209;
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TRANSMEM
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1A01_PANTR
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REVISIONS (A*0201).
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                                                  HLA-A OR HLAA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polymorphism.
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F
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                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLLINE; 90201944.
LAWLOR D.A., WARREN E., WARD F.E., PARHAM P.;
"Comparison of class I MHC alleles in humans and apes.";
Immunol. Rev. 113:147-185(1990).
-! FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1A02_HUMAN STANDARD; PRT; 365 AA.
P01892; P06338; P30514; P30444; P30445; P30446; Q29680; Q29899;
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                                                                                                                                      01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, A-1 ALPHA CHAIN PRECURSOR.
Pongo pygmaeus (Orangutan).
                                                                                                                                                                                      Eukāryotā; Metazoa; Chordāta; Craniata; Vertebrata; Mammalia;
Eutheria; Prīmates; Catarrhini; Hominidae; Pongo.
                                                                                                                                                                                                                                                                                     -i- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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Pred. No. 0.062;
0; Mismatches 1; Indels
           Length 365;
                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A-1 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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BY SIMILARITY.
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; FAD23315 CRC32;
          Score 44; DB 1;
Pred. No. 0.062;
                                                                                                                     365 AA.
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PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_I; 1.
MHC_I; Transmembrane; Glycoprotein; Signal.
                             0; Mismatches
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          86.3%;
90.0%;
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90.0%;
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Ouery Match
Best Local Similarity 90.۰۰
اجم 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                     STANDARD;
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110
365 AA;
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RVDLGTLRGY 108
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SEQUENCE
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ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
"Raptid cloning of Han-A,B cDNa by using the polymerase chain
reaction: frequency and nature of errors produced in amplification.";
Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Comparison of amino acid sequences of two human histocompatibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE; 89122144.
CIANETII L., TESTA U., SCOTTO L., LA VALLE R., SIMEONE A.,
BOCCOLI G., GIANNELLA G., PESCHLE C., BONCINELLI E.;
"Three new class I HLA alleles: structure of mRNAs and alternative mechanisms of processing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                        two
21-JUL-1986 (Rel. 01, Created)
13-A0G-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILLITY ANTIGEN, A-2 ALPHA CHAIN PRECURSOR
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MATISON D.H., HANDY D.E., BRADLEY D.A., COLIGAN J.E., COWAN E.P.,
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Immunogenetics 26:190-192(1987),
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 85132727.

KOLLER B.H., ORR H.T.;

"Cloning and complete sequence of an HLA-A2 gene: analysis of HLA-A alleles at the nucleotide level.";

J. Immunol. 134:2727-2733(1985).
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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KRANGEL M.S.;

"Unusual RNA splicing generates a secreted form of HLA-A2 in mutagenized B lymphoblastoid cell line.";

EMBO J. 4:1205-1210(1985).
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STROMINGER J.L.;
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MEDLINE; 87252273.
HOLMES N., ENNIS P., WAN A.M., DENNEY D.W., PARHAM P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        roc. Natl. Acad. Sci. U.S.A. 76:4395-4399(1979).
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MEDLINE; 85132727.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 881113844.

DOMENECH N., EZQUERRA A., CASTANO R., LOPEZ DE CASTRO J.A.;

"Structural analysis of HLA-A2.4 functional variant KNE. Implications for the mapping of HLA-A2-specific T-cell epitopes.";

Immunogenetics 27:196-202(1988).
"Multiple genetic mechanisms have contributed to the generation of
the HLA-A2/A28 family of class I MHC molecules.";
J. Immunol. 139:936-941(1987).
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DOMENECH N., CASTANO R., GOULMY E., LOPEZ DE CASTRO J.A.;
Molecular analysis of HLA-A2.4 functional variant KLO: close structural and evolutionary relatedness to the HLA-A2.2 subtype.";
Immunogenetics 28:143-152(1988).
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"Structure of the HLA-A*0211 (A2.5) subtype: further evidence for

"Selection-driven diversification of HLA-A2 antigens.";

Immunogenetics 35:344-346(1992).
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CASTANO N., EQUERRA A., DOMENECH N., LOPEZ DE CASTRO J.A.;
"An HLA-A2 population variant with structural polymorphism in the alpha 3 region."
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                                                                                                                                                                                        SEQUENCE OF 9-365 FROM N.A. (A*0204).
MEDLINE; 92033809.
CASTANO A.R., LOPEZ DE CASTRO J.A.;
"Structure of the HLA-A*0204 antigen, found in South American Indians. Spatial clustering of HLA-A2 subtype polymorphism.";
Immunogenetics 34:281-285(1991).
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"An Oriental HLA-A2 subtype is closely related to a subset of
Caucasoid HLA-A2 alleles":
Immunogenetics 29:112-116(1989).
                                                                                                                                                                                                                                                                                                                                                                                          WATKINS D.I., MCADAM S.N., LIU X., STANG C.R., MILFORD E.L., LEVINE C.G., GARBER T.L., DOGON A.L., LOND C.I., GHIM S.H., TROUP G.M., HUGHES A.L., LETVIN N.L.;
"New recombinant HLA-B alleles in a tribe of South American Amerindians indicate rapid evolution of MHC class I loci.";
Nature 357:329-333(1992).
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Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
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MEDLINE; 92218010.
                                                                                                                                                                                   OF 9-365 FROM N.A. (A*0204). 92039809.
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                                                                                                SEQUENCE FROM N.A. (A*0203/A*0205)
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Immunol. 137:1642-1649(1986).
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MEDLINE; 86305811.
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MEDLINE; 88014204.
BJORKMAN P.J., SAPER M.A., SAMRAOUI B., BENNETT W.S.,
STROMINGER J.L., WILEY D.C.;
"Structure of the human class I histocompatibility antigen, HLA-A2.";
Nature 329:506-512(1987).
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01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last sequence update)
CLASS I HISTOCOMPATIBLITY ANTIGEN, GOGO-A0401 ALPHA CHAIN PRECURSOR.
GOTILLA GOTILLA GOTILLA (Lowland gotilla)
Eukaryota, Metaso: Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrini; Hominidae; Gorilla.
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"HIA-A-NOS subtype distribution in Caucasians from northern Italy:
identification of A+0220.";
Issue Antigens 48:673-679(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KASHTWASE K., TOKUNAGA K., ISHIKAWA Y., OOHASHI H., HASHIMOTO M., AKAZA T., TADOKORO K., JUJI T.:
"A new A2 sequence HLA-A2K from Japanese.";
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A novel subtype of A2 (A*0217) isolated from the South American Indian B-cell line AMALA.";
Tissue Antigens 45:343-347(1995).
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FIEISCHHAUER K., ZINO E., MAZZI B., SEVERINI G.M., BENAZZI E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB 1; Length 365;
Pred. No. 0.062;
0; Mismatches 1; Indels
                                                    DE CASTRO J.A.;
subtype: HLA-A*0213.";
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"Nucleotide sequence of a novel HLA-A2 gene.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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MEDLINE; 91245570.
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                              MEDLINE; 94222455.
BARBER D.F., FERNANDEZ J.M., LOPEZ PRRERE D.F., FERNANDEZ J.M., LOPEZ IPTIMATY STRUCTURE Of a new HLA-A2 Immunogenetics 39:378-378(1994).
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90.0%;
                                                                                                                                                          SEQUENCE FROM N.A. (A*0216).
MEDLINE; 95278976.
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FROM N.A. (A*0213).
94222455.
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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P30377;
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1A03_GORGO
AD 1A03_GORDO
DT 01-APR
DT 01-APR
DE CLASS
OS GORILL
OC EURARY
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MW.
                                                                                                                    PIR, S03535; S03535.
HSSP; P01891; 2HLA.
PROSITE; PS00290; IG_MHC; 1.
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90.0%;
                                                                                                                                                                                                                                                                                                                     40822
                                                                                                                                                                                                                                                                                                                                                              Local Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                   365
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1115
207
209
3309
1125
110
365 AA;
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 MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                              1 RVDLRTLRGY 10
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
1A04_PANTR
ID 1A04_PANTR
AC P13749;
                                                                                                                                                                                                                                                                         DOMAIN
DISULFID
DISULFID
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TRANSMEM
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                   MEDLINE; 92078860.
LAWLOR D.A., MARREL E., TAYLOR P., PARHAM P.;
LAWLOR D.A., MARREL E. TAYLOR P., PARHAM P.;
GOTILLA class I major histocompatibility complex alleles: comparison to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1403_PANTR STANDARD; PRT; 365 AA.
P13749;
01-JAN-1990 (Rel. 13, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
01-APR-1993 (Rel. 25, Last annotation update)
CHAA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-108 ALPHA CHAIN PRECURSOR.
Pan troglodytes (Chimpanazee): Chandata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Nucleotide sequences of chimpanzee MHC class I alleles: evidence for trans-species mode of evolution."; EMBO J. 7:2765-2774(1988).
---i. FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                     Glycoprotein; Signal.

BY SIMILARITY.

CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G., KLEIN J.;
                                                                                               DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.3%; Score 44; DB 1; Length 365; 90.0%; Pred. No. 0.062; 1ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                    GOGO-A0401 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                CONNECTING PEPTIDE
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
i; C34850E8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                              40933 MW;
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                                                                                                                                                                                                                                                 PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
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Best Local Similarity 90.vv
                                                                                                                                                                                                                                                                                      MHC I; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMUNE SYSTEM
                                                                                              -!- SUBUNIT: DIMER ( MICROGLOBULIN).
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110
365 AA;
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[1]
SEQUENCE FROM N.A.
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DISULFID
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SEQUENCE
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"Nucleotide sequences of chimpanzee MHC class I alleles: evidence for
trans-species mode of evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-126 ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     trans-species mode of evolution.";
EMBO J. 7:2765-2774(1988).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 89030641.
MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE IMMUNE SYSTEM.

-1- SUBDINIT: DIER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 365;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A-108 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONNECTING PEPTIDE
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0.062;
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BC39DEDC CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB Pred. No. 0.060; Mismatches
                                                                                                                                                                                                                                                                          EMBL; X13113; CAA31505.1; ALT_INIT.
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us-08-653-294-37.rsp

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CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-126 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-2.
CONNECTING PEPTIDE.
                                                                                                                                      CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
A'; 94C6AFEB CRC32;
EMBL; X13114; CAA31506.1; -.
PIR; S01771; S01171.
HSSP: P01891; ZHLA.
PROSITE: PS00209; IG_MHC; 1.
PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
SIGNAL 1.
CHIA CLASS I HIST
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40656 MW;
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115
207
299
339
333
125
227
227
365 AA;
                                                                                          DOMAIN
DOMAIN
DOMAIN
TRANSMEM
DOMAIN
DISULFID
DISULFID
CARBOHYD
SEQUENCE
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Gaps ö

Query Match

86.3%; Score 44; DB 1; Length 365;
Best Local Similarity 90.0%; Pred. No. 0.062;
Matches 9; Conservative 0; Mismatches 1; Indels

Search completed: February 8, 2000, 01:26:03 Job time: 1563 sec

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bos taurus homo sapien bos taurus bos taurus rattus norv rattus norv

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leontopithe leontopithe

homo sapien homo sapien canis famil canis famil canis famil

ALIGNMENTS

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002949 PRELIMINARY; PRT; 344 AA.
002949;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MATURE MHC CLASS I ALPHA CHAIN (FRAGMENT).
RT1.A2F.
RATUS norvegicus (Rat).
ENKAIYOta; Metazoa (Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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SEQUENCE
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002949
002949 rattus norv
095567 rattus norv
P79599 rattus norv
070953 rattus norv
030441 callithrix
030441 callithrix
030421 ateles belz
030221 ateles belz
030221 ateles belz
045720 bos taurus
046720 bos taurus
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046734 bos taurus
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                                                          Search time 176.54 Seconds (without alignments)
3.927 Million cell updates/sec
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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095567
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sp_human:*
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sp_organelle:*
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                                            OM protein - protein search, using
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Listing first 45
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sp_bacteria:*
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1 RVDLRTLRGY 10
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sp_rodent:*
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Match Length DB
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Maximum DB seq length: 1000000
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Perfect score:
Sequence:
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521
531
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544
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Database :

Searched:

Run on:

ö Gaps STRAIN-LEWIS. 1F; TISSUE-SPENCYTES;
STRAIN-LEWIS. 1F; TISSUE-SPENCYTES;
SOLDE A.F., GONZALEZ A.L., MEHLING B., STEVENS J.,
COADWELL W.J., HUENIG T., HOWARD J.C., BUTCHER G.W.;
CUIT. Biol. 0:0-0(0).
EMBL; Y13579; CAA73907.1; -.
HSSP; P01901; 1KBG.
PFAM; PF00047; 1g; 1. ô Length 344; 0; Indels Created) Last sequence update) Query Match
100.0%; Score 51; DB 7;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 10; Conservative 0; Mismatches 0; 344 344 3417 MW; 7AB3EF04 CRC32; PRT; 345 AA. Q95567 PRELIMINARY; Q95567; P79601; 01-FEB-1997 (TrEMBLRE1. 02, 01-JUL-1997 (TrEMBLRE1. 04, 1 RVDLRTLRGY 10 RESULT 095567 ID 09 AC 09 DT 01 DT 01 ò g

Result

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P SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-NEDH; TISSUE-SPLENCCYTES;

A JOLY E., LE ROLLE A.F., GONZALEZ A.L., MEHLING B., STEVENS J.,

LC GLYC. BIOL. 0.0-0(0).

C CUT: BIOL. 0.0-0(0).

R EMBL; Y08532; CAA6848.1; -.

R PFAM; PF00129; MHC_I: 1.

R PFFAM; PF00129; MHC_I: 1.

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SEQUENCE 345 AA; 38953 MW; SA4ED67C CRC32;
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STRAIN-LEW. IF (F HAPLOTYPE);
STRAIN-LEW. IF (F HAPLOTYPE);
COADWELL W.J., HUENIG T., HOWARD J.C., BUTCHER G.W.;
CUTT. BIOL. 6:0-0(0).
EWBL: X14014; CAA74333.1; -.
HSSP; P01901; IKBG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 12, Last sequence update)
MHC CLASS I ALPHA CHAIN (FRAGMENT).
Rattus norvegicus (RAI).
Ebkaryota: Metazoa; Chordata; Cranlata; Vertebrata; Mammalia;
Eutaryota; Redentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 51; DB 11; Length 345; 100.0%; Pred. No. 0.022; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 51; DB 7; Length 346; 100.0%; Pred. No. 0.023; Live 0; Mismatches 0; Indels
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030441;
01-NOY-1996 (TEMBLrel. 01, Created)
01-NOY-1996 (TEMBLrel. 01, Last sequence update)
01-NOY-1999 (TEMBLrel. 12, Last annotation update)
MHC CLASS I CAJA-G*01 (FRAGMENT).
01-JUL-1997 (TrEMBLrel. 04, Last sequence update) 01-NOV-1999 (TrEMBLrel. 12, Last annotation update) PROTEIN INVOLVED IN PEPTIDE PRESENTATION (FRAGMENT)
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Best Local Similarity 100.C
Matches 10, Conservative
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Best Local Similarity 100.0
Matches 10, Conservative
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PFAM; PF00129; MHC_I; 1.
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01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MATURE ALPHA CHAIN OF MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I
ANTIGEN (FRAGMENT).
RTI.A2.
                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-RT1(0); TISSUE-SPLEEN;
JOLY E., LE ROLLE A.F., GONZALEZ A.L., MEHLING B., STEVENS J.,
COADWELL W.J., HUENTG T., HOWARD J.C., BUTCHER G.W.;
CHIT. 18101. 0:0-0(0).
EMBL: X90372; CAA62022.1; -.
HSSP; PO1901; 1KBG.
PFAM; PF00047; 19: 1.
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STRAIN-RILIO); TISSUE-SPLEEN;
STRAIN-RILIO); TISSUE-SPLEEN;
COADWELL W.J., HUENIG T., HOWARD J.C., BUTCHER G.W.;
CULT. B101. 0:0-0(1999).
EMBL; X90373; CAA62023.1; --
HSSP; P01900; 1B11.
                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
HISTOCOMPATIBILITY COMPLEX CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 51; DB 7; Length 345; Best Local Similarity 100.0%; Pred. No. 0.022; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 51; DB 7; Length 345; 100.0%; Pred. No. 0.022; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                          1
345 AA; 39139 MW; 8E486EB4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER 1 1 SEQUENCE 345 AA; 39221 MW; 602EBF79 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345 AA.
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P79599; Q95564;
01-MAY-1997 (TrEMBLRE1. 03, Cx
01-MAY-1997 (TrEMBLRE1. 03, La
01-NOY-1999 (TREMBLRE1. 12, La
MATURE ALPHA CHAIN OF MAJOR HI
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Best Local Similarity 100.
Matches 10; Conservative
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PFAM; PF00129; MHC_I; 1.
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RESULT P79599

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Gaps

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RESULT

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Gaps

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NON_TER SEQUENCE

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CADAVID L.F., SHUFFLEBOTHAM C., RUIZ F.J., YEAGER M., HUGHES A.L., MAKKINS D.I.;
"Evolutionary instability of the major histocompatibility complex class I loci in New World primates.";
Proc. Natl. Acad. Sci. U.S.A. 94:14536-14541(1997).
EMBL: U59648; AAB97491.1;
HSSP: PO1891; ZHLA.
                                                                                                                                    Sus scrofa (P1g).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.1%; Score 48; DB 7; Length 364; 90.0%; Pred. No. 0.094; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SULLIVAN J.A., OETTINGER H.F., SACHS D.H., EDGE A.S.B.;
J. Immunol. 159:0-0(1997).
EMBL; AFOJ4004; AAB69339.1; -.
HSSP; P30885; 1A9E.
PROSITE; PS00299; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ateles belzebuth (Long-haired spider monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Platyrrhini; Cebidae; Atelinae;
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I ANTIGEN.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
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Pred. No. 0.15;
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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PFAM; PF00129; MHC_I; 1.
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PFAM; PF00129; MHC_I; 1.
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NON_TER
SEQUENCE
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019744
ID 019744
AC 019744;
DT 01-JAN-
DT 01-JAN-
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Q30221
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MEDLINE, 96175158.
WANG M., STEPKOWSKI S.M., TIAN L., LANGOWSKI J.L., YU J., KAHAN B.D.;
WANG M., STEPKOWSKI S.M., TIAN L., LANGOWSKI J.L., YU J., KAHAN B.D.;
WANG M., STEPKOWSKI S.M., TIAN L., LANGOWSKI J.L., YU J., KAHAN B.D.;
WANG M., STEPKOWSKI S.M., TIAN L., LANGOWSKI J.L., YU J., KAHAN B.D.;
INCLEOCHIGE SEQUENCES of three distinct clones coding for rat heavy
chain class I major histocompatibility antigens.";
Immunogenetics 43:318-320(1996).
Immunogenetics 43:318-320(1996).
HSSP; P01900; IBII.
PFRM; PF001047; ig; 1.
PFRM; PF00129; MHC_I; 1.
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                                                                                                                         MEDLINE; 98070787.
CADAVID L.F., SHUFFLEBOTHAM C., RUIZ F.J., YEAGER M., HUGHES A.L., WATKINS D.I.;
"Evolutionary instability of the major histocompatibility complex class I loci in New World primates.";
Proc. Natl. Acad. Sci. U.S.A. 94:14536-14541(1997).
EMBL; U59637; AAB97480.1; -...
PRSP; P80685; 1ABE.
PROSITE; P800047; 10; I...
PFAM; PF00047; 10; I...
PFAM; PF00129; MHC_I; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
Callithrix jacchus (Common marmoset).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 51; DB 7; Length 356; Best Local Similarity 100.0%; Pred. No. 0.023; Matches 10; Conservative 0; Mismatches 0; Indels
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031254;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I RT1.AB HEAVY CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1
356 AA; 40093 MW; 728A4997 CRC32;
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    CHAIN
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    SEQUENCE
    367
    AA;
    41471
    MW;

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SIGNAL
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SEQUENCE
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Mammalia; Ateles.

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Gaps

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RESULT 019243 ID 0192 AC 0192 DT 01-3

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Length 356; Indels

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D 046734 PRELIMINARY; PRT; 166 AA.

AC 046734;
DT 01-JUN-1998 (TEMBLEel. 06, Created)
DT 01-JUN-1998 (TEMBLEel. 06, Last sequence update)
DT 01-JUN-1998 (TEMBLEEl. 06, Last sequence update)
DT 01-MY-1999 (TEMBLEEl. 10, Last annotation update)
DT 01-MY-1999 (TEMBLEEl. 10, Last annotation update)
DT 01-MY-1999 (TEMBLEEl. 10, Last sequence update)
DT 01-MY-1999 (TEMBLEEl. 10, Last sequence update)
DT 01-MY-1999 (TEMBLEEl. 06, Last sequence update)
DT 01-MY-1999 (TEMBLEEl. 06, Created)
DT 01-MY-1999 (TEMBLEEl. 06, Created)
DT 01-MY-1999 (TEMBLEEl. 06, Created)
DT 01-MY-1998 (TEMBLEEL. 06, CREATED)
D
      Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
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Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
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                                                                                                                                                               URAKAWA T., KODAMA M., MORITA M., IKEDA H.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO0856; BAA24716.1; -.
PFAM: PF00129; MHC_I: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     URAKAWA T., KODAMA M., MORITA M., IKEDA H.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: ABOO8589; BAA24719.1;
PFAM: PF00129; MHC_I: 1.
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUNY-1999 (TrEMBLrel. 10, Last annotation update)
MHC CLASS I HEAVY CHAIN (FRAGMENT).
Bos taurus (Bovine).
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Pred. No. 0.1;
0; Mismatches
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166 166
166 AA; 19338 MW; F0563A5A CRC32;
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166 166
166 AA; 19337 MW; 9321E1A4 CRC32;
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Pred. No. (
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
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Best Local Similarity
9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RVDLRTLRGY 10
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                                                                         Bovinae; Bos
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MEDILINE; 98211697.
KNAPP L.A. CADAVID L.F., WATKINS D.I.;
KNAPP L.A. CADAVID L.F., WATKINS D.I.;
"The MHC-E locus is the most well conserved of all known primate class in histocompatibility genes.";
J. Immunol. 166:189-196(1998).
EMBI, AF004922; AAC39880.1;
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                    "Polymorphism in the human class I MHC locus HLA-E in Japanese."; munuogeneetics 32:205-209(1990).
EMBL; M32506; AA463233.1; -.
PFAM; PF00129; MHC_I: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pithecia pithecia (White-faced saki).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Platyrrhini; Cebidae; Pitheciinae; Pithecia
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                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC HLA-E ALPHA-1 (FRAGMENT).
EA1.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
MHC CLASS I ANTIGEN (FRAGMENT).
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 46; DB 7;
Pred. No. 0.054;
L; Mismatches
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                                                                                                                                                               SEQUENCE FROM N.A. TISSUE-PERIPHEAL BLOOD; MEDLINE; 9103394 K., MIZUNO S.; OHYA K., KONDO K., MIZUNO S.;
                                                                                                                                                                                                                                                                                                                                                                     1 1
90 AA; 10505 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 90.2%;
Best Local Similarity 90.0%;
Matches 9; Conservative 1
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Matches 9; Conservative
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75 RVNLRTLRGY 84
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062875
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1999 (TrEMBLrel. 10, Last annotation update)
01-MAY-1999 (TREMBLREL. 10, Last annotation update)
MHC CLASS I HEAVY CHAIN (FRAGMENT).
MHC CLASS I MEAZOA: CHAIN (FRAGMENT).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
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90.2%; Score 46; DB 7; Length 166; Best Local Similarity 90.0%; Pred. No. 0.1; Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=303F;
URAKAWA T., KODAMA M., MORITA M., IKEDA H.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; ABOO8616; BAA24745.1;
PFAM; PF00129; MHC_I; 1.
                            URAKAWA I., KODAMA M., MORITA M., IKEDA H.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB008605; BAA24734.1; -.
PFAM; PF00129; MHC_I; 1.
                                                                                                                   1
166 166
166 AA; 19338 MW; F0563A5A CRC32;
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19236 MW;
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Best Local Similarity 90.03
Matches 9; Conservative
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166 1
166 AA;
SEQUENCE FROM N.A. STRAIN=303F;
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70 RVDLNTLRGY 79

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U59641 Callithrix faccus MH X79892 E.caballus EQMHCB4 m L02833 Bovine MHC class I r
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//dranslation="161:2182090"
//dranslation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (03-JUN-1997) E. Joly, The Babraham Institute,
Submitted (03-JUN-1997) E. Joly, The Babraham Institute,
Immunology, Babraham Hall, Cambridge CB2 4AT, UK
3 (bases 1 to 1035)
Joly,E., Le Rolle,A.F., Gonzalez,A.L., Mehling,B., Stevens,J.,
Coadwell,W.J., Huenig,T., Howard,J.C. and Butcher,G.W.
molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 1035)
Le Rolle, A.F., Hnig, T., Butcher, G.W. and Joly, E.
Unpublished
2 (bases 1 to 1035)
                                                                                                                                                                                                                                            RNRTIAZF 1035 bp mRNA ROD 12-FEB-1998
Rattus norvegicus mRNA for mature MHC class I alpha chain.
Y13579 1 GI:2182089
MHC class I alpha chain; RT1.A2f gene.
Norway rat.
Rattus norvegicus
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Gaps: 0
Percent Identity: 100.000
   1071
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1083
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/function="antigen presentation"
/codon_start=1
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Location/Qualifiers
1. 1035
/organism="Rattus norvegicus"
/dsrain="lewis.lr"
/db_xref="taxon:10116"
/chromosome="20"
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0.6496
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/clone_lib="8-21"
/dev_stage="adult"
/tissue_type="spenocytes"
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US-08-653-294-37.x RNRT1A2F
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LOCUS
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gb_pr3:CJU59641
gb_om:ECMHCB4
gb_om:BOVMHCIB
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1 X13579 Rattus norvegicus mRNA | AJ249705 Rattus norvegicus par | X90373 R. norvegicus mRNA for F | X90373 R. norvegicus mRNA for F | Y14014 Rattus norvegicus mRNA | Y08532 R. norvegicus mRNA for F | X14014 Rattus norvegicus mRNA | Y08532 R. norvegicus mRNA for F | AJ249704 Rattus norvegicus MHC | U38970 Rattus norvegicus MHC | U38970 Rattus norvegicus MHC | M301018 Rattus norvegicus MHC | M30548 R. sapiens HLA-E*01 varia | X87678 H. sapiens HLA-E*01 varia | X87678 H. sapiens HLA-E*01 varia | A3002533 Homo sapiens HLA-E*01 varia | A3002533 Homo sapiens HLA-E*01 varia | A3008505 Bos taurus mRNA for MHAB00850 Bos taurus mRNA for MHAB008602 Bos taurus mRNA for MHAB008602 Bos taurus gene for MHAB008602 Bos taurus gene for MHAB008603 Bos taurus gene 
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059643 Leontopithecus rosalia
X54375 G.gorilla MHC Class I
AJ249700 Rattus norvegicus par
                                                                                                                                                                                                                                                                         -MODEL-frame+_p2n.model -DEV=xlp
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-O=/cgn1_1/USPTO_spool/US08653294/runat_04D00 -GAPEXT=4.000
-OB-Gembla -CFWPT-fastap -SUFFIX=rege -GAPED=1.000 -GAPEXT=4.000
-GAPEXT=0.000 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPED=4.500
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                                                                                                                                            software, version 4.5,
       out_format : pfs
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6291
                                                                                                                                            About: Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
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   OM Of: US-08-653-294-37
                                                                         Date: Feb 8, 2000 10:26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query: US-08-653-294-37
Query length: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9D_rC: RNRT1A2F

9D_rC: RNRJ1A10G

9D_rC: RNRJ1A10G

9D_rC: RNRJ1A10G

9D_rC: RNRJ1A1014

9D_rC: RNRJ1A910

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9D_rC: RNRJ1A910

9D_rC: RNJ1B970

9D_rC: RNRT1A1CG

9D_rC: RNRT1A1CG

9D_RC: RNRT1A1CG

9D_RC: RNRT1A1CG

9D_RC: RNRT1A1CG

9D_RC: RNRT1A1CG
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gb_ro:RNO249700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       score_list:
Sequence
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LOCUS DEFINITION

ACCESSION VERSION

KEYWORDS

ORGANISM

SOURCE

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VGSDGSLLRGYRQDAYDGRDYIALNEDLKTWTAADFAAQITRNKWERARYAERLRAYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGTCVEWLRRYLELGKETLLRSDPPRAHVTLHPRPEGDYTLRCWALGFYPADISLSWQ
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SLSTDSNMETTVIXVVLGAVAIIAAVIIGAVVAVVRKRRRNTGGKGDYTPAPGRDSSQ
                                                                                                                                                                                                                                                                                                     Submitted (27-JUL-1995) E. Joly, The Babraham Institute, Babraham, Cambridge, CB2 4AT, UK
(Cambridge, CB2 14T, UK
(Dases I to 10.38)
Joly, E., Le Rolle, A. F., Gonzalez, A. L., Mehling, B., Stevens, J.,
(Coadwell, W. J., Huenig, T., Howard, J.C. and Butcher, G.W.
(Co-evolutation of rat tap transporters and MHC class 1 R11-A
                                       X90373.1 GI:1871632
alpha chain; class 1 antigen; major histocompatability complex.
                                                                                                                              Mammalia; Eutheria;
Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Curr. Biol. In press
On Mar 10, 1997 this sequence version replaced gi:940822.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 10
Gaps: 0
Percent Identity: 100.000
  norvegicus mRNA for RI1.A1(0) alpha chain
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                                                                            Norway rat.

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata;
Rodentia; Sciurognathi; Muridae; Murinae;
I (bases 1 to 1038)
Joly, E., Gonzalez, A.L. and Butcher, G.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Rattus norvegicus"
/strain="R71(0)"
/isolate="88(1) 29.6.92"
/db_xref="taxon:10116"
/chromosome="20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="spleen"
/cell_type="splenocyte"
1. .1038
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                                                                                                                                                                                                                                      2 (bases 1 to 1038)
Joly, E.
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                                                                                                                                                                                                                                                                                     Direct Submission
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US-08-653-294-37 x RNRT1A10G
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Ratio: 5.100
Percent Similarity: 100.000
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LOCUS RNRT1A20G
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VERSION
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DEFINITION
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AUTHORS
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REFERENCE
AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (16-SEP-1999) le Rolle A.F., Ceilular Immunology Program,
The Babraham Institute, CB2 4AF, Cambridge, UNITED KINGDOM
Location/Qualifiers
1 1038
/organism="Rattus norvegicus"
/strain="BUF"
/db_xref="taxon:10116"
/Abplotype="R11b"
/clone="Bb+8"
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VGTDGSLLRGYEQHAYDGRDYIALNEDLKTWTAADFAAQITRNKWDQAGAAERSRAYL
                                                                                                                                                                                                                                           major histocompatibility complex; MHC class IA antigen; RT1-A2b
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 1038)
LeROlle,A., Joly,E. and Butcher,G.
Characterisation of the rat MHC class I molecules
                                                                                                                                 29-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-1998
                                                                                                                              RNO249705 1038 bp mRNA ROD 29.NOV-19
Rattus norvegicus partial mRNA for MHC class Ia A2b antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_name="MHC class Ia antigen"
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223 CGAGTGGACCTGAGGACCCTGCGGGGCTAC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 CGAGTGGACCTGAGGACCTGCGCGCGTAC 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="RT1-A2b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="RT1-A2b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                    AJ249705.1 GI:5912595
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                                                                                                                                                                                                                                                                                     Norway rat.
Rattus norvegicus
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US-08-653-294-37 x RNO249705
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Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                          (RT1-A2b gene).
AJ249705
                                                                seq_name: gb_ro:RNO249705
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                                                                                                       seq_documentation_block:
LOCUS RNO249705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Le Rolle, A.F.
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LOCUS RNRT1A10G
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230

BASE COUNT

ORIGIN

alignment_scores:

Unpublished

JOURNAL REFERENCE AUTHORS TITLE

JOURNAL

REFERENCE AUTHORS TITLE

source

FEATURES

gene

12-FEB-1998

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VGSDGSLLRGYRQDAYDGSDYIALNEDLKTWTAADFAAQITRNKWERRYRYBELRAYL
EGTCVESLRGYLELGKETLLRSDPPEAHYTLHPRPEGDYTLRCWALGFYPADITLTWQ
LNGEDLYQDMELVETRPAGGGTFGKWASVVVPLGKEONYTCRYEHEGLEYPLGGRWEP
SPSTDSNMETTVIYVILGAVAMIGAVAHIGAMVAVVRRKRNTGGKGEYAPARGNDSS
                                                                                                                                                                                         Mehling B.

Jurect Submission

Submitted (A.7-JUN-1997) Mehling B., Universitaet Wuerzburg,

Institut fuer Virologie und Immunbiologie, Versbacherstr. 7 97078

Werzburg, GERMANN

Joly, B., LeRolle, A., Gonzalez, A.L., Mehling, B., Stevens, J.,

Co-Scolution of rat TAP transporters and MHC Class I RTI-A

molecquies
                                                                                                                                                                                                                                                                                                                                                                                                                        % (bases 1 to 1041)
Joly E., Le Rolle, A.F., Gonzalez, A.L., Mehling, B., Stevens, J.,
Joly E., Le Rolle, A.F., Gonzalez, A.L., Mehling, B., Stevens, J.,
Coadwell, W.J., Huenig, T., Howard, J.C. and Butcher, G.W.
Co-evolutation of rat tap transporters and MHC class 1 RT1-A
molecules

Curr. Biol. In press
Location/Qualifiers
J. 1041
/organism="Rattus norvegicus"
/strain="LEW-1F" (f haplotype)"
/db_xref="taxon:10116"
                                                                                                                                Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 1041)
        Rattus norvegicus mRNA for MHC class I alpha chain, partial.
Y14014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 10
Gaps: 0
Percent Identity: 100.000
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/note="alpha 1-domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271. .546
/note="alpha 2-domain"
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/note="alpha 3-domain"
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988. .>1041
/note="cytoplasmic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           958. .987
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                                                Y14014.1 GI:2225994
MHC class I alpha chain.
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                                                                                         Norway rat.
Rattus norvegicus
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Ratio: 5.100
Percent Similarity: 100.000
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US-08-653-294-37 x RNY14014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="GSHSLRYFYIAVSRPGLGEPRYMEVGYVDDTOFVRYDSDAENPR
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VGSDGSLLRGYRQDAYDGRDYIALNEDLKTWTAADFAAQITRNKWERARYAERLRAYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BGTCVESLRRYLELGKETLLRSDPPEAHVTLHPRPEGDYTLRCWALGFYPADITLTWO
LNGEDLTQDMELVETRPAGDGTFQKWASVVVPLGKEQNYTCRVEHEGLPEPLSGRWEP
SPSTNSNMETTVIYVVLGAIIGTLAIIGIVVAVVRRRRRNTGGKGGNYAPAPGRDSSQ
                                                                                                                                                                                                                                                                                                    E. Joly, The Babraham Institute, Babraham,
                                                                                                                                                                                                                                                                                          Submitted (27-301-1995) E. Joly, The Babraham Institute, Babraham, Cambridge, CB2 4AT, UK
Cambridge, CB2 4AT, UK
E. 3 (bases 1 to 1038)
S Joly, E., Le Rolle, A.F., Gonzalez, A.L., Mehling, B., Stevens, J., Coadwell, W.J., Huenig, T., Howard, J.C. and Butcher, G.W.
Co-evolutation of rat tap transporters and MHC class 1 RT1-A molecules
Curr. Biol. In press
On Mar 10, 1997 this sequence version replaced gi:940828.
Location/Qualifiers
on Mar 10, 1038
Curr. Biol. This sequence version replaced ji:940828.
Curr. Biol. This sequence version replaced ji:940828.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product-"Mature alpha chain of major histocompatibility complex class I antigen"
/protein_id="CAA62022.1"
/db_xref="GI:1871637"
/db_xref="SPTREMBL:Q95567"
                     X90372 X90372.1 GI:1871636 alpha chain; class 1 antigen; major histocompatability complex.
                                                                                                                        Mammalia; Eutheria;
Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-FEB-1998
      norvegicus mRNA for RT1.A2(0) alpha chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 0
Percent Identity: 100.000
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                                                                                     Norway rat.

Rattus norvegicus

Eukaryota: Metazoa; Chordata; Vertebrata;

Rodentia; Sciurognathi; Muridae; Murinae;

I (bases 1 to 1038)

Joly, E., Gonzalez, A.L. and Butcher, G.W.

Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="RT1(0)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="spleen"
/cell_type="splenocyte"
1. 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="RT1.A2(0)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="RT1.A2(0)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSDVSLPDCKA"
278 c
                                                                                                                                                                                                                                 (bases 1 to 1035)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /germline
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US-08-653-294-37 x RNRT1A20G
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Ratio: 5.100
Percent Similarity: 100.000
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LOCUS RNY14014
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                                                                                                                                                                                                                                                         Joly, E.
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to: 1047

from: 1

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2 (bases 1 to 1056)
Le Rolle,A.F.
Direct Submission
Submitted (16.5EP-1999) Le Rolle A.F., Cellular Immunology Program,
The Babraham Institute, CB2 4AF, Cambridge, UNITED KINGDOM
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AJ249704.1 GI:5912593 major histocompatibility complex; MHC class IA antigen; RT1-Alb
                                                                                                                                                                                                                                                                                                                             RNO249704 1056 bp mRNA ROD 29-NOV-1999
Rattus norvegicus partial mRNA for MHC class Ia Alb antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; I (bases 1 to 1055)
LeRolle, A., Joly E. and Butcher, G. Characterisation of the rat MHC class I molecules
                                                                                                                                                     223 CGAGTGGACCTGAGGACCTGCGCGGCTAC 252
                                                                                                                      1 ArgValAspLeuArgThrLeuArgGlyTyr
                                                           to: RNPEPPRES
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US-08-653-294-37 x RNPEPPRES
                                                                                                                                                                                                                                                                                                                                                                                     (RT1-Alb gene).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Norway rat.
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                                                                                                                                                                                                                                                                        RNDEPPRES 1047 bp mRNA ROD 12-FEB-1998
R. norvegicus mRNA for protein involved in peptide presentation
Y08532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 (bases 1 to 1047)
Joly,E., Le Rolle,A.F., Gonzalez,A.L., Mehling,B., Stevens,J.,
Coadwell,W.J., Huenig,T., Howard,J.C. and Butcher,G.W.
Co-evolutation of rat tap transporters and MHC class 1 RT1-A
molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Vertebrata; Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 1047)

Le Rolle,A.F., Butcher,G.W. and Joly,E.

(pases 1 to 1047)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="splenocytes"
/note="identical sequence obtained from PC12 cells'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Curr. Biol. In press
On Mar 10, 1997 this sequence version replaced g1:1619331.
Location/Qualifiers
1. 1047
/Organism...Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission submission Submitted (01-OCT-1996) E. Joly, The Babraham Institute, Immunology, Babraham Hall, Babraham, Cambridge CB2 4AT, 3 (bases 1 to 1047) Joly, E., Gonzalez, A.L. and Butcher, G.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 10
Gaps: 0
Percent Identity: 100.000
                               to: 1041
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/db_xref="taxon:10116"
/chromosome="20"
                                                                                                                                                     223 CGAGTGGACCTGAGGACCCTGCGCGGCTAC 252
                                                                                          1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                           Y08532.1 GI:1871630
peptide presentation protein.
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/haplotype="RT1g"
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                            Align seg 1/1 to: RNY14014 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="RT1.Ag"
<1. .1038
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Rattus norvegicus
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Ratio: 5.100
Percent Similarity: 100.000
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                                                                                                                                                                                                                seq_name: gb_ro:RNPEPPRES
                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS RNPEPPRES
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ORIGIN
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KEYWORDS
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/organism="Rattus norvegicus"

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YEPRARMEREREPEYWEOOTRIAKENBOVNRVDHTELAGYYNGSEGSHTIGERGGCD
VGSDGSLLRCYEQHAYDGROVIALNEDDLKTWAADFAAGITREKWERARYAERLRAYL
EGTCVEWLRRYLEHGKETLLRSDPPRAHVTLHPRPEGDVTLRCWALGFYPADISLSWO
INGEDLTOOMELVETRAAGGTFOKWASVYVPLGKEONYTCRYEHEGLEPLEORWEP
SLSEDSNMETYFTRAGGOTFOKWASVYVPLGKEONYTCRYEHEGLEPLEORWEP
GLSSDNSIMETYTVYVLGAVALIAAVIIAAVYTVYRRRRRNTGGKGGVYTPABGGEDS
GSSDVSLPDCKA"
                                                                                                                                                                                                       /standard_name="MHC class Ia antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                              /function="presentation antigen
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                                                                                                                                                                                                                                                                                          /protein_id="CAB56215.1"
/db_xref="GI:5912594"
                /db_xref="taxon:10116"
/chromosome="20"
/haplotype="RT1b"
/clone="Ba8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     354 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                             /gene="RT1-Alb"
                                                                                                                                      /gene="RT1-A1b"
                                                                                                                                                                                                                                                   /codon_start=1
/strain-"BUF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 C
                                                                                                                                                           <1. .1041
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US-08-653-294-37 x RNO249704
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Ratio: 5.100
Percent Similarity: 100.000
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KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL MEDLINE

TITLE

REFERENCE AUTHORS JOURNAL

ACCESSION VERSION

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Vances 1 to 1588)
Wang, M., Tlan, L., Langowski, J.L., Stepkowski, S.M. and Kahan, B.D.
Direct Submission
Submitted (20-071-1995) M. Wang, Division of Immunology & Organ
Transplantation, Department of Surgery, University of Texas Medical
School, 6431 Fannin Street MSB 6.255, Houston, TX 77030, USA
1. 1588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/podduc_winc class I RT1.Ab heavy chain precursor"
/product_winc class I RT1.Ab heavy chain precursor"
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/db_xref="d2:1263198"
/db_xref="d
                                                                                                                                                                                                                            Nucleotide sequences of three distinct clones coding for rat heavy chain class I major histocompatibility antigens Immunogenetics 43 (5), 318-320 (1996)
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Rattus norvegicus MHC class I RT1.Aa alpha-chain precursor mRNA,
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Rattus norvegicus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butherla; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 1590)
                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutherla; Rodentla; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 1588)
Wang, M., Stepkowski, S.M., Tian, L., Langowski, J.L., Yu, J. and
Rahan, B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
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/haplotype="RT1.Ab"
/tissue_type="ConA stimulated splenocytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"MHC class I RTI.Ab heavy chain" a 426 c 484 g 332 t
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Gaps: 0
Percent Identity: 100.000
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64. .1101
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Percent Similarity: 100.000
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US-08-653-294-37 x RNU38970
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (31-MAY-1996) Wisconsin Regional Primate Research Center,
University of Wisconsin-Madison, 1220 Capitol Court, Madison, WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="LLLLLSGALVLTETWAGSHSMRYFYTSVSRPGRGEPRFIIVGYV
                                                                                                                                                                                                                                                                             Callithrix jacchus.
Callithrix jacchus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Primates: Platyrrhini; Callitrichidae; Callithrix.
Eutheria: Primates: Platyrrhini; Callitrichidae; Callithrix.
I (bases I to 1071)
Cadavid.L.F. Shufflebotham, C., Ruiz, F.J., Yeager, M., Hughes, A.L. and Watkins, D.I.
Evolutionary instability of the major histocompatibility complex class I loci in new world primates
Proc. Matl. Acad. Sci. U.S.A. 94 (26), 14536-14541 (1997)
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Rattus norvegicus MHC class I RT1.Ab heavy chain precursor, mRNA, complete cds.
U38970.1 GI:1263197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 1071)
Cadavid, L.F., Shufflebotham, C., Ruiz, F.J., Yeager, M., Hughes, A.L.
and Watkins, D.I.
                                                    Length: 10
Gaps: 0
Percent Identity: 100.000
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1. 1071
/organism="Callithrix jacchus"
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1. 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <1. .1071
/gene="MHC class I Caja-G"
/note="Allele: 01"</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MHC class I Caja-G"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
                                                                                                                                                                                                U59637.1 GI:1389920
                                                                                                                                                                                                                                                                   Callithrix jacchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 c
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Ratio: 5.100
Percent Similarity: 100.000
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US-08-653-294-37 x CJU59637
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seq_name: gb_pr3:CJU59637
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source

FEATURES

gene

BASE COUNT ORIGIN

DEFINITION

ACCESSION

VERSION

major

MEDLINE REFERENCE AUTHORS TITLE JOURNAL

JOURNAL

AUTHORS

TITLE

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SDLGYTLRCWALGFYPKEISITWQREGODOSODMELVETRPSGDGTFOKWAALVVPPG
EEQSYTCHVQHEGLQEPLTIRWDPPQPPVPIVGIIVGLVLVLVAGAMVAGVVIWRKRR
SGEKGGSYTQAAGSDSAQGSDVSLTKDPRV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MRVRGPQAILILLSGALALTGTRAGPHSLSYFYTAVSRPDLGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFIAVGYVDDTQFVRFDSDANDRMERRAPWIEKEGOBYWDRETQIORDTSGYYRYDL
KTLRGYYNQSEAGSHTLQSMYGCYLGPDGLLLRGYROFAYDGADYLALNEDLRSWTAA
DWAAQISKRKWEAANAAEQERSYLQGRCVEWLRRYLEMGKDTLQRAEPPKTHYTRHPS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

I (bases 1 to 1095)

Sullivan, J.A., Oettinger, H.F., Sachs, D.H. and Edge, A.S.B.
Analysis of polymorphism in porcine MHC class I genes: Alterations in signals recognized by human cytotoxic lymphocytes

J. Immunol. 159 (1997) In press

(bases 1 to 1095)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Platyrrhini; Cebidae; Atelinae; Ateles.
[ (bases 1 to 1071)
Cadavid,L.E., Shufflebotham,C., Ruiz,F.J., Yeager,M., Hughes,A.L.
and Watkins,D.I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Evolutionary instability of the major histocompatibility complex class I loci in new world primates

Proc. Natl. Acad. Sci. U.S.A. 94 (26), 14536-14541 (1997)

98070787
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Cadavid, L.F., Shufflebotham, C., Ruiz, F.J., Yeager, M., Hughes, A.L.
and Watkins, D.I.
                                                                                                                                                                                                        Direct Submission
Submitted (16-UTL-1997) Molecular and Cellular Biology, Diacrin
Inc., Building 96, 13th Street, Charlestown, MA 02129, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU59648 1071 bp mRNA PRI 22-JAN-1998
Ateles belzebuth MHC class I (Atbe-B01) mRNA, partial cds.
U59648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="MHC class I antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAB69339.1"
/db_xref="GI:2352986"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 CGAGTGGACCTGAAGACCCTGCGCGGCTAC 324
                                                                                                                                                                                                                                                                                               1. .1095
/organism="Sus scrofa'/db_xref="taxon:9823"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1
                                                                                                                                                                                                                                                                                                                                                                                              /gene="PC14"
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Percent Similarity: 100.000
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US-08-653-294-37 x AF014004
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                                                                                                                                                                                        Edge, A.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211
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ACCESSION
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SOURCE
ORGANISM
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ORIGIN
                                                                          AUTHORS
TITLE
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AUTHORS
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JOURNAL
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Rada,C., Lorenzi,R., Powis,S.J., van den Bogaerde,J., Parham,P. and
Howard,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFAAQITRNKWERARYAĒRLRAYLEGTCVEWLSRYLELGKETLLRSDPPEAHVTLHPR
PEGDVTLRCWALGFYPADITLTWQLNGEDLTQDMELVETRPAGDGTFQKWASVVVPLG
KEQNYTCRVEHEGLPRPLSQRWEPSPSTDSNMETTVIYVILGAVAMIGAVAIIGAMVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation-"MEAMAPRTLLLLLAAALAPTQTRAGSHSLRYFYTAVSRPGLGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RFIAVGYVDDTEFVRFDSDAENPRMEPRARWMEREGPEYWEQOTRIAKEWEQIYRVDL
RTLRGYYNQSEGGSHTIQEMYGCDVGSDGSLLRGYRQDAYDGRDYIALNEDLKTWTAA
                                                                                                                                                                                                      Submitted (21-DEC-1990) The Institute for Genetics, University of Cologne, Cologne, 50674, Germany (bases 1 to 1590)
                                                                                                                                                                                                                                                                                                                           of
                                                                                                                                                                                                                                                                         Howard,J.C.
Direct Submission
Submitted (10-MAR-1997) The Institute for Genetics, University of Cologne, Cologne, 50674, Germany
Sequence update by submitter
On Mar 11, 1997 this sequence version replaced g1:205421.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
Locus AF014004 1095 bp mRNA MAM 03-SEP-1997
DEFINITION Sus scrofa MHC class I antigen (PC14) mRNA, complete cds.
ACCESSION AF014004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"MHC RT1.Aa alpha chain signal peptide"
82. .1122
                                                                          histocompatibility complex of murine rodents
Proc. Natl. Acad. Sci. U.S.A. 87 (6), 2167-2171 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/product="MnR RT1.Aa alpha-chain precursor"
/protein_id="AAB49324.1"
/db_xref="G1:1877416"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
/tissue_type="spleen and lymph node"
/coll_line="40 hour ConA blast cell line"
10. .1125
                                                  Concerted evolution of class I genes in the major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="5' end could be at nucleotide 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVRRRKRNTGGKGGDYAPAPGRDSSQSSDVSLPDCKA'
10. .81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 10
Gaps: 0
Percent Identity: 100.000
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/product="MHC RT1.Aa alpha chain"
1558. 1564
1 423 c 493 g 338 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /crganism="Rattus norvegicus"
/strain="DA"
/db_xref="taxon:10116"
/clone="3.3/1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1 to: 1590
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                                                                                                                                             (bases 1 to 1590)
                                                                                                                                                                  Howard, J.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
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US-08-653-294-37 x RATMHCRT
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Sus scrofa
                                                                                                                  90192768
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KEYWORDS
SOURCE
ORGANISM
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ORIGIN

source

FEATURES

COMMENT

Sas

AUTHORS TITLE JOURNAL REFERENCE

REMARK

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/db_xref="taxon:9606"
/chromosome="6"
/----"--1 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 bp
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                                    /map="p21.3
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lasczyk, R.
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US-08-653-294-37 x HSHLAE012
                                                                                                                                                                                                                                                                                                                                                                                  to: HSHLAE012
                                                                                                                                                                                                                                                           Quality: 46.00
Ratio: 4.600
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_prl:HSHLAE1E2
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LOCUS HSHLAE1E2
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                                                                                                                                                                                                                                            alignment_scores:
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AUTHORS
TITLE
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VERSION
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AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                             DDTQFVRFDSDAAIPRMEPRALWMEQEGPEYWEEQTRRVKAAAQTDRVDLQTLRGYYN
QSEAGSHTIQTWYGCDVGPEGRFLRGYRQDAYDGKDY IALNEDLRSWTAADMAAQNTK
RKWEAANVAEQLRAYLEGKCQESLRRYLENGKETLQRADPPKTHVTHHPVSDHEATLR
                                                                                                                                                                                                                                                                                                                                                CWALGFYPTEITLIWQRDGEDQTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCY
VQHEGLPEPLILRWEPSSQLIIPVGIIAGLAVLVAVVIGAAVTAVMWRRKSSGGKGGS
YSQAACSDSAQGSDVSLIACKA"
 Submitted (31-MAY-1996) Wisconsin Regional Primate Research Center,
University of Wisconsin-Madison, 1220 Capitol Court, Madison, WI
53715, USA
                                                                                                                                                                                                                                                                           translation="LLLLSGALALTQTRAGSHSMRYFYTSVSRPGRGEPRFIAVGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (31-MAY-1995) R. Blasczyk, Bloodbank, Dept of Internal
Medicine, Div. of Hematology & Oncology, Virchow-Klinikum,
Humboldt-Univ. Berlin, Augustenburger Platz 1, 13353 Berlin, FRG
3 (bases 1 to 254)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (07-DEC-1995) R. Blasczyk, Bloodbank, Dept of Internal
Madicine, Div. of Hematology & Oncology, Virchow-Klinikum,
Humboldt-Univ. Berlin, Augustenburger Platz 1, 13353 Berlin, FRG
On Dec 8, 1995 this sequence version replaced 91:871291.
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 254)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSHLAEO12 254 bp DNA PRI H.sapiens HLA-E*01C230), exon 2. x87678 2. x87678 11109758 alpha chain; HLA-E*01; MHC class I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                        /product="MHC class I Atbe-B*01"
/protein_id="AAB97491.1"
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                                                    173 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .254
/organism="Homo sapiens"
/isolate="940459"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 CGAGTGGACCTGCAGACCCTGCGCGGCTAC 300
                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ArgValAspLeuArgThrLeuArgGlyTyr
                                                                                                                                                                                          'note="Allele: 01"
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                                                                                                                                                           .1071
/gene="Atbe-B"
                                                                                                                                         /gene="Atbe-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 254)
                                                                                                                                                                                                                                                                                                                                                                                                    319 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 47.00
Ratio: 4.700
Percent Similarity: 100.000
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US-08-653-294-37 x ABU59648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_pr1:HSHLAE012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS HSHLAE012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blasczyk, R.
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JOURNAL
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AUTHORS
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JOURNAL
                                                                                                                         gene
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                                                    FEATURES
                                                                                                                                                         CDS
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Direct Submission
Submitted (31-MAY-1995) R. Blasczyk, Bloodbank, Dept of Internal
Medicine, Div. of Hematology & Oncology, Virchow-Klinikum,
Humboldt-Univ. Berlin, Augustenburger Platz 1, 13353 Berlin, FRG
3 (bases 1 to 254)
Blasczyk, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (07-DEC-1995) R. Blasczyk, Bloodbank, Dept of Internal
Medicine, Div. of Hematology & Orcology, Virchow-Klinikum,
Humboldt-Univ. Berlin, Augustenburger Platz 1, 13353 Berlin, FRG
On Dec 8, 1995 this sequence version replaced gi:871293.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 254)
Blasczyk,R., Forstmann,G. and Salama,A.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="alpha chain MHC class I glycoprotein"
77 c 90 g 41 t
                                                                                                                                     /product="alpha chain MHC class I glycoprotein"
78 c 90 g 40 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H.sapiens HLA-E*01 variant (HLA-E*01t230), exon 2. X87680
                                                                                                                                                                                                                                                                           Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRI
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'note-"allele HLA-E*01C230'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha chain; HLA-E*01; MHC class I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/isolate="940637"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
                   17. .254
/gene="HLA-E*01"
17. .>254
/gene="HLA-E*01"
/number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="HLA-E*01"
/number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="HLA-E*01"
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us-08-653-294-37.rge

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Direct Submission
Submitted (31-0CT-1997) Steffensen R., Aalborg Sygehus, Department
of Clinical Immunology and Blood Transfusion, 9000 Aalborg, DENMARK
2 (bases 1 to 270)
Steffensen, R., Christiansen, O.B., Bennett, E.P. and Jersild, C.
HLA-E polymorphism in patients with recurrent spontaneous abortion
99110147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codoi_start=3
/protein_id="CAA05526.1"
/protein_id="CAA05526.1"
/db_xxef="GT:3929739"
/translation="SHSINFFHTSVSRPGRGEPRFISVGYVDDTQFVRFDNDAASPRM
/translation="SHSINFFHTSVSRPGRGEPRFISVGYVNDSTQFVRFDNDAASPRM
/vPRAPMMEDEGSEYWNRETRRAFTRGYVNGSEA"
85 c 92 g 44 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Vertebrata; Mammalla; Eutherla;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 270)
                                                                                                                                                                                                                                                                                                                       19-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <1. >270
/gene="HLA-E"
/note="PCR product derived from human genomic DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leugth: 10
Gaps: 0
Percent Identity: 90.000
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                   Quality: 46.00 Length: 10
Ratio: 4.600 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 90.000
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                                                                                                                                                                                                                                                                                                                                                                     AJ002533.1 GI:3929738
HLA-E gene; human leukocyte antigen.
human.
                                                                                                                                                    to: 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. 270
7. Granism="Homo sapiens"
7db.xref="taxon:9606"
1. 270
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                                                                                                                                                                                                                            206 CGAGTGAATCTGCGGACGCTGCGCGGCTAC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 CGAGTGAACCTGCGGACGCTGCGCGCGTAC 251
                                                                                                                                                                                                                                                                                                                   HSAJ2533 270 bp DNA
Homo sapiens HLA-E gene exon 2.
AJ002533
                                                                                                                                                                                       1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                    from: 1
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                                                                                                                                                  Align seg 1/1 to: HSHLAE1E2
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Ratio: 4.600
Percent Similarity: 100.000
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US-08-653-294-37 x HSHLAElE2
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US-08-653-294-37 x HSAJ2533
                                                                                                                                                                                                                                                                seq_name: gb_pr1:HSAJ2533
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alignment_scores:
Quality:
Ratio:
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ORIGIN
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TITLE
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MEDLINE
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Human neuronal calcium chan
Human neuronal calcium chan
Human mitosin gene. Purifie
Mitosin nucleic acid sequen
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Tymphocytes - for producing cytotoxic T cells for immuno-therapy of
Cancers and viral infection
Example 2; Fig 10; 222pp; French.

Example 2; Fig 10; 222pp; French.

Control of antigen-specific lymphocytes comprises forming a complex
Control of antigen-specific lymphocytes comprises forming a complex
Control of antigen-specific lymphocytes compatibility complex (MHC) molecules,
confined antigen-specific lymphocytes. Expression of the MHC molecule in a cell
confined of antibody against the MHC molecule or by an antibody to
can specific lymphocytes. Expression of the MHC molecule or a cell
confined of antibodies against the MHC molecule or by an antibody to
can comprise the first 3 domains of the HLA-A2.1 heavy chain linked to human
confined to man a floatible linker. The method is also used to
detect and quantify tumour-specific T-cells and to generate CTC for
specific killing of tumour cells (solid tumours, leukaemia or lymphoma)
by infections.
                                                                                                                                                                                                                    14-OCT-1998 (first entry)
Chimeric HLA-A2.1/Deta-2 microglobulin coding sequence.
Antigen; major histocompatibility complex; MHC; lymphocyte; detection; immobilisation; cytotoxic T-cell; tumour; leukaemia; lymphoma; viral infection; chimeric; beta-2 microglobulin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "chimeric HLA-A2.1/beta-2 microglobulin"
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HLA-C exon Cb-1.
Human leukocyte antigen; probe; major histocompatibility complex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-NOV-1997.
21-MAY-1997; F00892.
21-MAY-1996; US-651925.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
(INSP ) INST PASTEUR.
Abastado J. Koutilsky P. Langlade-Demoyen P. Lone Y; WPI; 98-018653/02.
P-PSDB; W68385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Percent Identity: 90.000
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.6e+03
.3e+03
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1. .1239
/*tag= a
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88.25
88.18
86.31
86.31
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ID Q12116 standard; DNA; 1101
AC Q12116;
                                                                                                                                                                            seq_documentation_block:
ID V30457 standard; DNA; 1284
33.00
33.00
33.00
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                                                                                                                            seq_name: N_Geneseq_36:V30457
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US-08-653-294-37 x V30457
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Percent Similarity:
N_Geneseq_36:Q84662
N_Geneseq_36:Q84663
N_Geneseq_36:Q86851
N_Geneseq_36:V09076
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                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                         1284 | Chimeric Hia-A2.1/Deta-2 micro
1101 | Hia-C exon Cb-1. Hia-C gene, I
1101 | Hia-C exon Cb-2. Hia-C gene, I
13789 | Amycolatopsis mediterrane iri
11770 | Streptococcus pneumoniae genc
1265 | Streptococcus pneumoniae genc
28598 | Sorangium cellulosum soraphen
28958 | Sorangium cellulosum soraphen
28958 | Sorangium cellulosum soraphen
4937 | The soraphen biosynthesis gen
4937 | The soraphen biosynthesis gen
5127 | Swine HEV ORF I genomic DNA. N
51000 | Continuation (7 of 10) of
110000 | Continuation (8 of 10) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Taenia ovis antigenic polypepti
T. ovis vaccine candidate antig
I. para antigenic polypepti
I. Lipase modulating factor gene,
I. Lipase/lipase modulator fusion
Sequence encoding enzyme which
Sequence encoding enzyme which
Rhodococcus rhodochrous desulp
IDNA encoding enzymes capable
IDNA encoding enzyme capable
IDNA encoding an enzyme capable
I Drail base sequence of rice
VOR Hippel-Lindau disease gene
IHLA-B35 exon. HLA-B35 gene
VOR Hippel-Lindau disease gene
IHLA-B35 exon. HLA-B35 gene
IHLA-B7 expression vector. New
PHLA-B7 expression vector. New
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Tumour rejection antigen precu
Tumour rejection antigen precu
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Calcium channel alpha-1E subun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Hereditary haemochromatosis
| Hereditary haemochromatosis,
| Mouse NF-AT Interacting Protei
| Human secreted protein gene 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human calcium channel 27980/10
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                                                                                                                                                                                                 -MODEL-frame-pol.model -DEV-xlp
-Q=/Cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.2
-Q=/Cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.2
-Q=/Cgn1_1/USPTO_spool/US08653294/runat_04022000_16000
-QAPPETT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000
-QAPPETT=4.000 -OGAPEXT=0.000 -XGAPEXT=0.000
-FGAPOP=6.000 -FCAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP=6.000 -FCAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-pct
-ALIGN=15 -MODE=LOCAL -OUTFMT=Pfs -NORM-ext -MINLEN-0
-MAXLEN=1000000 -USER=US08653294 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
                                                                                                    Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
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2118
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1134525
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11019
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us-08-653-294-37.rng

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HIA-C gene, DNA probe and transformant cells - for immunisation of animals and monoclonal antibody development.

Claim 2; Page 1; 13pp; Japanese.

Probes comprising part of the sequence can be used to identify class I genes. The DNA can be expressed for immunisation of animals and produ. of monoclonal antibodies specific for the HIA-C antigen. See also 01216 (same patent) and J03112486 and J03112487. sequence 1101 BP; 215 A; 335 C; 379 G; 172 T;
                                                                                                                                                                                                     HIA-C gene, DNA probe and transformant cells - for immunisation of animals and monoclonal antibody development.

Claim 1; Page 1; 13pp; Japanese.

Probes comprising part of the sequence can be used to identify class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HIA-C animals and prodn. of monoclonal antibodies specific for the HIA-C sequence 1101 BP; 211 A; 337 C; 377 G; 176 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA-C exon Cb-2. Human leukocyte antigen; probe; major histocompatibility complex; MHC; class I; ss. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouality: 40.00 Length: 10 Ratio: 4.000 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                               Quality: 40.00 Length: 10
Ratio: 4.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 80.000
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(OLYU ) OLYMPUS OPTICAL KK.
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22-SEP-1989; 247695.
22-SEP-1989; UP-247695.
(OLVU ) OLYMPUS OPTICAL KK.
WPI; 91-182989/25.
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22-SEP-1989; 247695.
MHC; class I; ss.
Homo sapiens.
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                                                                                                                                                                                           P-PSDB; R12465
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                                                                                    J03112485-A
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seq_documentation_block:

ID V21187;
AC V21187;
DT 24-JUL-1998 (first entry)
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KW Amycolatopsis mediterranel: rifamycin; synthesis; gene cluster;

KW Amycolatopsis mediterranel: rifamycin; synthesis; gene cluster;

KW polyketide synthase; actinomycete; ansamycin; ds.

OS Amycolatopsis mediterranel:

FT CDS Li543

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                                       1 ArgvalAspLeuArgThrLeuArgGlyTyr 10
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 Align seg 1/1
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Streptococcus pneumoniae genome fragment SEQ ID NO:134. Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay; computer readable medium; vaccine; pharmaceutical composition; ds.

07-MAY-1998. 30-CCT-1997; U19588. 31-CCT-1996; US-029960. (HUMA-) HUMAN GENOME SCI INC. BATASH SC, Chol GH, Dillon PJ, Dougherty BA, Fannon M, Kunsch CA, Rosen CA:

11503 GATATGAGGACGTTAAAAGGTTAC 11480

seq_name: N_Geneseq_36:V52267

V52267 standard; DNA; 12665 BP.

seq_documentation_block

23-OCT-1998 (first entry)

Streptococcus pneumoniae

3 AspleuArgThrLeuArgGlyTyr 10

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by a process comprising: (a) streething agenomic DNA library using as a process comprising: (a) streething agenomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 (a) 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or CDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome. Products from the present fragments of the S. pneumoniae genome. Products from the present compositions and vaccines for S. pneumoniae. Some sead in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V5254) recorded on it, or a representative fragment or a sequence at least 958 identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391 (V52134 to V5.524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Computer readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae genome fragment SEQ ID NO:172.
Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
computer readable medium; vaccine; pharmaceutical composition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-0CT-1997; U19588.
31-0CT-1996; US-029960.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M,
Kunsch CA, Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to reverse of: V52305 from: 1 to: 11770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 6 Gaps: 0 Percent Identity: 75.000
                      Length: 9
Gaps: 0
Percent Identity: 77,778
                                                                                                                                                                                         to: V21187 from: 1 to: 53789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 1094-1101; 1409pp; English.
                                                                                                                                                                                                                                                                                       20272 AAGCTCGACCTGCGGACGCTGCGCGGC 20298
                                                                                                                                                                                                                                            Q
                                                                                                                                                                                                                                       1 ArgValAspLeuArgThrLeuArgGly
                                                                                                                                                                                                                                                                                                                                                                                                              V52305 standard; DNA; 11770 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-37 x V52305/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae.
                                                Ratio: 4.222
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                            seq_name: N_Geneseq_36:V52305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio: 4.625
Percent Similarity: 100.000
                         38.00
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                                                                                                                    alignment_block:
US-08-653-294-37 x V21187
                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
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                           Quality:
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alignment_scores
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The present invention describes a computer readable medium which has
The present invention describes a computer readable medium which has
The present invention describes a computer readable medium which has
The nucleotide sequences SEQ ID No.; it to 391 (752134 to V52524) recorded
The nucleotide sequences to a sequence at least 95% identical
To 391 (V52134 to V52524) are genomic fragments from Streptococcus
The present invention also describes an isolated nucleic acid
molecule encoding a homologue of any of the fragments of the S. pneumoniae
The present invention also describes an isolated nucleic acid
molecule encoding a homologue of any of the fragments of the S. pneumoniae
The process comprising; (a) screening a genomic DNA library using as a
probe a target sequence defined by any of the sequences in SEQ ID No: 1
That hybridise to the target sequence and isolating encoding to any produced
from an organism, amplifying nucleic acid molecules whose nucleotide
from an organism, amplifying nucleic acid molecules whose nucleotide
sequence is homologous to amplification primer the amplification and
isolating the amplified sequences. The computer readable medium can be
used in a computer-based system for identifying fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical
                                                                                                                   Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2890 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 12665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Percent Identity: 75.000
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Sorangium cellulosum soraphen gene cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: V52267 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12528 GATATGAGGACGTTAAAAGGTTAC 12505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seg_documentation_block:
ID T06769 standard; DNA; 28598 BP.
AC T06769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-37 x V52267/rev
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Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                compositions and vac
Sequence 12665 BP;
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                                                                                                                                                                                               oneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protecting plants against pathogens with genetically transformed biological control agent - which expresses all polypeptide(s) biological control agent - which expresses all polypeptide(s) an unverse protecting by protolitin biosynthetic pathway as 16; Column 104-128; 88pp; English.

This genomic DNA sequence encodes the Soraphen gene cluster. This sequence encodes two open reading frames (ORF's), the positions of which size and encodes 5 biosynthetic modules homologous to the erythromycin genes of Saccharopolyspora erythraea. Each module contains a genes of Saccharopolyspora erythraea. Each module contains a beta-ketoacylsynthase (KS), an acyltransferase (AT), a ketoreductase (KR) and an acyl carrier protein (ACP) domain. ORF2 is immediately adjacent to ORF1 and is thought to contain 3 modules. Soraphen is a crypt page (PRS) which has antiblotic activity.

Transgenic plants containing such antipathogenic genes like those encoded in the Soraphen cluster should have enhanced resistance to
                                                                                                                      7 14-DEC-1995.
7 10-MAY-1995. IBO414.
8 (CIBA ) CIBA GEIGY AG.
1 Beck JJ, Gaffney TD, Hammer PE, Hill DS, Lam ST;
8 Lighon J, Ryals JA, Schupp T, Uknes SJ;
8 Lighon J, Ryals JA, Schupp T, Uknes SJ;
8 Lighon J, Ryals JA, Schupp T, Uknes SJ;
8 WPI; 96-040226/04.
7 New genes for biosynthesis of anti-pathogenic substances - pref.
8 Pyrrolnitrin and soraphen, useful for disease control in plants pyrrolnitrin and soraphen, useful for disease control in plants
8 Claim 3; Page 140-158; 190pp; English.
9 This is the soraphen gene cluster from S. cellulosum. The gene cluster may be expressed recombinantly to produce soraphen, or expressed in a transgenic plant for disease-resistance.
9 Sequence 28598 BP; 4031 A; 11703 C; 8263 G; 4601 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     4601 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4655 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAR-1998 (first entry)
Sorangium cellulosum soraphen gene cluster genomic DNA.
Soraphen; polyketide synthase; PKS; antipathogenic; antibiotic; transgenic plant; phytopathogen; resistance; ss.
fungicide; posticide; myxobacterium; phenylpyrrole; antibiotic; Sorangum cellulosum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8356 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 28598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lenyth: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hill DS,
Uknes SJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: T06769 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191111111 | 11111111::: 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 | 3949 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hammer PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beck JJ, Gaffney TD, Hammer PE.
Ligon JM, Ryals JA, Schupp T,
WPI; 97-447901/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4084 A;
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ID T89956 standard; DNA; 28958 BP
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Sequence 28958 BP; 4
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01-JUN-1995; 457342.
20-JUL-1990; US-570184.
02-JUL-1992; US-908284.
31-AUG-1992; US-937648.
01-JUL-1993; US-087636.
08-JUN-1994; US-258261.
(CIBA ) CIBA GEIGY CORP.
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4.111
90.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
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                                                                                                    WO9533818-A2.
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11-MAY-1998 (first entry)
The soraphen biosynthesis gene cluster from Sorangium cellulosum.
The soraphen biosynthesis gene cluster from Sorangium cellulosum.
Polyketide synthase; PKS; blosynthesis; soraphen; SorR; SorB;
SorM; blosynthetic module; beta-kercacyisynthase; acyltransferase;
ketoreductase; beta-ketone processing domain; cytostatic agent;
antimicrobial agent; phytopathogenic fungl; transgenic plant;
Sorangium cellulosum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "gene product is highly homologous to type I PKSs that are known to be involved in the synthesis of polyketide compounds"
                                                                                                                                                                                                                                                                                                                                                                                ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note- "gene product is highly homologous
type I PKS genes"
19870. .24556
                                                                                                       from: 1 to: 28958
Length: 10
Gaps: 0
Percent Identity: 70.000
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                                                                                                                               /*tag- d
/note- "module 2 of Sk
/1455, 19616
/note- "module 3 of Sk
19871. 46318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note- "module 4 of S
40190. .46318
/*tag- 1
/note- "module 5 of S
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note= "module 1 of
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                                                                                                      to reverse of: T89956
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                                                                                                                                                                                                                      seq_documentation_block:
ID V05287 standard; DNA; 49377 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product- SorA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= g
/product= SorB
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/*tag= h
/prn
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.7115
                                                           alignment_block:
US-08-653-294-37 x T89956/rev
                  4.111
                                                                                                                                                                                           seq_name: N_Geneseq_36:V05287
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24638.
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   Quality:
Ratio:
                           Percent Similarity:
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SorB"

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Percent Similarity:
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                                                                                                                                                      contamination
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                                                                                                                                                                         Sequence
 888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence contains a cluster of genes that encode polyketide synthases (PKSs) that are involved in the synthasis of soraphens in sorangham cellulosum. The proteins encoded by the present sequence are Sorangium cellulosum. The proteins encoded by the present sequence are Soran, Sorah, SorB and SorM. SorA and SorB contain biosynthetic modules which contain a beta-ketoacylsynthase, an acyltransferase, a ketoreductase and an acyl carrier protein domain, as well as beta-ketone processing domains. S. cellulosum soraphens are useful as a cytostatic and antimicrobial agent active against phytopathogenic fungi. Soraphen-producing transgenic plants or biological control agents can also be produced, which may reduce crop losses and nutritional deprivation for local populations in many parts of the world. Sequence 49377 BP; 19522 C; 14477 G; 8131 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated swine hepatitis E virus - used to develop products for the diagnosis, prevention and treatment of hepatitis E virus infection in mammals, particularly humans Example 1; Fig 6A-C; 70pp; English.

This invention describes a swine hepatitis E virus (HEV) and its natural mutants which are capable of cross-reacting with antibodies reactive with a human HEV strain or natural mutants. The HEV and the proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JUN-1999 (first entry)
Swine HEV ORF 1 DNA.
Swine hepatitis E virus; HEV; cross-reaction; antibody; human; therapy;
vaccine; immunise; infection; detection; diagnosis; prevention; ss.
      foot...
/product = SorM
/product = SorM
/note= "gene product is homologous to the methyltransferase from Streptomyces methyltransferase from Streptomyces hygroscopicus that is involved in the synthesis of the polyketide rappamicin"
                                                                                                                                                                                                                                             DNA encoding Sorangium cellulosum polypeptide(s) - used for, e.g. blosynthesis of soraphen useful as antimicrobial agent against phytopathogenic fungi
                                                                                                     US5716849-A.
10-FEB-1998.
14-DEC-1996; 764233.
24-AUG-1993; WG-U07954.
08-JUN-1994; US-258261.
09-CCT-1996; US-729214.
(NOVS. ) NOVARTIS FINANCE CORP.
BECK JJ, HILL DS, Ligon JM, Neff S, Ryals JA, Schupp T; WPI; 98-158369/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 49377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.00 Length: 10
4.111 Gaps: 0
90.000 Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: V05287 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20281 AGGGTCGATGCCCGCACGCTCGAAGGCTTC 20252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JAN-1999.
17-JUL-1998; U14665.
18-JUL-1997; US-053069.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Emerson SU, Meng X, Purcell RH;
WPI: 99-132270/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID X23031 standard; DNA; 5127 BP.
.47891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-37 x V05287/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: N_Geneseq_36:X23031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis E virus.
WO9904029-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
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The diagnosis, prevention and treatment of hepatitis E virus for the diagnosis, prevention and treatment of hepatitis E virus for the diagnosis, prevention and treatment of hepatitis E virus for the diagnosis, particularly humans

Frample 1, Fig 7A-D; 70pp; English

Example 1, Fig 7A-D; 7app; English

Example 1, Fig 
can be used in vaccines for immunising against HEV infection. The swine HEV can be used in humans to prevent possible infection by human HEV. The swine HEV can also be used as a therapeutic treatment for infection by other strains of HEV. The swine HEV can also be used for the production of antibodies which can be used in therapy, detection and diagnosis. The products can also be used for determining the susceptibility of cells or organs to infection with swine HEV. The swine HEV is particularly useful for the development of agents for the prevention, treatment and detection of human HEV because it is not a human virus and thus can be handled both experimentally and clinically without fear of severe infection and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUN-1999 (first entry)
Swine HEV ORF I genomic DNA.
Swine hepatitis E virus; HEV; cross-reaction; antibody; human; therapy;
vaccine; immunise; infection; detection; diagnosis; prevention; ss.
W09904029-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1892 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1328 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1880 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1383 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 5127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouality: 36.00 Length: 9 Ratio: 4.500 Gaps: 0 Percent Similarity: 88.889 Percent Identity: 88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 9
Gaps: 0
Percent Identity: 88.889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1480 C;
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17-JUL-1998; U14665.
18-JUL-1997; US-053069.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Emerson SU, Meng X, Purcell RH;
WPI; 99-132270/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1527 CGGGTCGACCTCAGAACCCTCATAGGC 1501
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US-08-653-294-37 x X23031/rev
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4.500
88.889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5127 BP;
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Ratio:
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Talministry Tage 22-24; 36pp; English.

The antigenic polypeptide encoded by this sequence, its fragments and variants can be used in a vaccine to protect against infection by a cestode parasite, particularly in ruminants. The nucleic acids (See also T17934) can be used to produce recombinant viral vaccines. The DNA (preferably this DNA sequence) can also be labelled and used as a probe to identify nucleic acids encoding a protective antigen of an Echinococcus or Taeniid parasite other than Taenia ovis. Sequence 360 BP; 98 A; 99 C; 86 G; 77 T;
                                                                                                                                      Taenia ovis antigenic polypeptide coding sequence.
Taenia ovis; antigen; vaccine; infection; cestode; parasite; probe;
viral vaccine; Echinoccus; Taeniid parasite; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-MAY-1995 (first entry)
T. ovis vaccine candidate antigen.
Vaccine; protective antigen; tapeworm; glutathione-S-transferase; fusion protein; Escherichia coll; pGEX-2T; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Taenia ovis antigenic polypeptide - used to develop vaccines protect against infection by a cestode parasite, partic. in ruminants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lawrence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio: 4.375 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 87.500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 360
                                                                                                                                                                                                                                                                                                                                                                              31-JAN-1996.
07-APR-1994; 002410.
07-APR-1993; NZ-237361.
(PITM ) PITMAN MOORE NZ LTD.
Dempster RP, Gauct C, Harrison GBL, Heath DD,
Lightowlers MW, Richard MD, Robinson CM;
WPI, 96-139972/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dempster RP, Gauci C, Harrison GBL, Heath DD,
Lightowlers MW, Rickard MD, Robinson CM;
WPI; 94-333117/41.
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07-APR-1994; NZ0029.
07-APR-1993; NZ-247361.
(NZPA-) NW ZEALND PASTORAL AGRIC RES INST LTD.
(PITM ) PITWAN MOORE NZ LTD.
(UTME ) UNIV MELBOURNE.
                                                                                                                                                                                                                                                                                                                /*tag= a
/product= Antigenic polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
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10. .372
/*tag= a
                                                                                                                                                                                                                                                           Location/Qualifiers
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ID Q72739 standard; cDNA; 600 BP.
                    seq_documentation_block:

ID 71/935 standard; CDNA; 360 BP
T 16-AUG-1996 (first entry)
DE Taenia ovis antigenic polypep
KW Taenia ovis; antigenic polypep
KW Taenia ovis; antigenic vaccine
KW Taenia ovis; antigenic vaccine
KW Taenia ovis; antigenic vaccine
FT Key Location/Qual
FT AA402410-A.
PD 31-JAN-1996.
PR 07-APR-1996; 002410.
PR 07-APR-1996; 002410.
PR 07-APR-1999; N2-237361.
PR (7-APR-1993; 
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US-08-653-294-37 x T17935/rev
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        seq_documentation_block:

        Continuation (8 of 10) of x20248 from base 700001 (Borrella burgdorferi polynucleotide WP Sequence split into 10 fragments LOCUS x20248 Accession x20248

        WP Sequence split into 10 fragments LOCUS x20248 Accession x20248
        Accession x20248

        WP X20248_01
        Begin 1 10000
        End 2 10000

        WP X20248_02
        200001 310000
        310000

        WP X20248_03
        300001 410000
        410000

        WP X20248_04
        400001 510000
        510000

        WP X20248_05
        500001 610000
        510000

        WP X20248_06
        600001 710000

        WP X20248_06
        800001 910000

        WP X20248_08
        800001 910000

        WP X20248_08
        800001 910000

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                                                       to: 7207
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Gaps: 0
Percent Identity: 60.000
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Gaps: 0
Percent Identity: 60.000
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                                                       to reverse of: X23032 from: 1
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|||:::||||::
1283 AGAATTGACATAGGAACTCTTGAGGGTTAT 1254
                                                                                                                                                                                                                                                                                                                                                                                               1110000
210000
310000
510000
610000
610000
810000
910015
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                                                                                                               1 ArgValAspLeuArgThrLeuArgGly
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US-08-653-294-37 x X20248_06/rev
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US-08-653-294-37 x X20248_07/rev
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300001
400001
500001
600001
700001
900001
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US-08-653-294-37 x X23032/rev
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4.000
90.000
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Ratio:
Percent Similarity:
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X20248_01
X20248_03
X20248_03
X20248_03
X20248_05
X20248_06
X20248_06
X20248_07
X20248_08
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                                                       Align seg 1/1
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New protective antigen from Taenia ovis - and related DNA vectors, transformed cells and antibodies, useful in vaccines, also for detecting homologous genes and proteins Disclosure; page 22-23; 37pp; English.

A T. ovis oncosphere lambda gill cDNA library was screened with rabbit antibodies raised against a 16 kDa protective antigen of T. ovis. The insert from a selected clone was subcloned into vector pGEX-2T and expressed as a glutathione-S-transferase fusion protein in Escherichia coli JMIOI. The DNA and predicted amino acid sequences of the T. ovis portion of the fusion protein were
                                                                                                                                                                                                                                   sequenced
determined.
  P-PSDB; R62045.
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alignment_scores:

Quality: 35.00 Length: 8
Ratio: 4.375 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 87.500 alignment_block: US-08-653-294-37 x Q72739/rev

121 G;

153 C;

194 A;

Align seg 1/1 to reverse of: Q72739 from: 1 to: 600

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Soares
Sugano
Sugano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jorganism="Rattus sp."

Advaref="AttC (lahost):2004068"

Abvaref="AttC (lahost):2004068"

Abvaref="AttC (lahost):2004068"

Aclone="ReNAU72"

Aclone="Tax PC-12 cells, NGF-treated (9 days)"

Aclone="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:

Anote="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:

Anote:"Anote was purified from 9-day NGF treated pro12 cells. CDNA was constructed using an oligo-dT primer and directionally cloned using the Lambda ZAP II Vector

Kit by Stratagene" 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA 9712, Medical Center Drive, Rockville, MD 20850, USA Fax: (301)-838-0208

Email: nhlee@tigr.org

Exp. clone availability please contact the TIGR Database (tobhifo@tub.tigr.org) TC (Tentative Consensus) numbers represent assemblies of ESTs.
  AA197564 mu22d05.rl
AI529689 ui81c04.yl
AI047292 ud64e05.yl
                                                                                                                                                                                                                                                                                                                                                                 Rattus sp.

Rattus sp.

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,

Eutheria, Redentia, Sciurognathi, Muridae, Murinae, Rattus.

1 (bases 1 to 351)

Liee, N. H., Weinstock, K. G., Kirkness, E. F., Earle-Hughes, J. A.,

Fuldner, R. A., Marmaras, S., Glodek, A., Gocayne, J. D., Adams, M. D.,

Kerlavage, A. R., Fraser, C. M. and Venter, J. C.

Comparative expressed-sequence-tag analysis of differential gene
expression profiles in PC-12 cells before and after nerve growth
                                                                                                                                                                                                     ST 02-APR-1998
days) Rattus sp. cDNA
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5' end similar to
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Other_ESTS: TC508
                                                                                                                                                                                         H35352 351 bp mRNA EST 02
EST109782 Rat PC-12 cells, NGF-treated (9 days) Ratt
Clone RPNAU72 similar to MHC class I, mRNA sequence.
H35352 GI:980769
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LOCUS AA376928 113 bp mRNA EST
DEFINITION EST89412 Small intestine I Homo sapiens cDNA
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US-08-653-294-37 x H35352
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                                                                                                               seg_name: gb_est4:H35352
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  gb_est11:AA197564
gb_est28:A1529689
gb_est22:A1047292
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AA132653 zo2la05.r1 Stratagene
AI316043 u191616.r1 Soares infant
AA199357 mu14h06.r1 Soares DDB
AA790185 vv82e04.r1 Stratagene
AA790185 vv82e04.r1 Stratagene
AA70545 ms87h04.r1 Soares mous
AA305941 EST176934 Jurkat T-cel
AA175455 ms87h04.r1 Soares mous
AA017870 mh47h06.r1 Soares mous
H23377 ym57e02.r1 Soares infant
AA028838 mh90f04.r1 Soares mous
AA787144 u185406.r1 Soares mous
AA787144 u185406.r1 Soares mous
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AA88673 ms8607.r1 Soares mous
AA88670 u003a02.r1 Soares mous
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AA31847 EST185704 Colon carcin

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AA176192 zp24907.rl Stratagene

AA114126 ap30006.xl Schiller as

AA102538 EST21187 Normalized r

AA1313054 EST18381 Pancreas tum

AA134053 zol8911.rl Stratagene

AA134053 zol8911.rl Stratagene

AA134053 zol8911.rl Stratagene

AA146550 mul4408.xl Soares 2NDM

AA764120 vv45503.rl Soares 2NDM

AA764120 vv45503.rl Soares 2NDM
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-Q=/cgnl_1/USPTO_spool/US08653294/runat_04022000_160700_15770/app_query.fasta.2
-Q=-cgnl_1/USPTO_spool/US08653294/runat_04000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPCT=0.000 -GAPEV=4.500
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-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
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                                                                                                             About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Query: US-08-653-294-37
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Database: EST:*
Database sequences: 4538634
Database length: 1887811982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_est36:AI876777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_est9:AA125323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
gb_est4:H35352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_est9:C17443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_est2:R12066
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DEFINITION
                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                         ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE
COMMENT
                                                                                                                                                                                                KEYWORDS
SOURCE
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                                                                                                                                                     Duman.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheriata; Primates; Catarrhin; Hominidae; Homo.

Eutheria; Primates; Catarrhin; Hominidae; Homo.

Eutheria; Drimates; Catarrhin; Hominidae; Homo.

Eutheria; Lo 113)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.B., Brandon, R.C., Man-Wai, C., Man-Wai, C., Relley, J.M., Fitzprand, L.M., Fitzprand, L.M., Fitzprand, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hadhon, E.L., Hanna, M.C., Hainkley, S.M., Marrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hastings, G.A., Haymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Annow, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence

L. Nature 377 (6547 Suppl.), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: arkerlavetigr.org

For clone availability, additional sequence and expression

For clone availability, additional sequence and expression

Information related to this EST, please check the TiGR Human Gene

Index (http://www.tigr.org/tdb/hgi/hgi.html)

Seq primer: M13 Reverse.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="ATCC (inhost):181328"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dov_stage="adult"
/dov_stage="adult"
/note="Organ: small intestine; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoI"
a 33 c 35 g 18 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Sep 12, 1996 this sequence version replaced gi:1318560
  ы
similar to major histocompatibility complex, class I, (GB:M20022), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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Gaps: 0
Percent Identity: 90.000
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                                                                                 AA376928.1 GI:2029245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Other_ESTs: THC117633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio: 4.600
Percent Similarity: 100.000
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US-08-653-294-37 x AA376928
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Quality:
                                                                                                                                            human.
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                                                                                                                                                                ORGANISM
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MEDLINE
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                                                       ACCESSION
                                                                              VERSION
KEYWORDS
                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                         SOURCE
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seq_name: gb_est13:AA377133

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Human, Bukarota; Chordata; Craniata; Vertebrata; Mammalia; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 120)

8 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Mirkness,E.F., Weinstock, M.G., Mirkness,E.F., Weinstock, M.G., Mirkness,E.F., Weinstock, M.G., Mirkness,E.F., Weinstock, M.G., Man-Wai,C., Man-Wai,C., Man-Wai,C., Fliggerand,E.M., Flitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanan,M.C., Hedblom,E., Hinble,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nouyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,L.L., Saudek,D.M., Shilley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., Hugjun,J., Li,H., Melssner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Hugjun,J., Li,H., Melssner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Hugjun,J., Li,H., Melssner,P.S., Olsen,H., Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
9712 Medical Center Drive, Rockville, MD 20850 USA
9713 Medical Center Drive, Rockville, MD 20850 USA
9712 Medical Center Drive, Rockville, MD 20850 USA
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
information related
Seq primer: M13 Reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vector: pBluescript SK-;
          AA377<u>1</u>33 128 bp mRNA EST 21-APR-1997 EST89666 Small intestine I Homo sapiens CDNA 5' end similar to similar to major histocompatibility complex, class I, E (GB:W20022), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Sep 12, 1996 this sequence version replaced gi:1326664 Other_ESTs: THC117633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 10
Gaps: 0
Percent Identity: 90.000
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/db_xref-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Small intestine I"
/dev_stage="adult"
/note="Organ: small intestine;
Site_l: EcoRI; Site_l: *Noi"
35 c 44 g 20 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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                                                                                                                                                                         AA377133
AA377133.1 GI:2029461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 46.00
Ratio: 4.600
Percent Similarity: 100.000
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US-08-653-294-37 x AA377133
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seq_documentation_block:
LOCUS AA377133
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS TITLE

JOURNAL MEDLINE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

Eutherla; Primates; Catarrhini; Hominidae; Homo.

E (bases 1 to 377)

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,

Malte,O., Sutton,G., Blake,J.A., Brandon,R.C., Man Wai,C.,

White,O., Sutton,G., Blake,J.A., Earle-Hughes,J., Fine,L.D.,

Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,

Gloddk,A., Gnehn,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,

Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,

Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,

Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
                                                                                                                                                                                                                Eukaryotz, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 356)

1 (bybblished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS AA313847.1

DEFINITION EST185704 377 bp mRNA EST Homo sapiens CDNA 5'
DEFINITION EST185704 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5'
end similar to similar to major histocompatibility complex, class I, E (GB.M20022), mRNA sequence.
ACCESSION AA313847.1 GI:1966176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 on Sep 12, 1996 this sequence version replaced gi:1397543. Contact: Tsutomu Fujiwara Otsuka GEN Research Institute Otsuka Pharmaceutical Co.,Ltd 463-10 kagasuno Rawauchi-cho, Tokushima, Tokushima, 771-01 Japan Fax: 0886-37-1035.
C17443 356 bp mRNA EST 02-OCT-1996
C17443 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone
GEN-547C05 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GEN-547C05"
/clone_lib="Human placenta cDNA (TFujiwara)"
/issue_type="placenta"
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Gaps: 0
Percent Identity: 90.000
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                                                                                  C17443
C17443.1 GI:1579046
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Ratio: 4.600
Percent Similarity: 100.000
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US-08-653-294-37 x C17443
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                                                                                                                                                                     human.
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VERSION
KEYWORDS
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JOURNAL
COMMENT
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AUTHORS
                                                                                ACCESSION
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                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                               VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Strain="Sprague=Dawley"

/ Ab xref="taxon:10116"

/ Ab xref="taxon:10116"

/ Clone="ur=Fer-dn-h-09-0-ur"

/ Clone=lb="ur=Fer-dn-h-09-0-ur"

/ Ab host="bH10B (Life Technologies)"

/ Ab host="totor: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not1; Site_2: EcoRI; This library consists of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dr track which allows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.
Fatina Bonaldo, Ph.D. Clone distribution: clones will be available
through Research Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identification of the library of origin of a clone within the mixture." 124 g 47 t 1 others
                                                                          seq_documentation_block:
LOCUS AA900799 338 bp mRNA EST 05-FEB-1999
DEFINITION UI-R-E0-dn-h-09-0-UI.s1 UI-R-E0 Rattus norvegicus CDNA clone
UI-R-E0-dn-h-09-0-UI 3' similar to gill263201|gb|U38972|RW138972
Rattus norvegicus MHC class I RTI.Au heavy chain precursor, mRNA,
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodeniia; Sciurognathi; Muridae; Murinae; Rattus.
I (bases 1 to 318)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Apr 7, 1998 this sequence version replaced g1:3036153. Contact: Scares, MB Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, Fax: 319 335 9565
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Gaps: 0
Percent Identity: 90.000

    .338
    /organism="Rattus norvegicus"

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Rattus norvegicus
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Ratio: 4.600
Percent Similarity: 100.000
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US-08-653-294-37 x AA900799
                      seq_name: gb_est26:AA900799
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Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W. W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Wei, Y.F., Wingjun, J., Li, H., Melssner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wingjun, J., Xu, C., Yu, G.L., Ruben, S.M., Dillaon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

Fraser, G.M., Haseltine, W.A., Fields, C., Fraser, C.M., Massessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                         The institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA 9712 Medical Center Drive, Rockville, MD 20850 USA 11: 3018699055 Eax: 3018669423 Email: arkerlav@tigr.org Email: arkerlav@tigr.org information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgl.html)
Seg primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA243092 420 bp mRNA EST 11-MAR-1998 2Z155D01.rl Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:66433 5' similar to gb:MZ0022 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, E E*0101/E*0102 ALPHA (HUMAN); mRNA
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1 (bases 1 to 420)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Organ: colon; Vector: pBluescript SK-; Site_1: EcoRi; Site_2: XhoI"
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/db_xref="ATCC (inhost):110041"
/db_xref="taxon:9606"
/db_crone_lib="Colon carcinoma (HCC) cell line II"
/tissue_type="colon"
                                                                                                                                                                                                                                                                                                     On May 5, 1995 this sequence version replaced g1:798157.
Other_Ests: THC169518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="KM12C"
/cell_line="KM12C(HCC)-parental human colon
carcinoma;Dukes B2"
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/db_xref="footbased.general color of the col
                                       Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashD-NCI human EST Project
Unpublished (1997).

Unpublished (1997).

Contact: Wilson RK
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1647 Std Error: 0.00
Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 356.
Location/Qualiflers
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1 (bases 1 to 435)

13(a,L.B., Young,M.F., Touchman,J.W., Bouffard,G.G., Beckstrom-Sternberg,S.M., Green,E.D., Powell,J.I., Yang,L.M., Robey,P.G., Hotchkiss,R.N. and Francomano,C.A. SGAP: The Skeletal Genome Anatomy Project

Onpublished (1997)

On Feb 18, 1999 this sequence version replaced gi:4296314.
Moore, B., Schellenberg, R., Steptoe, M., Tan, F., , White, Y., Wylie, T., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 10
Gaps: 0
Percent Identity: 90.000
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National Human Genome Research Institute
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/organism="Homo sapiens"
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I (bases 1 to 448)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hultman,M., Rucaba,T., Lacy,M., Le,M., M., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rikin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               zp24g07.r1 Stratagene neuroepithelium (#937231) Homo saplens cDNA
clone IMAGE:610428 5' similar to gb:M20022 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, E E*0101/E*0102 ALPHA (HUMAN);, mRNA
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
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                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
./db_xref="taxon:9606"
./db_chone="NHDC_cno5002"
/clone_lib="Normal Human Trabecular Bone Cells"
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10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-126 Tel: 301-402-4877
Fax: 301-496-7157
Fax: 301-497
Fax: 30
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Gaps: 0
Percent Identity: 90.000
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/cell_type="Trabecular Bone Cells"
/lab_host="SURE"
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Fax: 314 286 1810
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AA176192.1 GI:1757314
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Percent Similarity: 100.000
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1. .448
/ Organism="Homo sapiens"
/ Ab_xref="GDB:4625687"
/ Ab_xref="Tamon:56687"
/ Ab_clone="IMAGE:610428"
/ Clone="IMAGE:610428"
/ Clone="IMAGE:610428"
/ Clone="IMAGE:610428"
/ Abost="Soln (kanamycin resistant)"
/ Abobost="Soln (kanamycin resistant)"
/ Abost="Soln (kanamycin resistant)"
/ Abost="
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IMAGE:1956698 3' similar to gb:M20022 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, E E*0101/E*0102 ALPHA (HUMAN);, mRNA
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400p from Gloco
High quality sequence stop: 339.
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1 (bases 1 to 469)

1 (bases 1 to 469)

1 (bases 1, Malen,M., Bowles,L., Dubuque,T., Geisel,G., Jost, Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Mylie,T., Waterston,R. and Wilson,R. Unpublished (1997)

On Jan 17, 1998 this sequence version replaced gi:1900422.
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Gaps: 0
Percent Identity: 90.000
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/organism="Homo sapiens"
/organism="texon:9606"
/clone="IMAGE:1956898"
/clone_lib="Schiller astrocytoma"
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High quality sequence stop: 110.
Location/Qualifiers
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AI214149
AI214149.1 GI:3777750
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Ratio: 4.600
Percent Similarity: 100.000
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US-08-653-294-37 x AA176192
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alignment_scores:
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                                                                /note="Organ: brain; Vector: pBluescript SK- (Stratagene); Ste_1: ECORI; Site_2: Khof; Double-stranded cDNA was prepared from human astrocytoma using primer.
5'-GAGGAGAGAGAGAGAACTAGTCTGAGT(18)-3'. An ECORI adaptor was used on the 5' end of the CDNA as follows: AATTCGGCAGGAG.' The library was size-selected and went through one round of amplification. Average insert size is 1.7 kb, with a range from 0.4-12 kb. Tumor identification by consensus pathology. This library was University)."
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1 (bases 1 to 501).

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project
On Jan 17, 1998 this sequence version replaced gi:1900329.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 295.
Location/Qualifiers
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Gaps: 0
Percent Identity: 90.000
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/db_xref="taxon:9606"
/clone="inAdE:1956874"
/clone_lib="Schiller astrocytoma"
/sex-"male"
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/tissue_type="astrocytoma"
/dev_stage="44 years"
/lab_host="SOLR"
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AI214126.1 GI:3777727
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Ratio: 4.600
Percent Similarity: 100.000
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US-08-653-294-37 x AI214149
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JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
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AI102538 648 bp mRNA EST 08-JAN-1999
EST211827 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
REMBO96 3' end, mRNA sequence.
                                                                           /note="Organ: brain; Vector: pBluescript SK- (Stratagene); Stel: ECORI; Site_2: KhOI; Double-stranded CDNA was prepared from human astrocytoma using primer 5.-GAGNGAGAGAGAGAACTAGTCTGAGT(18)-3. An ECORI adaptor was used on the 5' end of the CDNA as follows: 5.-AATTCGGCAGGAG." The library was size-selected and went through one round of amplification. Average insert size is 1.7 kb, with a range from 0.4-12 kb. Tumor dentification by consensus pathology. This library was constructed by Dr. Martin Schiller (Johns Hopkins University)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus sp.

Rattus sp.

Rattus sp.

Rattus sp.

Rattus sp.

Butheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

I (bases I to 648)

Lee, N. H., Glodek, A., Chandra, I., Mason, T. M., Quackenbush, J.,

Rerlavage, A. R. and Adams, M.D.

Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Normalized rat embryo, Bento Soares"
/dev_stage="embryo 8, 12, 18 dpc"
/note="Vector: pT/T78Pac; Site_1: EcoRI; Site_2: NotI"
_189 c 228 g 102 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1998)
On Aug 21, 1998 this sequence version replaced gi:3704683.
Other_ESTs: TC51871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                           3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 10
Gaps: 0
Percent Identity: 90.000
/tissue_type="astrocytoma"
                                                                                                                                                                                                                                                                                                                                                                                                           81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199 CGAGTGAACCTGCGGACGCTGCGCGGCTAC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus sp."
/db_xref="taxon:10118"
/clone="REMB096"
                        /dev_stage="44 years"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                     170 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI102538.1 GI:4134091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seg primer: M13-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 46.00
Ratio: 4.600
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-37 x AI214126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AI214126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Lee, NH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_est26:A1102538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene Index
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodenia; Sciurognathi; Muridae; Murinae; Mus.

Eutheria; Rodenia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (Dases 1 to 344)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Rucaba,T., Lacy,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

The WashJ-HMIM Mouse EST Project
Unpublished (1996)

On Jan 19, 1998 this sequence version replaced gi:2284822.

Contact: Marra M/Mouse EST Project
WashJ-HHMI Mouse EST Project
Fax: 314 286 1800

Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL ; contact the IMMGE Consortium (info@image.linl.gov) for further information. MGI:920168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI158411 344 bp mRNA EST 30-SEP-1998 ud24e07.rl Soares 2NbMT Mus musculus cDNA clone IMAGE:1446852 5' similar to 9b:J00400 Mouse MHC class I H2-K gene (MOUSE);, mRNA
                                                                                               Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: -28ml3 rev2 ET from Amersham.
Location/Qualifiers
1. .344
/organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares 2NbMT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="IMAGE:1446852"
                                                                                                                                                                                                                                                                                                                                    1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                       31 CGAGTGGACCTGGGGACCCTGCGCGGCTAC 60
                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AII58411
AI158411.1 GI:368680
                                                                                                                          4.889
                                                                                                                                                                                                                                                                                Align seg 1/1 to: AA313054
                                                                                                                                                                                                      alignment_block:
US-08-653-294-37 x AA313054
                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_est23:A1158411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse.
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                                                                                                                                                Percent Similarity:
                                                                                                                                Ratio
                                                                         alignment_scores:
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DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E 1 (Dases 1 to 245)
S Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Rirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanne, M.C., Hedblom, E., Hinkle, P.S.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Mquyen, D.T., Pelligrino, S.M.,
Phillips, C. A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Link, Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS AA313054 245 bp mRNA EST 19-APR-1997
DEFINITION EST183851 Pancreas tumor, subtracted (abundant clones) Homo sapiens
CDNA 5' end similar to similar to major histocompatibility complex,
ACCESSION AA313054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: arkerlar@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
Seq primer: MI3 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="ATCC (1nhost):172202"
/db_xref="taxon:9666"
/clone_lib="Pancreas tumor, subtracted (abundant clones)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="adult"
/note="organ: pancreas; Vector: pBluescript SR-; Site_1:
ECORI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On May 8, 1995 this sequence version replaced gi:801299.
Other_ESTs: THC183330
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 others
                Canyun: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 t
                                                                                                                                                                                                      to: 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bioinformatics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                     248 CGAGTGAACCTGAGGACCTGCGGGGGTAC 277
                                                                                                                                                                                                                                                       1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                      from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA313054.1 GI:1965382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 C
                                                                                                                                                                                                      to: AI102538
                                              Ratio: 4.600
Percent Similarity: 100.000
                                                                                                                          alignment_block:
US-08-653-294-37 x AI102538
                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_est12:AA313054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ď
                        Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
alignment_scores:
                                                                                                                                                                                                    Align seg 1/1
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ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

AUTHORS REFERENCE

source

FEATURES

MEDLINE JOURNAL

COMMENT

TITLE

BASE COUNT

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alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA125323 382 bp mRNA EST 18-FEB-1997 m080C08.17 SOARES STOAD INAGE:57534 5% similar to gb:x00492_cds1 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-3 A*0301 ALPHA (HUMAN); gb:M69073 Mus musculus mRNA, complete cds (MOUSE); mRNA sequence. AA125323.1 GI:1684491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 382)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Marra,M., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
This Consortium (info@lmage.llnl.gov) for further information.
MGI:350182
Seq primer: -28M13 rev2 from Amersham.
Location/Qualifiers
1. .382
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1282198.
Contact: Marra M/Mouse EST Project
WashIngton University School of MedicineP
H44 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
                                                                                                                                                                                                                                                                           to: 344
                                                                                             Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                           Align seg 1/1 to reverse of: Al158411 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="IMAGE:575534"
/clone_lib="Soares_2NbMT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                          tissue_type="Thymus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="4 weeks"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strain-"C57BL/6J
                                                                                                                                                                                                alignment_block:
US-08-653-294-37 x AII58411/rev
                                                                                                4.889
90.000
                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_est9:AA125323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS AA125323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
                                                                                                                            Ratio:
Percent Similarity:
                                                                                                  Ouality:
                                                                           alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
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JOURNAL
COMMENT
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ORIGIN
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96 t
107
124 C
55 a
BASE COUNT
ORIGIN
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Gaps: 0 Percent Identity: 90.000 Length: 44.00 4.889 90.000 Quality:
Ratio:
Percent Similarity:

alignment_block: US-08-653-294-37 x AA125323/rev

to: 382 from: 1 to reverse of: AA125323 Align seg 1/1

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058407 pyrococcus
065157 mus musculu
033348 mycobacteri
055457 synechocyst
083484 treponema p
095430 oryza sativ
044103 amycolatops
020152 chlorella v
095066 bomo sapien
025032 haemonchus
025032 haemonchus
095044 caenorhabdi
09441 mycobacteri
06160 caenorhabdi
09442 homo sapien
05872 homo sapien
054819 mycobacteri
061419 mycobacteri
                                                                  Search time 209.03 Seconds (without alignments) 3.317 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                             OM protein - protein search, using sw model
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sp_unclassified:*
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Match Length DB
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ALIGNMENTS

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800 Bound West And Control of Con		PRELIMINARY;				IY POTHETIC.		orikoshii	yarchaeot		OM N.A.		344137.	L Y., SAWA	SEKINE M	SURA K., O	, TANAKA	CAMURA Y.,		equence an	archaeba	55-76(1998	03; BAA29	151 AA; 1		vat)ER 104		PRELIMINARY;		(TremBLrel.
NESCO SON MARCH STATE SON	07	058407	058407;	01 - ATG-1998	01-JAN-1999	151AA LONG F	PH0674.	Pyrococcus 1	Archaea; Eur	[1]	SEQUENCE FRO	STRAIN-OT3;	MEDLINE; 983	KAWARABAYAS1	YAMAMOTO S.,	SAKAI M., OG	FUNAHASHI T.	AOKI K., NAR	KIKUCHI H.;	"Complete se	thermophilic	DNA Res. 5:5	EMBL; AP0000	SEQUENCE	ery Match	st rocal simi				062157	062157;	01-NOV-1996 01-NOV-1996
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BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
COLE S.T.;
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                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.4%; Score 35; DB 11; Length 506; ilarity 77.8%; Pred. No. 40; Conservative 1; Mismatches 1; Indels
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TAKAHASHI M.;
SUBMILTER (OCT-1993) to the EMBL/GenBank/DDBJ databases.
slumitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
-! - SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
EMBL; X75343; CAA53092.1; -.
PROSTE: PS00518; ZINC_FINGER_C3HC4; 1.
PFAM: PF000622; SPRY; 1.
PFAM: PF000623; ZF-B-Dox; 1.
PFAM: PF00067; zf-C3HC4; 1.
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
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PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL 10.2 KD PROTEIN.
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
ZINC FINGER PROTEIN (FRAGMENT).
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EMBL, AL1008883; CAA15528.1; -
Hypothical protein
SEQUENCE 87 AA: 10237 MW; 62B840DE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     506 AA; 57882 MW; AEE397C3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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NON_TER 1 1 SEQUENCE 506 AA; 57882
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Best Local Similarity
Matches 7; Conserv
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STRAIN-PCC6803;
MEDLLINE, 97061201.
MEDLLINE, 97061201.
MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAWADA M., YASUDA M.,
TABATA S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).

EMBL; D64006; BAA10800.1; -

Hypothetical protein.

SEQUENCE 132 AA; 15240 MW; 53B23658 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUGIURA M., TABATA S.,
"Sequence analysis of the genome of the unicellular cyanobacterium
"Sequence systis sp. strain PCC6803. I. Sequence features in the 1 Mb
region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-PCC6803;
MEDLINE; 96127529.
KANEKO T., TANEKA A., SATO S., KOTANI H., SAZUKA T., MIYAJIMA N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 98332770.
FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
DODSON R., GWINN M., HICKEX E.K., CLAYTON R., KETCHUM K.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Cyanobacteria; Chroococcales; Synechocystis
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Bacteria, Spirochaetales; Spirochaetaceae; Treponema
                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
HYPOTHETICAL 15.2 KD PROTEIN.
Synechocystis sp. (strain PCC 6803).
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL 53.0 KD PROTEIN.
                                                                                                                                                                                                                  132 AA.
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1 YRLLIRLDE
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Gaps

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1; Indels

2; Mismatches

69.4%; Score 34; DB 2; Length 87; 66.7%; Pred. No. 11;

Query Match
Best Local Similarity 66.7
Matches 6; Conservative

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MEDLINE: 97303241.
WAKASUGI T., NARALIMA K., SUGITA M., ITO M., ITO S.,
WAKASUGI T., NARASHIMA K., TSUDZUKI T., SUZUKI Y., HAMADA A., OHTA T.,
INDMURA A., YOSHINAGA K., SUGIURA M.;
"Complete nucleotide sequence of the chloroplast genome from the green
alga Chlorella vulgarias: the existence of genes possibly involved in
chloroplast division..;
Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlorella vulgaris.
Chloroplast.
Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
                                                                                                                 STRAIN-DSM 5908;
MEDLINE: 97449857.
MEDLINE: 97449857.
MEDLINE: 97449857.
"Cloning and analysis of a peptide synthetase gene of the ballimycin producer Amycolatopsis mediterranei DSM5908 and development of a gene disruption/replacement system.";
J. Biotechnol. 56:115-128 (1997).
EMBL: X97860; CAA66454.1;
PROSTE: PSO0455; AMP_BINDING; 1.
PPRAM: PFO0501; AMP-Dinding; 1.
PPRAM: PF00509; DP-binding; 1.
                    Amycolatopsis mediterranei.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1324;
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Pred. No. 2.6e+02;
1; Mismatches 2; Indels
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Last sequence update)
Last annotation update)
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70.0%;
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60.0%;
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Best Local Similarity 70.00
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Best Local Similarity 60.0
Fra 6; Conservative
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17 FLLLVELDER 26
                                                                                                    SEQUENCE FROM N.A.
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Q9Y058;
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AC Q9Y058
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                                                                                                                                                                          FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G., PODDSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A., SODERGREN E., HARDHAM J.M., MOLEOD M.P., SALZBERG S., PETERSON J., KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK I., MCDOMALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJI C., GARLAND S., VENTER B., HORST K., ROBERTS K., WATTHEY L., WELDMAN J., SMITH H.O.,
SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J., KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T., MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S. HARCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O., VENTER J.C.;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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                                                                                                  'Complete genome sequence of Treponema pallidum, the syphilis
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TOZAWA Y., HASEGAWA H., TERAKAWA T., WAKASA K.;
TOZAWA Y., HASEGAWA H., TERAKAWA T., WAKASA K.;
TICE-CDNA encoding anthranilate synthase alpha subunit.";
Submitted (Jan. 1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB022602; BAA82094.1; -.
SEQUENCE 577 AA; 63947 MW; 057FE09C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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EMBL; AE001223; AAC65460.1; -.
TIGR: TP0471; -.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
ANTHRANILATE SYNTHASE ALPHA 1 SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                  ll protein.
469 AA; 52960 MW; F76800E7 CRC32;
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                                                                                                                                         Science 281:375-388(1998).
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Best Local Similarity
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81 YRCLVREDDR 90
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| 140 YTLLIRLD 147
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                                                                                                                       spirochete.
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"Cloning and sequence comparisons of four distinct cysteine proteases expressed by Haemonchus contortus adult worms.";
Mol. Biochem. Parasitol. 51:209-218(1992).
EMBL; M80388; AAA29178.1;
HNSSP; P07888; ICSB.
PFAM; PF00112; Peptidase_C1; 1.
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SHIRAYAMA M., KAWAKAMI K., MATSUI Y., TANAKA K., TOH-E A.;
"MSI3, a multicopy suppressor of mutants hyperactivated in the RAS-
CAMP pathway, encodes a novel HSP70 protein of Saccharomyces
                                           Haemonchus contortus.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Strongylida;
Trichostrongyloidea; Trichostrongylidae; Haemonchinae; Haemonchus.
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WATANABE Y., IRIE K., MATSUMOTO K.;
"Yeast RLM1 encodes a serum response factor-like protein that may function downstream of the Mpk1 (Slt2) mitogen-activated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
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MEDLINE; 90078303.
DESHALES R.J., SCHEKMAN R.;
"SEG5 encodes a putative membrane protein required for protein translocation into the yeast endoplasmic reticulum.";
J. Cell Biol. 109:0-0(0).
                                                                                                                                  SEQUENCE FROM N.A.
MEDILIN: 92244291.
PRITI D., ARMES L.G., HAGEMAN R., REYNOLDS V., BOLSVENUE R.J.,
COX G.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 5; Length 341
Pred. No. 1.1e+02;
Pred. no. 1.2e+02; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 89345597.
GAMPEL A., TZAGOLOFF A.;
"Homology of aspartyl- and lysyl-tRNA synthetases.";
Proc. Natl. Acad. Sci. U.S.A. 86:6023-6027(1989).
  01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYSTEINE PROTEINASE (FRAGMENT).
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Last annotation update)
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341 AA; 38342 MW; 2520FB2D CRC32;
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01-NOV-1996 (TrEMBLrel. 01, Last segu
01-NOV-1998 (TrEMBLrel. 08, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.3%;
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nes 6; Conserv
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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Q02895;
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Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                             DEAN F.B., LIAN L., O'DONNELL M.; "CDNA cloning and gene mapping of human homologs for Schizosaccharomyces pombe radil, radi, and husl and cloning homologs from mouse, Caenorhabditis elegans, and Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.3%; Score 32; DB 5; Length 267; 55.6%; Pred. No. 86;
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Pred. No. 1e+02;
0; Mismatches 1; Indels
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BAUER C., WILLIAMS D.;
The sequence of Homo sapiens PAC clone DJ0669B10.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases EMBL; AC004853; AAC64378.1; -. SEQUENCE 317 AA; 35293 MW; B32AE3AE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WATERSTON R.H.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
    Created)
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01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-WAY-1999 (TrEMBLrel. 10, Last annotation update)
WUGSC: H_DJ0669B10.1 PROTEIN.
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(TrEMBLrel. 01, Last sequence update)
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EMBL: AF076843: AAC95525.1; -.
SEQUENCE 267 AA: 29910 MW: A91CD2BF CRC32;
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87.5%;
01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12,
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Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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                                                                                                           Caenorhabditis elegans.
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                                                                    RAD1-LIKE PROTEIN.
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                A BUSSEY H., STORMS R.K., AHMED A., ALBERNANN K., ALLEN E., ANSORGE W., ARAUJO R., APARICIO A., BARELL B., BACCCK K., BENES V., BOSTEIN D., BOWMAN S., ENCKNER M., CARPENTER J., CHUGG E., CHUGGHER C., COSTER F., DAVIS R.W., DIETRICH F.S., CHUGG E., DELIUS H., DIPAOLO T., DUBOIS E., DUSTERHOFT A., DUNCAN M., FLOETH M., FRIEZE C., GOFFEAN A., HYMAN R., HILBERT H., HILLIER E., HUMLCKE-SMITH S., HYMAN R., JOHNSTON M., KALMAN S., KLEINE K., KOMP C., KURDI O., LASHKARI D., LAW H., LIN D., LOUIS E.J., MARATHE R., MESSENGUY F., NEWEYS H.W., MIRTIPATI S., MOESTL D., MULLER ADER S., NAMATH A., PURNELLE D., SCHRFEN M., SCHREEN B., SCHREBN S., SCHRAMM S., SCHRODER M., SDICU A.M., TETTELIN H., URRESTARZU L.A., USHINSKY S., WIERENDELS F., VISSERS S., VOSS H., WARLEL S., WANBUTT R., WANG Y., WENDLER E., WENDLER H., WINNETT E., ZHONG W.W., ZOLLNER A., VO D.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
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OKINAKA R.T., CLOUD K., HAMTON O., HOFFMASTER A., HILL K.K., KEIM P.,
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AVRAM D.A., BAKALINSKY A.T.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
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HILL J.E., TZAGOLOFF A.A.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
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Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U43281; AAB68211.1; -.
SEQUENCE 342 AA; 39682 MW; 9EAC1CD5 CRC32;
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Best Local Similarity
Matches 7; Conserv
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Q9X314;
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BONFIELD J., BURTON J., CONNELL M., COPSETT T., COOPER J., COULSON A.,
BONFIELD J., BURTON J., CONNELL M., COPSETT T., COOPER J., COULSON A.,
GARDNER A., GREEN P., HAWINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., KOOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
WATENSTON R.,
WATENSTON R.,
WALIKINSON -SPROAT J., WOLLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
KOEHLER T., LAMKE G., KUMANO S., MAHILLON J., MANTER D., MARTINEZ Y., RICKE D.O., SVENSOND R., JACKSON P.J.;

"The sequence and organization of pvJ.;
plasmid harboring the Anthrax toxin genes.";
J. Bacteriol. 0:0-0(1999).

Bacteriol. AF065404; AAD32348.1;
Plasmid.
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Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                        Score 32; DB 2; Length 428
Pred. No. 1.4e+02;
3; Mismatches 1; Indels
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STRAINERSTOL N2;
WATERSTON N2;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF022976; AAC69086.1; -.
PFAM; PF01362; DUF12; 1.
SEQUENCE 441 AA; 51624 MW; DE523A9B CRC32;
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DAVIDSON S., WOHLDMANN P., BAUER C.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
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01.JAN-1998 (TrEMBLrel. 05, Last sequence update)
01.MAY-1999 (TrEMBLrel. 10, Last annotation update)
SIMILARITY TO C4-TYPE ZINC FINGERS.
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Pred. No. 1.4e+02;
3; Mismatches 2;
                                                                                                                         428 AA; 50415 MW; FOFE581D CRC32;
                                                                                                                                                                                                                                                                                                                                                                       441 AA
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50.0%;
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Best Local Similarity 55.6%;
Matches 5; Conservative
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Best Local Similarity 50.0°
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Caenorhabdítís elegans.
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DT 01-JUL-1997 (TREMBLICE). 08, Last annotation update)
DT 01-NOV-1998 (TREMBLICE). 08, Last annotation update)
ON MYCObacterium tuberroulosis.
OC Actinomycetales: Corynebacteriaes: Mycobacteridaes:
OC Actinomycetales: Corynebacterines: Mycobacteridaes:
OC Actinomycetales: Corynebacterines: Mycobacterium.
RP SEQUENCE FROM N.A.
RA SEQUENCE FROM N.A.
RA SEQUENCE FROM N.A.
RA BARRELL B.G., RAJANDREAM M.A.;
RA SEQUENCE FROM N.A.
RA BARRELL B.G., RAJANDREAM M.A.;
RA SEQUENCE FROM N.A.
RA PHILIPP W.J. POULET S., EIGLMEIER K., PASCOPELLA L.,
RA BALLASUBRAWANIAN V., HEYM B., BERGH S., BLOOM B.R., JR.OR SA BALLASUBRAWANIAN V., HEYM B., BERGH S., BLOOM B.R., JR.OR RA BALLSUBRAWANIAN V., HEYM B., BERGH S., BLOOM B.R., JR.OR RA BALLSUBRAWANIAN V., HEYM B., BERGH S., BLOOM B.R., JR.OR RA BALLSUBRAWANIAN V., HEYM B., BERGH S., BLOOM B.R., JR.OR RA BALLSUBRAWANIAN V., HEYM B., BERGH COMPATISON WIth Mycobacterium tuberculosis HJRV, and comparison with Mycobacterium RT Proc. Natl. Acad Sci. U.S.A. 93:3132-3137(1996).
DR EMBL: 29558: CAB08966.1:
SEQUENCE 554 AA. 57835 MW; C42C89FC CRC32;
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Search completed: February 8, 2000, 13:17:42 Job time: 32491 sec

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Gaps

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Query Match 65.3%; Score 32; DB 2; Length 554; Best Local Similarity 66.7%; Pred. No. 1.8e+02; Matches 6; Conservative 2; Mismatches 1; Indels

2 RLLIRLDER 10 || :|:||| 48 RLHVRIDER 56

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sapiens (sapiens)
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**NOTE: This is a 'working draft' sequence. It currently consists of 93 contigs. The true order of the pieces

**is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

**This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                   seq_documentation_block:
LOCUS ACO08337 187246 bp DNA HTG 02-SEP-1999
DEFINITION Homo sapiens chromosome 19 clone CIT-HSPC_490E21, *** SEQUENCING
PROGRESS ***, 93 unordered pieces.
ACCESSION ACO08537
VERSTON ACO08537.1 GI:5686530
SETWING HTG: HTGS_PHASE1.
SOURCE human
     HOMO
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HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 187246)
AC009643 H
AC004618 H
AC004670 H
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contig of 635 bp in length
gap of unknown length
gap of unknown length
contig of 700 bp in length
contig of 263 bp in length
gap of unknown length
contig of 643 bp in length
gap of unknown length
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9 of 675 bp in length
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9 of 261 bp in length
E unknown length
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of 657 bp in length
unknown length
of 629 bp in length
unknown length
of 400 bp in length
unknown length
of 40 bp in length
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of 273 bp in length
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of 610 bp in
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gb_htg4:AC009643
gb_htg2:AC004618
gb_htg2:AC004670
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187246 | AC008537 Homo sapiens chrome
211769 | AC008591 Homo sapiens chrome
142336 | AL035457 Human DNA sequence
323792 | AC004965 Homo sapiens clone
34051 | AL022305 S.pombe chromosome
146996 | U88310 Caenorhabditis elegans
63852 | AC014106 Drosophila melanogas
94468 | AC001406 Drosophila melanogas
117732 | AC010690 Caenorhabditis elegans
1170136 | AC008496 Homo sapiens chrome
170136 | AC008496 Homo sapiens chrome
170136 | AC006586 Caenorhabditis eleg
299719 | AC006586 Caenorhabditis eleg
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1 U00050 Caenorhabditis elegans
1 Z68136 S. pombe chromosome I
1 AC010028 Drosophila melanogas
1 AC007167 Arabidopsis thalian
1 AC000815 Oryza sativa genomi
1 AC012259 Homo sapiens chromd
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S68137 orf 5' of mpal, mpal-Pu
M93021 Pasteurella haemolytica
J03474 Human serum amyloid A g
Y11829 A.thaliana hsp88.1 gene
                                                                                                                                                                                          Command line parameters:
-MODEL-framet-p2n.model-DEV-x1p
-Q=/cgn1_1/GSPTO_spool/US08653294/runat_04022000_160701_15779/app_query.fasta.1
-Q=/cgn1_1/GSPTO_spool/US08653294/runat_04022000_160701_15779/app_query.fasta.1
-DB=Genemb1 -QFWT=fastap -SUFFIX*rse -GAPOP=12.000 -GAPEXT*-4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GGAPOP=6.000
-GGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOPE-6.000
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                                                                                                                About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Submitted (0.3-Angu-1999) Production Sequencing Facility, DOB Joint Genome Institute.

LEST (Submitted (0.3-Angu-1999) Production Sequencing Facility, DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA ON Oct 31, 1999 this Sequence version replaced gi:5686476.

* NOTE: This is a "working draft, sequence. It currently tonsists of 60 contigs. The true order of the pieces and their order in this sequence record is arbitrary. Gaps between the contigs are represented as truns of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                      DNA HTG 31-OCT-1999
5 clone CIT-HSPC_575N7, *** SEQUENCING IN
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 211769)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
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LOCUS AC008591 211769 bp DNA
DEFINITION Homo sapiens chromosome 5 clone CI
PROGRESS ***, 60 unordered pieces.
ACCESSION AC008591 GI:6165161
KEYWORDS HTG: HTGS_PHASE1.
4014 CGCCTTCTCATCAGGTTGGACGAGAGA 3988
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Submitted (30-OTT-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. Email enquiries: humquery@sanger.ac.uk CDne requests: clonerequest@sanger.ac.uk

On Oct 29, 1999 this sequence version replaced g1:6058975.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Ems., EMBL: Sw.; SWISSPROT: Tr.; TREMBL: Wp:, WORNPEP: Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep IMPORTANT: This sequence is not the entire insert of clone 1106NLB. It may be shorter because we only sequence overlapping sections once, or the contract because we arrange for a small overlap between neighbouring
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS HS1106N18 142336 bp DNA PRI 23-NOV-1999
DEFINITION Human DNA sequence from clone 1106N18 on chromosome 20q13.2-13.2,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                 others
164838: contig of 10529 bp in length gap of unknown length 177853: contig of 13015 bp in length 192072: contig of 14219 bp in length gap of unknown length 192079: contig of 19697 bp in length.
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Percent Identity: 70.000
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AL035457
AL035457.13 GI:6143575
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Ratio: 4.100
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Direct Submission
Submitted (12-JUN-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20 1106N18 is from the library RPCI-5 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpc.med.buffalo.edu/ VECTOR: pCYPAC2.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 323792)
Waterston, R.H.
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of 2301 bp in length
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of 1836 bp in length
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4.333 Gaps: 0
90.000 Percent Identity: 80.000
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/organ1sm="Homo sapiens"
/db_xref="taxon:9606"
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/map="q13.2-13.2"
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US-08-653-294-15 x HS1106N18/rev
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g of 89226 bp in length
f unknown length
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Protein coding regions (CDS) have been predicted with the help of computer analysis using the Genefinder program in Pombase (an ACEDB database) with additional predictions for the branch-acceptor sites supplied by the program spisplice. CAUTION: It is possible that for number of introns/exons or we may not have chosen the correct splice donor/acceptor sites. CDS are numbered using the following system eg SPBC25H2.Olc. SP (S. pombe). B (chromosome 2), c25H2 (cosmid name). Ol (first CDS), c (complementary strand). The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

IMPORTANT: This sequence MAX NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (27.74R-1998) European Schizosaccharomyces genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk applied biologiese Universiteit Leuven, Faculty of Agricultural and Applied Biological Sciences, Laboratory of Gene Technology, Kardinaal Mercierlaan 92 Blok F, B-3001 Leuven, Belgium 2 (bases 18652 to 34051)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS
SPBC14C8 34051 bp DNA 19-OCT-1998
DEFINITION S.pombe chromosome II cosmid c14C8.
AL022305.1 GI:3647356
KEYWORDS acetolactate synthase regulatory subunit; beta transducin; cdc18; repeat; quicoamylase procursor; methionine aminopeptidase; pol5; procean import protein; ribosomal protein; RNA polymerase II subunit; rpb8; transcription factor; triacylglycerol lipase; WD
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On Sep 25, 1998 this sequence version replaced gi:3006158.
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1 (bases 1 to 34051)
Lyne,M., Rajandream,M.A., Barrell,B.G. and Volckaert,G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                               775 others
11 322078: gap of unknown length
9 323792: contig of 1714 bp in length.
Location/Qualifiers
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Gaps: 0
Percent Identity: 80.000
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MLPRIMESYGKENAFPVTPISNRNGTKGAGSKRAPLGSTKQSNA
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MQNKATSVTIRNTPASDFHVYKEFSDDDPIQFPLLSVDGDSPLTEKDTMLTTPATLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   membrane translocase subunit tim44 precursor, (431 aa),
fasta scores: opt: 893, E():0, (43.0% identity in 430 aa)"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AELKKSOELODSVRALQDSSGSLSESDTFKRRDATBEARSGTTAASSFTGKTVGKAG
AKIGSYAQKAWESAPVQLSKKVISSTANTVATGVDTATKPVRETAFYKTIKQTMSDGS
TSSRYGFYADKEQRKKLREEFERRNRWFASSARIQPNEDVQSVVVHSNPSWKNKVEQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="G1:3006160"
/db_xref="SPTREMBL:060084"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNESTLVRKIQELKKSYQESEHPIVSSIRDMADSISGVWSRMFSETEASQVMRRFKEI
DPSFNTEHFLQYLREYIVPEVTEAYVKGDKEVLKTWLSEAPFSVYETTTKEYAKHGVV
SVGKILDIRGVDIMSQRLLQPNDIPVFIVTFRTQEVHMFKDASSGELVAGKDDRIQQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEKKKKKKKKKKSSKKKKTPQEQTNPPTVGLSKIFVNKKYPVGEVCDYAEDNLWRTTDEE
KRALDRQNFDQYNDLRRAAEVHRQARQYAQSVIKPGMSMMDVVNTIENTTRALVEEDG
overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid c14C8 is overlapped at the 3' end by c15C4. Details of yeast sequencing at the Sanger Centre are available on the World Wide Web. (URL, http://www.sanger.ac.uk/Projects/S_pombe/) buring 1995 to 1996 about 66% of S. pombe chromosome 1 was sequenced by the Sanger Centre. The sequencing of the S. pombe genome is now being continued with funding from The European Commission. Fourteen European sequencing laboratories, including the Sanger Centre, are participating in the project.
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/note="SPBC14C8.03, len:426, SIMILARITY:Arabidopsis
factor., (431 aa), fasta scores: opt: 1697, E():0, (59.48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="mitochondrial import inner membrane translocase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="SPBC14C8.02, len:427, SIMILARITY:Saccharomyces cerevisiae, IM44_YEAST, mitochondrial import inner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2261. .2284
/gene="SPBC14C8.02"
/note="PS00017 ATP/GTP-binding site motif A (P-loop)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative methionine metallopeptidase"
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                                                                                                                                                                                                                                                                                                                                                            /organism="Schizosaccharomyces pombe"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(<1. .661)
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1994. .3277
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                                                                                                                                                                                                                                                                                                                                                                                         /strain="972h-"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="cut2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="IIR"
                                                                                                                                                                                                                                                                                                                                    .34051
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PQYDNLLAAVKAATNKGIEEAGIDARLNEIGEAIQEVMESYEVEINGKTHQVKSIRNL
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PDAGHIPLRLPRAKALLNTITQNFGTLPFCRRYLDRIGESKYLLALNNLVSAGIVQDY
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complement(8460. 9812)
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complement(8460. 9812)
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OKRAWODGYFARRIGAPDQAALYORTIEPIDLKLGEFWDPGMGVIKGYKGRYDRSGL
OCSTILASLY SNEFDMHILPTLLKLOETWTRDYPVNGWKQAMGRYPEDVYDGWSKSI
GNPWFICTSGAAEITYKAIAYYENGUKOLPELTEYNIHFFWKFAEFGDPYNMSVTRKNMH
TYADNFLKAVAEFQHPNGSMSEQFSRDDGHQKGARDLTWSYSSLLNAIYRREAIKGSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation-"MSTPFNRVQRPKRHVFNCLVQNEPGVLSRLSGILAARGFNIDSL
VVCATEVENLSRWTIVLRGADEVVEQAKRQIEDIVSVWAVLDYTGTSMVERELLLAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLLGPDHFQEHFERSEKVAESTNAKAKSDGEGVMNANAALGLRASQLAAINQLTTLFH
GRVADISTETIILELTATPDRVDNFLSLLRPYGVLEACRTGTSAMTRAPHSNEVTEEA
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LKSGIGFPTGVSLNHCAAHYTPNAGDTTILKEKDVMKVDIGVHVNGRIVDSAFTMSFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /jour 252.145,7526. .8036)
/gone="SPBC14C8.04"
/note="SPBC14C8.04"
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/gene="SPBC14C8.03"
/note="PS01202 Methionine aminopeptidase subfamily 2
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/gene="sop2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="gtatgt, splice donor sequence" 7511. .7525
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7258. .803
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
I (bases I to 46996)
Milson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M.,
Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,
Coulson, A., Craeno, P., Hawkins, T., Hillier, L., Jier, M.,
Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,
Latreille, P., Lightning, J., Lloyd, C., MoMurray, A., Mortimore, B.,
O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A.,
Saunders, D., Shownkeen, R., Sanldon, N., Smith, A., Sonnhammer, E.,
Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Wilkinson-Sproat, J. and Wohldman, P.,
Wilkinson-Sproat, J. and Wohldman, P.,
D. 2, Mo of contiguous nucleotide sequence from chromosome III of C.
                                           LAAGCADRKAYVLSAYVRDVDAKPEASVWGSRLPFNTYCAEYPSGGWTHAVGFSPSGN
ALAYAGHDSSVT IAYPSAPEQPPRALITVKLSQLPLRSLLWANESAIVAAGYNYSPIL
LQGNESGWAHTRDLDAGTSKTSFTHTGNTGEGREEEGPVSFTALRSTFRNMDLKGSSQ
WKHARTFSDHDKIVTCVDWAPKSNRIVTCSQDRNAYVYEKRPDGTWKQTLVLLRLNRA
                         ATFVRWSPNEDKFAVGSGARVISVCYFEQENDWWVSKHLKRPLRSTILSLDWHPNNVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-1997
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St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
                                                                                                SISSLPTWHOWNIATLRPYAGTPGNITAFTSSGTDGRVLWTL"
10951. .10956
/gene="sop2"
                                                                                                                                                                                              /note="gtacag, splice donor sequence"
                                                                                                                                                                                                                                                                  Length: 10
Gaps: 0
Percent Identity: 80.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans strain-Bristol N2.
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence of C. elegans cosmid C24G7
Unpublished (1997)
3 (bases 1 to 46996)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 34051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans cosmid C24G7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1109 TATTCGCTCCTCATTGAATTAGACGAGAGG 21238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TyrArgLeuLeuIleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 46996)
Goela, D. and Wilson, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46996 bp
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                                                                                                                                                                                                                                                                38.00
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90.000
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                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-15 x SPBC14C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_in1:CELC24G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                     Quality:
Ratio:
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94150718
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                                                                                                                                              misc_feature
                                                                                                                                                                                                                                            alignment_scores
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MEDLINE
REFERENCE
AUTHORS
TITLE
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AUTHORS
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JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE
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NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions

Cambridge CB10 IRQ, England e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk

IROPTFSQPISEELESKYGK"

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone

NEIGHBORING COSMID INFORMATION:

cosmid is CO9D1, 13199 bp overlap; 3' end lies in a gap. start of this cosmid is at base position 197 of CELC24G7; end is at 46996 of CELC24G7 The 5' Actual actual

NOTES:

Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation). Location/Qualifiers .46996
 /organism="Caenorhabditis elegans" //strain="Bristol N2"
 /db_xref="taxon:6239"
 /chromosome="1" /clone~"C24G7" source gene CDS FEATURES

15823. .24728 /gene="C24G7.5" /gene="C24G7.5" /gene="C24G7.5" /gene="C24G7.5" 15860,16237. .16593,16703. .16967,17315. .17601, 18125. .18246,18366. .18769,19326. .19526,20957. .21484, 21758. .22079,22456. .23239,23596. .23924,23983. .24201, 24248. .24487,24629. .24728) /gene="C24G7.5" /note="similar to the protein kinase domain of myosin light chain kinases; coded for by C. elegans CDNA ykl3188.5; coded for by C. elegans CDNA yk1299.5; coded for by C. elegans CDNA yk912.5; coded for by C. elegans coded for by C. elegans CDNA yk1294.5; coded for by C. elegans CDNA yk1394.5; coded for by C. elegans CDNA yk13188.3; coded for by C. elegans CDNA yk1294.3; coded for by C. elegans cDNA yk9412.3; coded for by C. elegans CDNA yk13188.3; coded for by C. elegans CDNA yk1294.3; coded for by C. elegans cDNA yk9412.3; coded for by C. elegans CDNA yk13188.3; coded for by C. elegans cDNA yk1394.3; coded for by C. elegans coded for by C. elegans cDNA yk133h10.3; coded for by C. elegans CDNA yk131c10.5. .17601,

/codon_start=î

DEVERBARA PONLEKER I. PODECET SHEKEKTOH PURITA STATEMENT OF THE STREET SHEKEKTOH SHERE SHEKEKTOH SHEKESPHOT SHERE SHEKESPHOT SHERE SHEKESPHOT SHERE SHEKESPHOT SHERE SHEKET /translation="MAEQYEQKORTLYANSTIDGLSSLAHPGVEIAEPKGVNRETCVR
VFVQLLLALAKHMHDLRIAHPETTLQDDRKLKADFGGARELLEGETKGS
PEFVSPETVAS PLILATDWARTTULTOFTLLGDEKKLADFGGARELLEGETKGS
PEFVSPETVAS PLILATDWARTTULTYVLLTGLSPFHGDNONETLANVDSCOFDSS
IGNESYDAGDFVKKLLTEIPVSRLTVDBALDHPWINDEKLKTEPLSADTLREFKYQHK
VERKVFQQTPSEQTLEALIGPATAQAQQNAPABCRREAEIYDYLLRIQPKKRPPT
VEXVPQQPREHPPFTDFGQLILGGAFDRPGGTGFEFRQPPQPPQPPQPTPPQPQAHD
SRRHEQQPQHQGQPQRIPVDQYGRPLVDPRILNDFSHRPSSLDDAFFYVDKYGAAHD
SRRHEQQPQHQGQPQRIPVDQYGRPLVDPRILNDFSHRPSSLDDAFFYVDKTGNRVAH SLRDGQHENVQRLIAAFNNSNFLYLLSERLYEDVFSRFVFNDYYTEEQVALTMRQVTS ALHFLHFKGIAHLDVNPHNIMFQSKRSWVVKLVDFGRAQKVSGAVKPVDFDTKWASPE FHIPETPVTVQSDMWGMGVVTFCLLAGFHPFTSEYDREEEIKENVINVKODPNLIPVN ASQECLSFATWALKKSPVRRMRTDEALSHKFLSSDPSMVRRESIKYSASRLRKLAAM SNLØLØTDDPTGRFØIGGLKFKGRFSVIRDAVDSTTEGHAHCAVKIRHPSSEAISEYE **RIVQTHGKGAPKLQIDVLKSEIRLNVVSMPQKSTNQLGGISEESEEDSEARTANEDMK** /protein_id="AAB42336.1" /db_xref="GI:1825742"

CDS

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/tanslation="MIPTISKENTHOSTKSARKSSNESPYPSVTFRPNSSLSHLIIEV
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FRLSPQPGFFDCCSISTPVLFPLGKCYTLDLLESTKPSMHKOTFPGIQAGLATLDA
HLEBQPDGSNGMDALFTNSFVNGFOYFVHPPRIPHLSSDEFTVTPNSVAYTAISSER
FELLPTNKWGNCTEHYPSGIKSDLPYLTGNCVSLCKAKFFMENCGCTPAVXNNERNLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA HTG 16-NOV-1999
*** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
This sequence was identified as CDM:10211010 by the submitter.
This sequence will be replaced
* This sequence will be replaced
* This sequence as soon as it is available and
* the finished sequence as soon as it is available and
* the accession number will be preserved.

Location/Qualifiers

1. 63852
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AC014106.1 GI:6437229
HTG: HTGS_PHASE2.
Etuit fly melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. [ (bases 1 to 63852) Adams, M. and Venter, J.C. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 46996
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/db_xref="taxon:7227"
12714 c 12710 g 19962 t
                                                                                                                                                                                                                                                                                                                                                                 Length: 10
Gaps: 0
Percent Identity: 70.000
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Gaps: 0
Percent Identity: 70.000
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Drosophila melanogaster,
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US-08-653-294-15 x CELC24G7/rev
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Percent Similarity: 100.000
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US-08-653-294-15 x AC014106
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LOCUS AC014106 (
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44312. .44399,44447. .44678,44726. .45044,45323. .45488,
45545. .45610,45653. .45815,46110. .46201,46250. .46395,
46445. .46512,46563. .46686)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               jóin(38014. 38120,38786. 38931,38976. 39021,39089. 39197,
39250. 39337,39384. 39615,40120. 40438,40757. 40922,
40978. 41046,41091. 41233,41342. 41433,41480. 41625,
41677. 41744,41862. 42000)
                                 join(28911. .28981,29343. .29464,29894. .30247,30296. .30386,
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/gene="C24G7.4"
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LLOTINDAME LESULATIONE FAVITY CURT PLANS Y RELINYSGDITGETLEY
CLOTINDAME LESULATIONE FATE FOR THE FORM TH
                                                                                                                                                                                /note="similar to degenerins; coded for by C. elegans cDNA CEMSH05F; coded for by C. elegans cDNA yk35e3.3; coded for by C. elegans cDNA yk35e3.5"
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ILLQMYFSKPTLSQVSFIVNEGGMDFPAVTVCNFNPIKKSYVRELNVSGDLTGETLEY
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HKLNECWQDIVEHDGTYN"
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KTYVNEINKTGEVSPPMINYMMKWFTEIPTLIGGADRPTLHEGNEELKLYMKNHLNFT
VDSFFMNSGFSCPDIFKLCSFQGEIFDCCTLSTEVLTPLGKCFTLDLSSSTKASMHKQ
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SPRIVAVERS ISSDRYVLLPHUMGWOTTBNFPDGIQSNLSTSGSNCLEEKTAKFYMEN
CGCTPALYN TENNIKECTPVETTGLDNILARPNKEFGKIEFOTPNCKACAQGUNSLY
YRAYNSYGSQFSAGAPHYLKSINPEWTDGHMRANFQMINIFYRDMSYTEYNQVQDASV
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NFRYNOSRSQMIIEVPVAQLKKLRKLEGTVSIKRETQHFCETTTMHGPKRIFQGKRWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1QLLSDIGGNMGMFLGMSVITITEICLFFSKMFWLGFSKKRRDYMYSKRVNEKTHERE
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join(33868. .32898,32979. .33141,33227. .33569)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to degenerins"
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/codon_start=1
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32868. .33569
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28911. .32411
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join(28911. .289
30573. .30894,30
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CDS

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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL REFERENCE RUTHORS TITLE JOURNAL

COMMENT

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Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Perygota; Metazoa; Arthropoda; Tracheata; Brachycera;

Muscomorpha; Ephydroldea; Drosophilidae; Drosophila.

1 (Dases 1 to 11772)

8 Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K.,

8 Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K.,

8 Bodota, B., Bouck, J., Bowle, S., Brooks, A., Buhay, C., Bunac, C.,

9 Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,

10 David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N.,

10 Buyan-Rocha, S., Durbin, K.J., Ferantz, P., Ganesh, R., Gorrell, J.H., Gorrell, J., Forcum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J.H., Gorrell, J., Forcum-Tansey, J., Frantz, P., Forcum-Tansey, J., Frantz, P., Kovar, C., Leal, B., Li, Z.,

Relly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z.,

11chtarge, O., Liu, J., Liu, W., Logan, O., Lu, J., Lucier, R.,

Martin, R., Martinez, C., McLeed, M.P., Mei, G., Morgan, M., Morris, S.,

Naly, S., Nelson, A., Nguyen, R., Nguyen, S., Oswal, G.,

Relter, D., Rives, M., Samuel, S., Say, J., Scherer, S., Shah, E.,

Shen, H., Simon, M., Sparks, A., Stamps, A., Stener, S., Shah, E.,

Bristor, D., Weinstock, I.R., Williamson, A., Worley, K., Wren, J.,

Wensford, G., Weinstock, I.R., Williamson, A., Worley, K., Wren, J.,

117732)
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Subsess 1 to 11732)

Direct Submission

Submitted (11-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Oct 16, 1999 this sequence version replaced gi:5881454.

* NOTE: This is a "working draft' sequence. It currently consists of 23 contigs. The true order of the pieces

* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as trues of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                      Drosphila melanogaster chromosome 3L/71F1 clone RPC198-21K15, SEQUENCING IN PROGRESS ***, 23 unordered pleces. AC010050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      838: contig of 838 bp in length
1645: contig of 807 bp in length
3495: contig of 847 bp in length
3495: contig of 847 bp in length
4351: contig of 866 bp in length
6048: contig of 1697 bp in length
7829: contig of 1697 bp in length
17320: contig of 1823 bp in length
17531: contig of 2568 bp in length
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17531: contig of 2403 bp in length
17531: contig of 2403 bp in length
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24775: contig of 3821 bp in length
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46290: contig of 4685 bp in length
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79413: contig of 18185 bp in length
79413: contig of 18185 bp in length
79413: contig of 18185 bp in length
101611: contig of 18195 bp in length
101611: contig of 18195 bp in length
101611: contig of 16041 bp in length
                                                                                                                                                                                                                                                   Drosophila melanogaster
                                                                                                                                                                     ACO10050.3 GI:6056153
HTG: HTGS_PHASE1.
fruit fly.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (24-FEB-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, Mo 63108, USA
Mo 108, USA
Mo 11099 this sequence version replaced gi:4263446.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pleces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                         Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditina; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis:
Materston, R.H.
AC006902 96468 bp DNA HTG 26-FEB-1999
Caenorhabditis elegans clone Y74AllY, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2040: contig of 2040 bp in length 2055: gap of unknown length 10950: contig of 8905 bp in length 10975: gap of unknown length 21821: contig of 10846 bp in length 21836: gap of unknown length 30779: gap of unknown length 30779: gap of unknown length 30779: contig of 6721 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 others
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of 10050 bp in length
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contig of 11154 bp in length
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93051: gap of unknown length
96468: contig of 3417 bp in length.
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of 9675 bp in length
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                                                                                                                                                                                                                                                                                     The sequence of Caehorhabditis elegans clone Unpublished
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Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Caenorhabditis elegans'
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30222 a 17588 c 18100 g 30408 t
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                                              ***, 11 unordered pieces. AC006902
                                                                                               AC006902.2 GI:4309900
                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 96468)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21836: 9
30764: 9
30779: 9
37500: 4
47190: 47205:
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US-08-653-294-15 x AC006902/rev
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Ratio: 3.800
Percent Similarity: 100.000
                                                                                                                         HTG; HTGS_PHASE1
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10961
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21822
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93037
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source

FEATURES

BASE COUNT

ORIGIN

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40855 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (03-3406-1999) Production Sequencing Facility, DOE Joint Common Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Oct 31, 1999 this sequence version replaced gi:5686571.

* NOTE: This is a "working draft sequence. It currently consists of 6 contigs. Gaps between the contigs.

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 13545c)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * This sequence will be replaced
* This sequence will be replaced
* by the finished sequence as it is available and
* the accession number will be preserved
* 1 32143: contig of 32143 bp in length
* 32144 42505: contig of 10362 bp in length
* 42506 76913: contig of 34408 bp in length
* 76914 94682: contig of 17769 bp in length
                                                                                                               others
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                                                                                                                                                                                                                                                                                                                                       to: 117732
                 1. .117732
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22525 c 23405 g 35555 t 26
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Gaps: 0
Percent Identity: 70.000
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                                                                                                                                                                                                                                                                                                                                                                                                99919 TATCGACTTTTAATGCAATTAGATAAGAGA 99890
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   Location/Qualifiers
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DOE Joint Genome Institute.
Direct Submission
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US-08-653-294-15 x AC010050/rev
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Ratio: 3.800
Percent Similarity: 100.000
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   FEATURES
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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Erric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (06-NOV-1997) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
SUBMITTED BY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone RGG11J21 is from the first release of the human BAC library CITB-978SK-B. The library contains cloned DNA from the male fibroblast cell line 978SK. See: Shizuya et al., Proc. Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (Dases 1 to 170136)
Graves, T. Becker, M and Hawkins, M.
The sequence of H. sapiens BAC clone RG011J21
Unpublished (1997)
Q. (Dases 1 to 170136)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-1997
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LOCUS AC003082 170136 bp DNA PRI 06-N
DEFINITION Human BAC clone RG011J21 from 7q31, complete sequence.
ACCESSION AC003082. GI:2588625
318 others
                                                                                                                                                  Length: 10
Gaps: 0
Percent Identity: 70.000
28075 g 36803 t
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Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                       to reverse of: AC008496
                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-15 x AC008496/rev
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29385 c
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                                                                                                                                               Quality: 38.00
Ratio: 3.800
Percent Similarity: 100.000
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Anote—"similar to EST AA489840 (NID:92220715) ab04f12.s1"
52387. .52466
Anote—"similar to EST AA366493 (NID:9221859)"
Complement(52387. .52480)
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Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1995). This clone is available from Research Genetics, Inc. (http://www.resgen.com). VBCTOR: Belobach. Selection: chloramphenicol
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complement(23173. .23302)

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complement(23173. .23344)

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                                                                                                                  The clone sequenced to the left is RG067E13, 200 bp overlap. Actual start of this clone is at base position 196 of RG011J21; actual end is at 170136 of RG011J21.
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Location/Qualifiers
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complement(28082. .28155)
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29513...29694
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/rpt_family="L1"
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8018. .28045
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1086. .28175
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to: 299719

from: 1

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to reverse of: AC006780
                                                                                                            seq_name: gb_htg2:AC006858
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LOCUS AF026087
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LOCUS AC006858 2
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Direct Submission

AL Submission

A Submission

A Gailog, USA

ON Mar 1, 1999 this sequence version replaced gi:4263158.

* NOTE: This is a "working draft' sequence. It currently

* consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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                                                                                                                                                                                                                                                                                                                                                   3047; contig of 3047 bp in length 3061; gap of unknown length 6816: contig of 3755 bp in length 6830; gap of unknown length 35765; contig of 28935 bp in length 35779; gap of unknown length 299719; contig of 263940 bp in length.
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                                                                      Length: 10
Gaps: 0
Percent Identity: 60.000
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Percent Identity: 70.000
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HTG; HTGS_PHASE1.
Caenorhabditis elegans.
Caenorhabditis elegans
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US-08-653-294-15 x AC006780/rev
                                                                      Quality: 38.00
Ratio: 3.800
Percent Similarity: 100.000
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US-08-653-294-15 x AC003082
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HTG; HTGS_PHASE1.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 299719)
                                                                                                                                                                                         AC006858 299719 bp DNA HTG 25-FEB-1999 Caenorhabditis elegans clone Y47D9x, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (24-FEB-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. 1 Mo 3108, UBA.

**NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION Schizosaccharomyces pombe Satl gene, partial cds. ACCESSION AF026087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 299719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence of Caehorhabditis elegans clone Inpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio: 3.800 Ercent Similarity: 100.000 Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55063 c 53844 g 95007
                             163290 TACAGGTTATTGATTCGTATGGAGCACAGA 163261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to reverse of: AC006858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1 TyrArgLeuLeuIleArgLeuAspGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TyrArgLeuLeuIleArgLeuAspGluArg
                                                                                                                                                                                                                                           ***, 4 unordered pieces. AC006858
                                                                                                                                                                                                                                                                                                     AC006858.1 GI:4263490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 299719)
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US-08-653-294-15 x AC006858/rev
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Louis,

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1832 TACCAGCTTTTACTACAAATGGATGAAGA 1803
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                                                                                                                                                                                                                                                                                                                                   source
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ORIGIN
                                                                   JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAB84238.1"
/db_xref="G1:2612955"
/translation="ILTDKE@KQENAIPVLLTRPDILGVDITLSPGEEKCFRLKRRIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KOKVLCRLELSKSRYRTGEMMITELEGLDAMVRQVHMOLESVERIVPDIRIRNSVGTE
RATRKVWCRITRGVFELENMSASMVVPEECPETFETQQFGVEHFLRVELLRAVNKKRE
MOGPAHPRYSEEVOSPSRSRYSEEVORVSEGRLSEEVSKEEEFKGGRESGQHKRMASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKLLDGESNEEGGGEFQDHGMRSEINEEVLEEEDEEKIALLKKLESKQPMATRFEITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /iunction="restores G1 arrest under starvation conditions to sat1- \max- mutant"
                                                                                                                                                                                                                  1 (bases 1 to 2253)
Seth-Smith, H., Kominami, K. and Toda, T.
Direct Submission
Submitted (19-SEP-1997) Cell Regulation, Imperial Cancer Research Fund, 44 Lincoln's Inn Fields, London WC2A 3PX, UK
Location/Qualifiers
1. 2253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMMGPR 2428 bp mRNA PRI 07-JAN-1995
Human cation-dependent mannose 6-phosphate-specific receptor mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2428) Pohlmann, R., Nagel, G., Schmidt, B., Stein, M., Lorkowski, G., Krentler, C., Cully, J., Meyer, H.E., Grzeschik, K.-H., Mersmann, G., Hasilik, A. and von Figura, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNSREMOIQHAPTTFAAETIQCVLPĪRIEKRVVWMEDGMEGGMEGMOPV"
342 c 595 g 566 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Schizosaccharomyces pombe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 9 Gaps: 0 Percent Identity: 88.889
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                                                                                                             Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4896"
<898. .>2223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="972h-"
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   GI:2612954
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/gene="sat1"
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US-08-653-294-15 x AF026087/rev
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4.625
88.889
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   AF026087.1
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Ratio:
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ORIGIN
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                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
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VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
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KEYWORDS
SOURCE
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ELALVERLKPLFNKSFESTVGGSDTYIYIFRVCREAGNHTSGAGLVOINKSNGKETV
VRALNETHIFNGSNMIALLIYGGDEDTOHAGGESORRAVVNISCORNHTLADNFNPYSEE
RGKVQDGFYLFEMDSSLACSPEISHLSVGSILLLYTFNSLVAVVVGGFLYGVYVGGA
GMEQFPHLAFWQDLGNLVADGCDFVCRSKPRNVPAAYRGVGDDQLGEESEERDDHLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref-"GDB:G00-120-162"
/db_xref-"dd-"AA55542.1"
/db_xref-"G1-37147"
/translation="MPPFYSCWRTGLLLLLAVAVRESWQTEEKTCDLVGEKGKESEK
                                                                                                           though the cleavage
Cloning of a cDNA encoding the human cation-dependent mannose 6-phosphate-specific receptor Natl. Acad. Sci. U.S.A. 84 (16), 5575-5579 (1987) 87289647

The protein is a presumptive prepropeptide, though the cleavag site for the mature peptide was not determined. Draft entry and computer readable copy of sequence [1] kindly provided by K.von Figura, 01-OCT-1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"mannose 6-phosphate-specific receptor protein" 618 a 534 c 576 g 700 t 319 bp upstream of HindIII site; chromosome 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="mannose 6-phosphate-specific receptor protein signal peptide"
146, .979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146. .979
/gene="M6PR"
/note="mannose 6-phosphate-specific receptor protein
precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 2428
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Percent Identity: 60.000
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                                                                                                                                                                                                                                                                                                                                   <1..2428
/note="mps receptor mRNA"
146..223
/gene="M6PR"</pre>
                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to reverse of: HUMM6PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="M6PR"
146. .979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene-"M6PR"
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US-08-653-294-15 x HUMM6PR/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.00
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Percent Similarity: 100.000
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Quality:
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Chlamydomonas reinhardtii R
Sequence of the tapetum-spe
Scytalidium catalase gene.
Human secreted protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide(s) and proteins derived from Staphylococcus aureus rotored on computer readable medium and used in the production of anti-S.aureus vaccines

Protorio on computer readable medium and used in the production of anti-S.aureus vaccines

Protorio on computer readable medium and used in the production of anti-S.aureus vaccines

Colim 1; Page 1230-1231; 3271pp; English.

Colim 1; Page 1230-1231; 3271pp; English.

Colim 2; Page 1230-1231; 3271pp; English.

Colim 4; Producino. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access of the invention. The DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences of computer readable medium.

Computer readable medium.

Sequence 1816 BP; 539 A; 307 C; 240 G; 657 T;
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers

241. 300

**Atag= a /**Atag= a /**Atag= a /**Atag= a /**Atag= a /**Atag= a /***Atag= a /***At
                                                                                                                                                                                                                                         Staphylococcus aureus contig SEQ ID #351.

Computer readable medium; vaccine; S.aureus infection; immunodetection cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.

Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-0UL-1997; ...
05-JAN-1997; ...
05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Chol GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 1816
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Gaps: 0
Percent Identity: 88.889
  2413
2569
2794
3791
  1.6e+03
1.7e+03
1.9e+03
2.7e+03
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  91.88
91.33
90.59
87.92
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                                                                                                                                                                             V74662 standard; DNA; 1816 BP. V74662;
                                                                                                                                                                                                                      16-MAR-1999 (first entry)
31.00
31.00
31.00
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US-08-653-294-15 x V74662/rev
                                                                                                              seq_name: N_Geneseq_36:V74662
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                                                                                                                                                        seq_documentation_block
  N_Geneseq_36:V41261
N_Geneseq_36:Q36520
N_Geneseq_36:T42791
N_Geneseq_36:V59714
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                            Key
misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA;
                                                                                                                                                                                 Contiguous sequence determined

A Brassica napus genomic clone
Enterococus faecalis genome
Polynucleotide sequence from t

Hybrid srmc/tylG ORF1. DNA er

DNA encoding Factor-VIIIC. Pr

T Platenolide synthase gene clu
Primer for HIV RNA. Inhibiting r

Primer for HIV RNA. Inhibiting r

DNA sequence of the specificati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1816 | Staphylococcus aureus contig S
14024 | E. Coli Ol57 antigen gene clu
2485 | Rabbit GnT I CDNA clone. Human
2485 | Floral organ-specific chitinas
110000 | Continuation (11 of 17) of
603 | Human anti-angiogenic l6K hPRL
1498 | Rice anthranilate synthase fir
1734 | Human biallelic polymorphic DNA
174 | Staphylococcus aureus contig SE
174 | Staphylococcus aureus contig SE
174 | Bacillus thuringiensis ssp is
175 | Staphylococcus sequence of f
175 | Totol contiguous sequence of f
176 | A Brassica napus genomic clone
176 | A Brassica napus genomic clone
177 | Hybrid synthase gene clu
177 | Platenolide synthase gene clu
177 | Platenolide synthase gene clu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BRCA2 cancer susceptibility ge
Mouse G3BP cDNA. New ubiquitin
Granulocytic Ehrlichia protein
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                                                                                                                                                                      -MODEL-frame-pol. model - DEV-xlp
-MODEL-frame-pol. model - DEV-xlp
-MODEL-frame-pol. model - DEV-xlp
-Q-(cgn1_1/USPTO_Spool/US08653294/runat_04022000_160701_15807/app_query.fasta.1
-DB-VGGenseq_36 - OFMT-fastap - SUFFIX-rng - GAPOP-12.000
-GAPDXT-4.000 -MINMATCH-0.100 -LOOPEXT-0.000
-GAPDXT-4.000 -MINMATCH-0.100 -LOOPEXT-0.000
-GAPDEXT-6.000 -GAPDEXT-0.000 -YGAPOP-10.000 -YGAPDEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -YRAPOP-10.000 -YGAPDEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -YAAPOP-10.000
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-MALIGN-15 -MODE-LOCAL -OUTFWT-pfs - NORM-ext -MINLEN-0
-MAXLEN-1000000 -USER-US08653294 -NCPU-6 - ICPU-3 -NO_XLPXY -WAIT
                                                                                     About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
  out_format : pfs
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1128
1147
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646.49
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5 1.7e+04
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3.0e+0.3
3.2e+0.3
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1.5e+03
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1.4e+03
  N_Geneseq_36:*
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103.58
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38.00 1
37.00 36.00 1:
36.00 10
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Database length: 125096042
Search time (sec): 590.520000
  OM of: US-08-653-294-15 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Search information block:
Query: US-08-653-294-15
Query length: 10
                                                                                                                                                      Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database: N_Geneseq_36:*
                                         Date: Feb 8, 2000 1:28
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N_Geneseq_36:Q29262
N_Geneseq_36:T29774
N_Geneseq_36:N90712
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N_Geneseq_36:V74662
N_Geneseq_36:X06749
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N_Geneseq_36:V49983
N_Geneseq_36:V21209_
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N_Geneseq_36:X01701
N_Geneseq_36:X23749
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N_Geneseq_36:V83003
N_Geneseq_36:X26856
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N_Geneseq_36:T80415
N_Geneseq_36:N50107
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N_Geneseq_36:Q87446
N_Geneseq_36:X12081
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N_Geneseq_36:V15570
N_Geneseq_36:V36099
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N_Geneseq_36:T79695
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N_Geneseq_36:V84064
N_Geneseq_36:T58392
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_Geneseq_36:V81791
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N_Geneseq_36
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N_Genesed_3
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Q25594 standard; cDNA; 2485
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US-08-653-294-15 x X06749/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-NOV-1990; US-620098.
(HSCR-) HSC RES & DEV LP.
                                                                                                                                                                                                                                                                                                                                            seq_name: N_Geneseq_36:025594
                                                                                                                                                                                                                          Ouality: 37.00
Ratio: 4.111
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sarkar M, Schachter H; WPI; 92-217073/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUN-1992.
29-NOV-1991; CA0417
                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; R24779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polya_signal
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                                                                                                                                                                                                                                                                                         Align seg 1/1
                                                                                                                                                                                         Sequence
/*tag= a
/product= sugar_transferase
/note= "wdN gene (ORF1), this region is
specifically claimed in Claim 6; encodes W88312"
858. .2042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              it= N-acetyl_transferase
"wbdR gene (ORF12), this region is
specifically claimed in Claim 6; encodes W88323"
                                                                                                                                                                        encodes W88313"
                                                                                                                                                                                                                  encodes W88314"
                                                                                                                                                                                                                                                              encodes W88315"
                                                                                                                                                                                                                                                                                                                                             encodes W88317"
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                        26-APR-1999 (first entry)

E. coll 0157 antigen gene cluster.
O antigen; 0157 antigen; diagnosis; wbdN gene; wzx gene; wzy gene; wbdP gene; wbdO gene; wbdR gene; transferase; polymerase; flippase; Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "H-repeat, may play a role in gene cluster
assembly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene (ORF10); encodes W88321"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene (ORF11); encodes W88322'
                                                                                                                                                                                                /product= sugar_transferase
/note= "wbdo gene (ORF3), this region is
specifically claimed in Claim 6;
                                                                                                                                                                                                                                           /product- O_antigen_flippase
/note- "wzx gene (ORF4), this region is
specifically claimed in Claim 6;
                                                                                                                                                                                                                                                                                                                           /product= sugar_transferase
/note= "wbdP gene (ORF6), this region is
specifically claimed in Claim 6;
                                                                                                                                                              /note= "wzy_gene_(ORF2), this region is specifically claimed in Claim 6;
                                                                                                                                                                                                                                                                                        -- perosamine_synthetase
'per gene (ORF5); encodes W88316"
                                                                                                                                                    /product = O_antigen-polymerase
                                                                                                                                                                                                                                                                                                                                                                    /noté= "ÓRF7; encodes W88318"
7606. .8578
                                                                                                                                                                                                                                                                                                                                                                                                  "ORF8; encodes W88319"
                                                                                                                                                                                                                                                                                                                                                                                                                            "ORF9; encodes W88320"
                                                                                Location/Qualiflers
       X06749 standard; DNA; 14024 BP.
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/note= "wb
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22-JUL-1997; AU-008162.
01-MAY-1997; AU-006545.
(UNSY ) UNIV SYDNEY.
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                                                                                                                                                                                                                           2744.
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                                                                                                                                                                                                                                                                                                                                                      6491.
seg_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reeves PR, Wang L;
WPI; 99-059669/05.
P-PSDB; W88312, W86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9850531-A1.
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PROTECT STATEMENT OF CARGARDING SPECIFIC TRADECTELL PONYAGEOFATIGA

PARTITIONS - USECHI FOR CASCACHING SPECIFIC STEALER IN C. 9. 1000,
PR. CALLEGES OF PARTIES SERVICES.

C. This is the molective sequence of a gene cluster involved in the steam of a state of the state of the state of the sequence of a gene cluster involved in the state of the sequence of a gene cluster involved in the sequence of a gene cluster of the sequence of a gene cluster involved in the sequence of a gene cluster involved in the sequence of a gene cluster of the sequence of the sequence of a gene cluster of the sequence of the sequen
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claim 1; Pages 40'41; 67pp; Japanese.

This represents a floral organ-specific chitinase encoding gene sequence along with a floral organ-specific promoter sequence. The promoter derived from rice associated with chitinase is specific to floral organs and allows expression of genes in the flower parts of monocotyledonous plants. The expression of desired genes specifically in the floral parts
                                                                                                                                                                                                                                                                                                                                                                                               V49983;
10-NOV-1998 (first entry)
Floral organ-specific chitinase gene with promoter sequence.
Floral organ specific gene: chitinase; promoter; Orga sativa; rice;
flower part; monocotyledonous plant; bacterial resistance; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .1234
/*tag= a
//otce= "floral-organ specific promoter sequence"
//tag= b
/*tag= b
insert in a positive clone was 1.6kb. An 80bp riboprobe was prepared from the 5' terminal of the 1.6kb insert and used to rescreen the library. The largest cDNA insert was cloned into pGEM-7z to obtain pGEM-7z-rcgntl. The full-length rabbit GnT coding sequence was eventually obtained from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Promoter sequence associated with chitinase, specific to floral organs - allows expression of genes in the flower parts of monocotyledonous plants
                                                                                       669 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "floral-organ-specific chitinase"
/note= "contains introns"
                                                                                                                                              Percent Identity: 66.667
                                                                                                                                                                                                                                                    to: 2485
                                                                                         644 G;
                                                                                                                                                                                                                                                    from: 1
                                                                                       623 C;
                                                                                                                                                                                                                                                                                                1072 TACAAACTGCTGCTTCAGCTTGATGAA 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NISB ) JAPAN TOBACCO INC.
Inoue T, Ito T, Saito H, Takakura Y;
WPI; 98-388123/33.
P-PSDB; W64776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                1 TyrArgLeuLeuIleArgLeuAspGlu 9
                                                                                                                                                                                                                                                    Align seg 1/1 to reverse of: Q25594
                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
ID V49983 standard; DNA; 2636 BP.
                                                                                       549 A;
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2109. .2502
/*tag= g
/number= 3
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1235. .1691
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1777. .1909
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/number= 2
1910. .2108
/*tag= f
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/*tag= d
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US-08-653-294-15 x Q25594/rev
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                                                                                                                                               Ouality: 36.00
Ratio: 4.000
Percent Similarity: 100.000
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26-DEC-1997; J04892.
27-DEC-1996; JP-349505.
                                                                                       2485 BP;
                                                                           See also Q25595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9829542-A1.
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                                                                                                                                     alignment_scores:
                                                                                          Sequence
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V21209 from base 1000001 (Methanococcus jannaschii circula
ragments LOCUS V21209 Accession V21209
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X01698 standard; DNA; 603 BP.
X01698

08-JUN-1999 (first entry)

Human anti-anglogenic hPRL Met-1Cys199 antisense DNA. HPL; anglogenesis; growth hormone; hGH; hGH-V; capillary endothelial cell proliferation; placental vascularisation; pregnancy; treatment; anglogenic disease; tumour; inhibitor; malignant; anglofibroma; arteriovenous malformation; arthritis; atheroscalerotte plaques; corneal graft neovascularisation; arthritis; anglogeneration; granulation; glaucoma; ocular; uveitis; fracture; Osler-Weber syndrome;
of monocotyledonous plants, allows modifications to be made in the structure or function of these parts allowing the introduction of desired characteristics such as increased resistance to bacterial attack. Sequence 2636 BP; 722 C; 696 G; 561 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 110000
                                                                                                                                  Length: 9
Gaps: 0
Percent Identity: 77.778
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Gaps: 0
Percent Identity: 60.000
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9
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210000
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1610000
1664976
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                                                                                                                                                                                                                                                                                                                                           213 TACAGGGCATTAATTAAACTAGATGAA 187
                                                                                                                                                                                                                                                                                                         σ
                                                                                                                                                                                                                                                                                                                                                                                                                Seq_documentation_block:
Continuation (11 of 17) of v21209 from
WP Pragment Name Begin 110
WP V21209_01 100001 1110
WP V21209_02 200001 3110
WP V21209_03 300001 4110
WP V21209_04 400001 3110
WP V21209_05 500001 4110
WP V21209_05 500001 7110
WP V21209_06 600001 7110
WP V21209_08 900001 1010
WP V21209_10 1000001 1110
WP V21209_11 1100001 1310
WP V21209_12 1200001 1310
WP V21209_13 1300001 1410
WP V21209_14 1400001 1510
WP V21209_14 1400001 1510
WP V21209_14 1400001 1510
                                                                                                                                                                                                                                                                    to reverse of: V49983
                                                                                                                                                                                                                                                                                                         1 TyrArgLeuLeuIleArgLeuAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-15 x V21209_10/rev
                                                                                                                                                                                                                                                                                                                                                                                    seq_name: N_Geneseq_36:V21209_10
                                                                                                                                  36.00
4.500
88.889
                                                                                                                                                                                                          alignment_block:
US-08-653-294-15 x V49983/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.00
3.889
90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: N_Geneseq_36:x01698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
                                                                                                                                                     Ratio:
Percent Similarity:
                                                                                                                alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                      Align seg 1/1
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arthritis; atherosclerotic plaques; corneal graft neovascularisation;

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08-JUN-1999 (first entry)
Human anti-anglogenic 16K hPRL Met-1Prol42 antisense DNA.
Human; anti-anglogenic 16K hPRL Met-1Prol42 antisense hPL; anglogenesis;
Human; anti-anglogenic; prolactin; placental lactogen; hPL; anglogenesis;
growth hormone; hGH; hGH-V; capillary endothelial cell proliferation;
placental vascularisation; pregnancy; treatment; anglogenic disease;
tumour; inhibitor; malignant; anglofibroma; arteriovenous malformation;
psoriasis; fibroplasia; scleroderma; Kaposi's sarcoma; vascular adhesion;
                                                                                                                                                                                                                                                                                                                                                                                  pre-eclampsia, intrauterine growth retardation, and placental
       ulcer; leukaemia; reproductive disorder; contraceptive agent; gene therapy; pre-eclampsia; intrauterine growth retardation; placental dysfunction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                    ÷
                                                                                                                                                                                                                                                                                                                                                                                                    161
                                                                                                                                                                                                                                                                                                                                                                                                                                     10
3.667 Length: 10
90.000 Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                    173 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: X01698 from: 1 to: 603
                                                                                                                                                                                                                                                                                                                                                                                                    134 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TyrArgLeuLeuIleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 x01701 standard; DNA; 603 BP.
                                                                                                                                                                                                                                                                                                                                                                                                   135 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: N_Geneseq_36:X01701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-15 x X01698
                                                                                                                                                                                                                                                                                                                                                                                                    603 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                           WO9851323-A1.
                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                            dysfunction
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X01701;
                                                                                                                                                                                                                                                                                                                                                                                    with
K K K K E E E E E
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wound healing; proliferative retinopathy; macular degeneration; trachoma; granulation; glaucoma; ocular; uveitis; fracture; Osler-Weber syndrome; postiasis; fibroplasia; soleroderma; Kaposi's sarcoma; vascular adhesion; ulcer; leukaemia; reproductive disorder; contraceptive agent; gene therapy; pre-eclampsia; intrauterine growth retardation; placental dysfunction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JUN-1999 (first entry) Rice anthranilate synthase first isozyme alpha-subunit DNA fragment. Anthranilate synthase; alpha-subunit; ASA; rice; isozyme; plant; seed;
                                                                                                                                                                                                                                                                                                                                                            156 T;
                                                                                                                                                                                                                                                                                                                                                                                         Length: 10
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                            180 G;
                                                                                                                                                                                                                                                                                                                                                             132 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TyrArgLeuLeuIleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: X01701 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID X23749 standard; DNA; 1498 BP.
                                                                                                                                                                                                                                                                                                                                                            135 A;
                                                                                                                                                                                                                                                                                                                                                                                                 3.667
90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: N_Geneseq_36:X23749
                                                                                                                                                                                                                                                                                                                                                                                          33.00
                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-653-294-15 x X01701
                                                                       12-MAY-1998; U09691
                                                                                                                                                                                                                                                                                                                                                             603 BP;
                                                                                                                                                                                                                                                                                                                                                                                           Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                  Homo sapiens.
WO9851323-A1.
                                                                 19-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                      dysfunction
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E E E E E
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Quality:
Ratio:
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Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa
                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
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  Rice anthranilate synthase first isozyme alpha-subunit DNA variant.
Anthranilate synthase; alpha-subunit; ASA; rice; isozyme; plant; seed;
maize; wheat; tryptophan content; nutritional value; ss.
                                         /product= "ASA synthase"
/note= "Partial coding sequence. Incomplete exon 2"
1102. .1233
                                                                                                                                                                                                                                                                                       DNA ancodes "a-subunit of first isozyme of rice anthranilate synthase - used for improving tryptophan production and nutritional value of crops, e.g. rice, malze or wheat Example 5; Page 131-133; 152pp; Japanese.
This invention describes a novel rice anthranilate synthase first isozyme alpha-subunit. The encoding DNA can be used to produce transformant plants and seeds, of e.g. rice, maize or wheat, with enhanced tryptophan content and nutritional value of the crops. Sequence 1498 BP; 343 A; 362 C; 404 G; 389 T;
maize; wheat; tryptophan content; nutritional value; ss
Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 10
Gaps: 0
Percent Identity: 60.000
                                                                                                                      /*tag= c //number= 1 1318. .1498 //number= 2 //number= 2 //number= 2 //note= "partial exon 2 sequence"
                                                                                                                                                                                                                        29-AUG-1997; JP-235049.
(HOKK ) HOKKO CHEM IND CO LTD.
(NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
HASSEGAWA H, TETAKAWA T, TOZAWA Y, WAKASA K;
WPI; 99-228982/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-AUG-1998; J03883.
29-AUG-1997; JP-235049.
(HOKK ) HOKKO CHEM IND CO LTD.
(NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
HORQ ) JAPAN MIN AGRIC FORESTRY WAKASA K;
WPI; 99-228982/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: X23749 from: 1 to: 1498
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/product= "ASA synthase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualiflers
1. .1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TyrArgLeuLeulleArgLeuAspGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
ID X23754 standard; DNA; 1734 BP.
AC X23754;
DT 25-JUN-1999 (first entry)
                                  1102. .1498
/*tag= a
                                                                                                              1234. .1318
                                                                                                                                                                                                                                                                                                                                                                                                                             33.00
4.125
80.000
                                                                                        /*tag= b
                                                                                                  /number-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: N_Geneseq_36:X23754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-15 x X23749
                                                                                                                                                                                                    11-MAR-1999.
31-AUG-1998; JO3883.
                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
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Percent Similarity:
                                                                                                                                                                                          WO9911800-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9911800-A1
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                                                                                                               intron
                                                                                                                                               exon
                                                                                exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
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25-JUN-1999 (first entry) first isozyme alpha-subunit DNA. Rice anthranilate synthase first isozyme alpha-subunit; ASA; rice; isozyme; plant; seed; maize; wheat; tryptophan content; nutritional value; ss.
P-PSDB; W93815.

NAM encodes ^a-subunit of first isozyme of rice anthranilate
Synthase - used for improving tryptophan production and
nutritional value of crops, e.g. rice, maize or wheat
Claim 8; Pages 142-145; 152pg; Japanese.
This invention describes a novel rice anthranilate synthase first
isozyme alpha-subunit. The encoding DNA can be used to produce
transformant plants and seeds, of e.g. rice, maize or wheat, with
enhanced tryptophan content and nutritional value of the crops.
Sequence 1734 BP; 82 A; 889 C; 505 G; 418 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by Anoches "a-subunit of first isozyme of rice anthranilate synthase - used for improving tryptophan production and nutritional value of crops, e.g. rice, maize or wheat claim 2; Page 125-128; 152pp; Japanese.

This invention describes a novel rice anthranilate synthase first isozyme alpha-subunit. The encoding DNA can be used to produce transformant plants and seeds, of e.g. rice, maize or wheat, with enhanced tryptophan content and nutritional value of the crops.
                                                                                                                                                                                                                                                                                                                                                                           Length: 10
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 10
Gaps: 0
Percent Identity: 60.000
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31-AUG-1998. JO3883.
31-AUG-1997. JP-235049.
(HOKK ) HOKKO CHEM IND CO LTD.
(NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
(NORQ ) JAPAN MIN AGRIC FORESTRY WAKASA K;
WPI; 99-228982/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: X23754 from: 1 to: 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product= "ASA synthase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 TACCGCTGCTCAGGGAGGACGACCGC 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 1.1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
ID X23748 standard; DNA; 1734 BP.
AC X23748;
                                                                                                                                                                                                                                                                                                                                                                           33.00
4.125
80.000
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80.000
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US-08-653-294-15 x X23754
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US-08-653-294-15 x X23748
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intron

exon

exon

intron

intron

exon

exon

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6716. .6940
/*tag- e
/note- "encodes residues 177 to 251 of OCIF, see R99925"
6941. .8960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8961. .9349
/*tag= 9
/note= "encodes residues 252 to 380 of OCIF, see R99925"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis for bone resorption control, apanese fragment of osteoporosis the sequences given in 1318pp; Japanese fragment of the genomic DNA encoding the full length osteoclastogenesis inhibitory factor (OCIF) of the invention mas a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. C or 30 mins at 56 deg. C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore
                                                                                                                                                                                       23-APE-1997 (first entry)
Fragment of human OCIF genomic DNA-2.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          deg.C. OCIF is useful in the control of bone resorption and therefor in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-AUG-1996.
20-FEB-1995; J00374.
20-FEB-1995; JP-054977.
21-ULL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashlo K, Kobayashl F, Mochizuki S, Morinaga T; Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H; 96-403320/40.
                                                                                                                                                                                                                                                                                                                        130. 499
/*tag= a
/note= "encodes residues -11 to 112 of OCIF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 10
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1920 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 10190
Align seg 1/1 to: V20767 from: 1 to: 9898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TyrArgLeuLeuIleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                    Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3184 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: T33183 from: 1
                                                                                                                                                 seq_documentation_block:
ID T33183 standard; DNA; 10190 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -ncc
/*tag= f
8961.
                                                                                                                                                                                                                                                                                                                                                            /*tag= P
4504.
                                                                                                               seq_name: N_Geneseq_36:T33183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio: 3.300
Percent Similarity: 100.000
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US-08-653-294-15 x T33183
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Quality:
                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                    Intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    intron
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                                                                                                                                                                                                                                                                                                                          exon
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                                                                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
                                                                                                                                                                         Claim 1; Page 16-26; J6pp; English.

Claim 1; Page 16-26; J6pp; English.

The present sequence represents human OCIF genome DNA which is specifically claimed in the present invention. The present invention of coreclasts specifically claimed in the present invention. The present invention of coreclasts of and/or antipyretic proteins, which have the following characteristics:

(1) And determined by SDS-PAGE of approximately 60 kDa under reducing conditions, and 60 kDa and 120 kDa under non-reducing conditions; and 60 kDa and 120 kDa under non-reducing conditions; and 60 kDa and 120 kDa under non-reducing conditions; (ii) a sequence (III) (see W53239); (iii) affinity to cation exchangers and heparin; (iv) its osteoclast formation inhibiting activity reduced by heating at 70 degrees Celsius for 10 minutes, and (2) a method for preparing at 90 degrees Celsius for 10 minutes, and (2) a method for preparing the above proteins. The proteins are useful for, e.g. treatment and convention of osteoprosis, rheumatism or multiple sclerosis, and also as antigens for immunological diagnosis of these diseases and disorders. Sequence 9898 BP; 3110 A; 1835 C; 1871 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; W53238.
Inhibition of osteoclast formation and/or antipyretic activity useful for, e.g. treating osteoporosis, rheumatism and multiple
                                                                                                                                                 Human, OCIF; genome; osteoclast; antipyretic; osteoporosis; rheumatism; multiple sclerosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                 /*tag= a
/note= "contains introns"
130. .499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-AUG-1997; JO2859.
19-AUG-1996; JP-235928.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
MODINGGE T, NAKAGAWA N, YASUGA H;
WPI: 98-169150/15.
                                                                                                                                                                                                         Location/Qualifiers
130. .9057
                                                       seq_documentation_block:
ID V20767 standard; DNA; 9898 BP.
                                                                                                                                                                                                                                                                               /*tag* b /*tag* b /*tag* b /*tag* b /*tag* c /*tag* c /*tag* c /*tag* /*tag* d /*tag* d /*tag* d
                                                                                                                                                                                                                                                                                                                                                                                                                                          /number= 2
4696. .6715
/*tag= e
/number= 2
6716. .6940
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /number= 3
6941. .8668
/*tag= 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /number= 3
8669. .9057
/*tag= h
/number= 4
                                                                                                           15-JUL-1998 (first entry)
duman OCIF genome DNA-2.
                 seq_name: N_Geneseq_36:V20767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 33.00
Ratio: 3.300
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-08-653-294-15 x V20767
                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores
                                                                                                                                   Human OCIF
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3187 T;

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PER WOSSOLIDSTANDER WAS AND WELLIOUS TREED TO TAKE THE WAS TREED TO THE WAS TREED TO THE WELLIOUS TREED TO THE WELLIOUS TREED THE WELLIOUS TREED THE WELLIOUS TREED THE WELLIOUS TO THE WELLIOUS TO WE WELLIOUS TO THE WELLIOUS THE WELLIOUS TO THE WELLIOUS THE WELLIOUS TO THE WELLIOUS THE WELLIOUS THE WELLIOUS TO THE WELLIOUS TO THE WELLIOUS THE WELLIOUS THE WELLIOUS THE WELLIOUS THE WELLIOUS TO THE WELLIOUS THE W
                                                                                             WPI: 95-131177/17.

WPI: 95-131177/17.

P-PSDB: R71384.

P-PSDB: R71384.

Potent modulators of nerve cell growth and regeneration better growth and regeneration.

Example 2: page 85-88; 10tpp: English.

Example 3: page 85-88; 10tpp: English.

Example 4: page 85-88; 10tpp: English.

Example 5: page 85-88; 10tpp: English.

Example 6: page 85-88; 10tpp: English.

Example 7: page 85-88; 10tpp: English.

Exa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human biallelic polymorphic DNA fragment EST91495b.
Polymorphism: biallelic; human: forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 13
Gaps: 1
Percent Identity: 69.231
                                                                        Matthes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           544 TACCGCCTACTAATATCGAAGTTTCGTCTTGATTCAAGA 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TyrArgLeuLeulle.....ArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: Q87446 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  577 C;
                                                                        Kolodkin AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  681 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X12081 standard; DNA; 150 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.50
3.250
76.923
13-SEP-1993; US-121713.
(REGC ) UNIV CALIFORNIA.
Bentley DR, Goodman CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-653-294-15 x Q87446/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: N_Geneseq_36:X12081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
WO9820165-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
   Semaphorin; grasshopper; human; vaccinia virus; Drosophila; Tribolium; variola major virus; smallpox; semaphorin receptor binding activity; modulation; nerve cell growth; immune response; viral pathogenesis; neurological disease; neuro-regeneration; oncological infection; ds. Tribolium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated Borrella burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease claim 1, Page 908-914; 1128pp; English.

X20248 to X20402 represent polynucleotide sequences isolated from Borrella burgdorfer! (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrella belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrella causes epidemic and endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                      Borrelia burgdorferi polynucleotide sequence #11.

Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis; infection; diagnosis; characterisation; detection; ds.

WO9958943-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3760 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clayton R, Dougherty BA, Fraser C, Lathigra R, Smith HO,
White OR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1401 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1 to: 10502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 8
Gaps: 0
Percent Identity: 75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1402 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= semaphorin I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to reverse of: X20258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3939 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q87446 standard; cDNA; 2504 BP.
                                                                                                                                        X20258 standard; DNA; 10502 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-NOV-1995 (first entry)
Tribolium semaphorin I cDNA.
                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355. .2493
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US-08-653-294-15 x X20258/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JUN-1998; U12764.
03-SEP-1997; US-057483.
20-JUN-1997; US-050359,
22-JUL-1997; US-053344.
22-JUL-1997; US-053377.
                                    seq_name: N_Geneseq_36:x20258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: N_Geneseq_36:Q87446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio: 4.125
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MEDI-) MEDIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10502 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-1995.
13-SEP-1994; U10151.
                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 99-081217/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9507706-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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to: 2504

632 T;

614 G;

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syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or prophylaxis of such diseases.

Sequence 150 BP; 38 A; 38 C; 32 G; 41 T;
      8888888888
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alignment_scores:
Quality: 32.00
Ratio: 4.000
Percent Similarity: 100.000

Length: 8
Gaps: 0
Percent Identity: 62.500 alignment_block: US-08-653-294-15 x X12081/rev

to: 150

from: 1

Align seg 1/1 to reverse of: X12081

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D73590 CELK060G3F Yuji Kohar
D74728 CELK084F3F Yuji Kohar
D75423 CELK104C7F Yuji Kohar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .491

/organism="Trypanosoma brucei"
/strain="Trypanosoma brucei"
/strain="Trypanosoma brucei"
/strain="Trypanosoma brucei"
/db_xref="taxon:5691"
/clone="Sheared DNA-22K17"
/clone="Sheared DNA-22K17"
/clone="Sheared DNA-22K17"
/clone="Sheared DNA-22K17"
/clone="Sheared DNA-22K17"
/clone="Sheared DNA-22K17"
/clone="Trypanosoma brucei from a cloned population of Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTAt 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb).
The v + imethod used for the library construction is described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barelli, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Int. Sheared UNA 1107aTy
Unpublished (1999)
Other_GSSs: Sheared DNA-22KI7.TR
Contect: Najlb M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Fax: 301 838 0208
Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
Seg primer: M13-Forward
Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                 Trypanosoma.

1 (bases 1 to 491)
El-Sayed,N., Zhao,H., Gill,S., Suh,E., Malek,J., Fujil,C., Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S.,
Donelson,J., Fraser,C. and Adams,M.
Determination of clone end sequences from Trypanosoma brucei GUTat
10.1 sheared DNA library
                                                                                                                                                                       AQ652500 491 bp DNA GSS 22-JUN-1999
Sheared DNA-2ZKI7.TF Sheared DNA Trypanosoma brucei genomic clone
AQ652500 GI:5145686
                                                                                                                                                                                                                                                                                                                        Trypanosoma brucei.
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 491
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Gaps: 0
Percent Identity: 77.778
360
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160.90
160.90
160.90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: AQ652500
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130.80
130.80
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US-08-653-294-15 x AQ652500/rev
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36.00
36.00
36.00
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Percent Similarity: 100.000
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                                                                                                   seq_name: gb_gss15:AQ652500
                                                                                                                                                seq_documentation_block:
LOCUS AQ652500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores
gb_est5:D73590
gb_est5:D74728
gb_est5:D75423
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                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Documentation ... | AQ652500 Sheared DNA-22KI7.TF S | AQ652500 Sheared DNA-22KI7.TF S | AA05573 ml84g04.rl Stratagene | AA107217 y290407.rl Soares_multip | A1837241 UI-M-AKO-ade-f-09-0-UI | AA040214 zf03b06.rl Stratagene | AA085256 znl2g08.rl Stratagene | A87592 ywl7g08.rl Soares_placen | A1413784 me91h02.xl Soares mous | A1413784 me91h02.xl Soares mous | AA465578 aa24f06.rl NCI_CGAP_GC | AW048953 UI-M-BHI-amo-q-04-0-UI | AA137143 zl02f08.rl Soares_melanc | AA137143 zl02f08.rl Soares_preg | A1849304 UI-M-AA1-aha-b-09-0-UI
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A4036922 zk32f05.r1 Soares_preg

A4423708 ve81b03.r1 Soares_preg

A4423708 ve81b03.r1 Soares_preg

A44314917 zt03f09.r1 Soares_preg

A4489970 ab05b01.r1 Stratagene

N53340 yz03f12.r1 Soares_multip

N53340 yz03f12.r1 Soares_multip

N53201 yx7f603.r1 Soares_multip

N53204 yz03f12.r1 Soares_multip

N53204 yz03f12.r1 Soares_multip

N53204 yz0800.r1 Knowles Sol

A4632641 np87b04.s1.NCI_CGAP_rF

AA12242 zt01e12.r1 Soares_preg

AA122536 x146c03.x1 NCI_CGAP_PR

A1956148 wt35609.x1 NCI_CGAP_PR

A1956148 wt35609.x1 NCI_CGAP_PR

A188864 wn34d10.x1 NCI_CGAP_PR

A188864 wn34d10.x1 NCI_CGAP_PR

AN103547 xf52h02.x1 NCI_CGAP_GR

AN035538 tz79e04.x1 NCI_CGAP_PR

AN03538 tz79e04.x1 NCI_CGAP_PR
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B29703 T16A22TRB TAMU Arabidops
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CELK051H2F Yuji Kohara
                                                                                                                                                                     Command line parameters:

-MODEL=frame+_p2n.model_DEV=x1p
-Q=/cgnl_1/USPTO_spool/US08653294/runat_04022000_160700_15770/app_query.fasta.1
-Q=/cgnl_1/USPTO_spool/US08653294/runat_04.000 -GAPEXT=4.000
-DB=EST -OPMT=fastap -SUFFTX=rst -GAPEYT=0.000 -GGAPEXT=4.000
-MINNATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GGAPOP=4.500
-GGAPEXT=0.050 -KGAPOP=10.000 -KGAPEXT=0.500 -EGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-LIST=45 -DOCALIGN=200 -TRR_SCORE=pct -ALIGN=15 -MODE-LOCAL
-OUTPWT=pfs -NORM=ext -MINLEN=0 -MALLEN=1000000 -USER=US08653294
-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1
                                                                                                      software, version 4.5,
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148.99
160.90
                                                                                                   About: Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.00 Per 19.00 
     to: EST:*
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Query: US-08-653-294-15
Query length: 10
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 8553.360000
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  OM of: US-08-653-294-15
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9b_est9 AA085256

9b_est9 AA106940

9b_est27 A1413784

9b_est15 AA465578

9b_est18 AA048963

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gb_est9:AA114917
gb_est15:AA489970
gb_est6:N53340
gb_est5:N34201
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gb_gss8:AQ036625
gb_est25:AI310218
gb_gss3:B29703
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gb_est8:AA036922
gb_est7:W88510
gb_est14:AA423708
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gb_est17:AA632641
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gb_est20:AA897536
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gb_est6:N92217
gb_est35:A1837241
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gb_est7:W22057
gb_est22:A1066787
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gb_est30:AI635238
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gb_est5:D73508
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ORGANISM

ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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N92217 222 bp mrNA 220 down the property of the property 290d07.r1 Soares multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:290317 5' similar to gb:X56253_rnal CATION-DEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR PRECURSOR (HUMAN); contains element THR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia) digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis G. Becker (NIDS/NIH).

G. Becker (NIDS/NIH).

a 48 c 47 g 75 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. 222

/organism="Homo sapiens"

/db_xref="GDB:2300157"

/db_xref="GDB:2300157"

/db_xref="GDB:230317"

/clone_lib="Soares_multiple_sclerosis_2NbHMSP"

/sex="male"

/sex="male"

/dsv_stage="male 46"

/lab_host="PHIOB (ampicillin resistant)"

/note="Vector: pT77B5 (pharmacia) with a modified

polylinker V_TYPE: phagemid; Site_1: Not I: Site_2: Eco

RI: 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ETPFIME.
High quality sequence stop: 47.
                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Butheria, Primates, Catarrhini, Hominidae; Homo.

1 (bases 1 to 223)

Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The WashU-Merck EST Project
Unpublished (1995)
On Sep 21, 1992 this sequence version replaced gi:276322.
Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 10
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222
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                                                                                                                          repetitive element ;, mRNA sequence.
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                                                                                                                                                                           N92217.1 GI:1264526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-15 x N92217/rev
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Percent Similarity: 100.000
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seq_documentation_block:
LOCUS N92217
DEFINITION y290407.r1 So
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ORGANISM
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
COMMENT
                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                           VERSION
                                                                                                                                                                                                                                           Mus musculus

Bukaryota. Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Bukaryota. Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 189)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                 EST 04-FEB-1997 (#937315) Mus musculus cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston, R.
The Washur-HMMI Mouse EST Project
Unpublished (1996)
On Apr 14, 1993 this sequence version replaced gi:693450.
Contact: Marra M/Mouse EST Project
Washur-HHMI Mouse EST Project
Washington University School of MedicineP
H44 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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/db_xref="taxon:10090"
/db_ore="INAGE:518742"
/clone="INAGE:518742"
/clone=|lb="Stratagene mouse kidney (#937315)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 9
Gaps: 0
Percent Identity: 88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGI:312>yu
Putative full length read
vector to vector length is 372
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 140.
Location/Qualifiers
                                                                       seq_documentation_block:
LOCUS AA105773 AA105774
DEFINITION m184904.rl Stratagene mouse kidney (#
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="females"
                                                                                                                                                                                             AA105773.1 GI:1654862
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US-08-653-294-15 x AA105773/rev
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4.625
88.889
                         seq_name: gb_est9:AA105773
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FEATURES

125 TACCAGCTTTTACTACAAATGGATGAAGA 96

seq_name: gb_est6:N92217

Align seg 1/1

BASE COUNT ORIGIN

LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

MEDLINE JOURNAL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butharyota; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 285)

11 (bases 1 to 285)

12 (bases 2 to 285)

13 (bases 3 to 285)

14 (bases 4 to 285)

15 (bases 5 to 285)

16 (bases 6 to 285)

17 (bases 7 (biapelli, B., Chissoe, S., Dietrich, W., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Hawkins, M., Mortala, M., Parsons, J., Prange, C., Rikin, L., Rohlifing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Prangeskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS AA040214 285 bp mRNA
DEFINITION zf03b05.r1 Soares_fetal_heart_NDHH19W Homo sapiens cDNA clone
IMAGE:375825 $' similar to gb:X56253_rnal CATION DEPENDENT
MANNOSE.6-PHOSPHATE RECEPTOR PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Oct 18, 1995 this sequence version replaced gi:1023753.
Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 10
Gaps: 0
Percent Identity: 60.000
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         ٠.
و
                                                                                                                                       239 TACCTCCTCATCAGACTGGATGAG 265
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                                                                                           σ
    from: 1
                                                                                           1 TyrArgLeuLeuIleArgLeuAspGlu
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to: AI837241
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Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                          seq_name: gb_est8:AA040214
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Align seg 1/1
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AUTHORS
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JOURNAL
MEDLINE
COMMENT
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KEYWORDS
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/clone="101-"Ax0-ade-f:09-0-UI"
/clone="101-"N-XX0-ade-f:09-0-UI"
/clone="101-"N-XX0-ade-f:09-0-UI"
/clone="101-"N-XX0-ade-f:09-0-UI"
/dev_stage="107-32 page |
/dab_host="DH10B (Life Technologies)"
/dab_host="bH10B (Life Technologies)"
/dab_host="mbH10B (Life Technolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence contained an oligo-dr track that was present in the oligonuclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the CDNA between the NoI site and the oligo-dr track served to verify it as a clone from the non-normalized hypothalamus library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP CDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP CDNA clones, this record will be updated accordingly when that means is determined. Seg primer: MI3 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodenita; Sciurognathi; Muridae; Murinae; Mus. [ toases 1 to 275)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                         AI837241 275 bp mRNA EST 14-JUL-1999 UI-M-AKO-ade-f-09-0-UI.s1 NIH_BMAP_MHY Mus musculus cDNA clone UI-M-AKO-ade-f-09-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Jun 5, 1998 this sequence version replaced gi:3188055.
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 9
Gaps: 0
Percent Identity: 88.889
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/organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 6 (9), 791-806 (1996) 97044477
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TAG_TISSUE=hypothalamus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                            AI837241.1 GI:5471494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.00
4.625
88.889
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US-08-653-294-15 x AI837241
                                      seq_name: gb_est35:AI837241
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LOCUS AI837241
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Ratio:
Percent Similarity:
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source

FEATURES

BASE COUNT

ORIGIN

alignment_block:

DEFINITION

ORGANISM

SOURCE

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS

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H87592 344 bp mRNA EST 21-NOV-1995
W1709B.T. SOATES placenta, 8to9weeks_ZNbHP8tc9W Homo sapiens CDNA clone IMAGE:25242 5' similar to 9b:X56253_rnal CATION-DEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stops: 330
Source: INAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (life@image.llnl.gov) for further information.
Insert Length: 658 Std Error: 0.00
Seq primer: MI3RPI
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases: 1 to 344)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Mashu-Merck EST Project
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:635818.
Contact: Wison RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fal: 314 286 1800
Fax: 314 286 1810
Email: esf@watson.wustl.edu
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                 to reverse of: AA085256 from: 1
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/organism="Homo sapiens"
/db_xref="GDB:3885608"
                                                                                                                                                                                                                                                                                        1 TyrArgLeuLeuIleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                                           128 TACCAGCTTTTACTACAAATGGATGAAGA 99
                                                                                                                                          US-08-653-294-15 x AA085256/rev
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Ratio: 3.700
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wilson, R.
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                                                                                                            alignment_block
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VERSION
KEYWORDS
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ORIGIN
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          zn13q08.rl Stratagene hmr. neuron (#937233) Homo sapiens cDNA clone
IMAGE:547262 5' similar to gb:X56253_rnal CATION-DEPENDENT
MANNOSE-6-PHOSPHATE RECEPTOR PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib-"Stratagene hNT neuron (#937233)"
/dev_stage="hNT neurons"
/lab_host="SOLR (kanamycin resistant)"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT.
Bifferentiated, post mitotic hNT neurons. Average insert Size: 15 kb; Uni ZAP XR Vector; -5' adaptor sequence: 5'
GRATTGGGGAGGAGGAG 3' adaptor sequence: 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalla;
Eukaryota: Primates; Catarrhini; Hominidae; Homo.

( bases 1 to 328)
Hiller,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W.,
Mawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: estewarson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should likept in mind should you use this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807\text{-}828 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On May 5, 1995 this sequence version replaced gi:797884. Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Fax: 314 286 1880
                                                                                                                                             to: 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                                                          Align seg 1/1 to reverse of: AA040214 from: 1
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/organism="Homo sapiens"
/db_xref="GDB:3925452"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCGAGTTTTTTTTTTTTTTTTTT
                                                                                                                                                                                                                                                          216 TACCAGCTTTTACTACAAATGGATGAAAGA 187
                                                                                                                                                                                                                 1 TyrArgLeuLeulleArgLeuAspGluArg 10
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/clone="IMAGE:547262"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA085256
AA085256.1 GI:1627314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 bp
                                                                   US-08-653-294-15 x AA040214/rev
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                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_est9:AA085256
                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS AA085256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
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TITLE JOURNAL MEDLINE COMMENT

10

alignment_scores

BASE COUNT

ORIGIN

FEATURES

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US-08-653-294-15 x AA106940/rev
                                                                                                                                            seq_name: gb_est27:AI413784
                                                                                                                                                                                  seq_documentation_block:
LOCUS AI413784
                                                                                                                                                                                                                                                                                                                 house mouse.
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Ratio:
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                                    Align seg 1/1
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KEYWORDS
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                                                                                                                                                                                                                    DEFINITION
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Manmalia, Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Manmalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus. 1 (bases 1 to 351).

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The Washu-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marsa M/Mouse EST Project
Washington University School of Medicinep
Washington University School of Medicinep
H444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108
Tel: 314 286 1800
                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS AA106940 351 bp mRNA EST 04-FEB-1997
DEFINITION m192h06.r1 Stratagene mouse kidney (#937315) Mus musculus cDNA clone IMAGE:519515 5' similar to 9b:M22810 Mouse androgen-regulated protein mRNA, complete cds (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps: 0
Gaps: 0
Percent Identity: 88.889
Gaps: 0
Percent Identity: 60.000
                                                                                                            to: 344
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High quality sequence stop: 448.
Location/Qualifiers
1. .351
                                                                                                          from: 1
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/strain="C57/B16"
/db_xref="taxon:10090"
                                                                                                                                                               1 TyrArgLeuLeuIleArgLeuAspGluArg 10
                                                                                                          Align seg 1/1 to reverse of: H87592
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EST.
                                                   alignment_block:
US-08-653-294-15 x H87592/rev
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Ratio: 3.700
Percent Similarity: 100.000
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Ratio:
Percent Similarity:
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KEYWORDS
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SM Musc musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
E 1 (bases 1 to 398)

SM Marra, Hillar, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.
The Washu'NcI Mouse EST Project 1999
Unpublished (1999)
L. On Apr 21, 1998 this sequence version replaced gi:3071892.
Contact: Marra M/Washu-NcI Mouse EST Project 1999
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800
Fax: 314 286 1800
Email: mouseest@atson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. IMAGE Consortium sequenced on the 5' end only, this new High quality sequence stop: 375.
High quality sequence stop: 375.
                                                                                                                                                                 AI413784 398 bp mRNA EST 09-FEB-1999 me91h02.x1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:402963 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:402963"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
to: 351
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Gaps: 0
Percent Identity: 88.889
from: 1
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                  to reverse of: AA106940
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                                          σ
                                          1 TyrArgLeuLeulleArgLeuAspGlu
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4.625
88.889
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LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

sed_name:

ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

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Email: mESTemail.ilh.gov

The sequence contained an oligo-dr track that was present in the coligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dr track served to identify it as a clone from the normalized pineal glands library cDNA Library Preperation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. POLYA-YES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polylinker; Site_1: Not I; Site_2: Eco RI; The WILBAMP_M.S. library is a subtracted library derived from NIH_BMAP_M.S.1 which in turn is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amydala, basal gangila, pineal gland, striatum, hipoccampus). The driver used for subtraction consisted of a pool of 5,000 clones from the NIH_BMAP_M.S.1 library and a pool of 5,000 clones obtained from non-normalized and normalized mouse brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 407)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                     AW048963 407 bp mRNA EST 18-SEP-1999 UI-M-BH1-amo-g-04-0-UI.SI NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-BH1-amo-g-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C57BL/6J"
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/dev_stage="127-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Mar 16, 1998 this sequence version replaced gi:2961735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
20892-9643, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Gaps:
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Res. 6 (9), 791-806 (1996)
97044477
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205 TACCAGCTTTTACTACAAATGGATGAAAGA 176
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TAG_TISSUE=pineal-gla
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91 c
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Fax: 301 443 9890
                                                                                                              gb_est38:AW048963
                                                                                                                                                                                      seq_documentation_block:
LOCUS AW048963
                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
Mus musculus
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Quality:
Ratio:
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                                                                                                                                                                                                                                                             DEFINITION
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AUTHORS
TITLE
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COMMENT
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | FIGURE | TOTAL | TOTAL | FIGURE | FIG
                                                                                                                                                                                                                                                                                                                                                                                                AA465578 402 bp mRNA EST 15-AUG-1997 and 402 bp mRNA EST 15-AUG-1997 saddfor.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814211 5' similar to gb:X56253_rna1 CATION-DEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMMGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 Er from Amersham High quality sequence stop: 313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 402)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              constructed by Bento Soares and M. Fatima Bonaldo." 87 c 106 g 119 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
Unpublished (1997)
On May 9, 1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:814211"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 402
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Percent Identity: 60.000
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                                                                                                              to: 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="GDB:6032206"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TyrArgLeuLeulleArgLeuAspGluArg 10
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                                                                                                                                                                                                                                                             233 TACCTCCTCTCATCAGACTGGATGAG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: AA465578
                                                                                                                                                                                      1 TyrArgLeuLeulleArgLeuAspGlu 9
                                                                                                              from: 1
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US-08-653-294-15 x AA465578/rev
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Ratio: 3.700
Percent Similarity: 100.000
                                                                                                          to: AI413784
alignment_block:
US-08-653-294-15 x AI413784
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LOCUS AA465578
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BASE COUNT

ORIGIN

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases 1 to 43)

Hiller,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hulman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Mortis,M., Parsons,J., Prange,C., Rikin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thlerry Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Variation University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 315 180 1810
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LOCUS AA137143 433 bp mRNA EST 14-MAY-1997

LOCUS 1202f08 r.1 Somets_pregnant_uterus_NbHPU Homo sapiens CDNA clone
DEFINITION IMAGE:491175 5' similar to 9b:X56253 rnal CATION-DEPENDENT
MANNOSE-6-PHOSPHATE RECEPTOR PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Sep 12, 1996 this sequence version replaced gi:1393248.
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism-"Homo sapiens"
/db_xref="GDB:3805762"
/db_xref="Actions : 1805762"
/clone="ImAce:491175"
/clone_lib="Soares_pregnant_uterus_NDHPU"
                                                                                                                                to: 432
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Gaps:
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                                                                                                                                to reverse of: N28776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA137143
AA137143.1 GI:1698378
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                                                              US-08-653-294-15 x N28776/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.00
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                                                                                                                                                                                                                                                                                                                                   seq_name: gb_est10:AA137143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
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                                  alignment_block:
                                                                                                                                Align seg 1/1
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VERSION
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SOURCE
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JOURNAL
MEDLINE
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Contact: Wilson KK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: essewatson.wustl.edu
High quality sequence stops: 323
Source: IMAGE Consortium, Linit, This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: T7
High quality sequence stop: 323.
High quality sequence stop: 323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."
                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:

132 bp mRNA

LOCUS

N28776

DEFINITION TAC6909.11 Sources melanocyte 2NbHM Homo sapiens cDNA clone images:267040 5' similar to 9b:X55253_rnal CATION-DEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 432)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:9606"
/clone="INAGE:267040"
/clone=Ilb="Soares melanocyte 2NbHM"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps: 0
Percent Identity: 60.000
Percent Identity: 88.889
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                                                                                                                                                                407
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/db_xref="GDB:3876682"
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t
                                                                                                                                                                                                                                                                     The WashU-Merck EST Project
                                                                                                                                                                                                                                  1 TyrArgLeuLeulleArgLeuAspGlu 9
                                                                                                                                                            from: 1
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Ratio: 3.700
Percent Similarity: 100.000
                                                                                                                                                                Align seg 1/1 to: AW048963
88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .432
                                                              alignment_block:
US-08-653-294-15 x AW048963
                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_est5:N28776
Percent Similarity:
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ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS TITLE JOURNAL COMMENT

source

FEATURES

BASE COUNT

ORIGIN

No.

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Ratio:
Percent Similarity:
                                                                                                                       Quality:
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                                                                                   alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
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VERSION
KEYWORDS
SOURCE
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ORIGIN
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AUTHORS
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JOURNAL
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/strain="C57BL/6J"
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/dbexref="taxon:10090"
/clone="lib-"NuH_BMAP_MB-D-09-0-UI"
/clone="lib-"NuH_BMAP_MB-N"
/dev_stage="27-32 days"
/dev_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Jun 22, 1998 this sequence version replaced g1:3247013.

Contact: Chin, H
National Institute of Mental Health
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 1706
Fax: 301 443 9890
Email: mESTGmail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the Oligo-dT track served to verify it as a clone from the normalized olfactory bulbs library CDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP CDNA clones will be made available by the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI849304 433 bp mRNA EST 15-JUL-1999 UI-M-AJI-aha-b-09-0-UI.sl NIH_BMAP_MOB_N Mus musculus cDNA clone UI-M-AJI-aha-b-09-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 433) Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotides present between the Not I site and the oligo-dT track. The library was constructed as describly By Bonnido, Lennon and Soares, Genome Research 6: 791-806, 1996. Tissue provided by Ms. Annie Novakovich, Zivic-Miller Laboratories.
TAG_IIS-NIH_BMAP_NOB_N
TAG_IIS-SUPE-CATGG
   Percent Identity: 60.000
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                                                                                                                                                                                                                                                                      1 TyrArgLeuLeuIleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                           from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI849304.1 GI:5493210
                                                                       alignment_block:
US-08-653-294-15 x AA137143
                                                                                                                                                                                       Align seg 1/1 to: AA137143
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_est35:AI849304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
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1 others

129

110 g

95 a

BASE COUNT ORIGIN

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Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.linl.gov) for further information.
Seq primer: T7
High quality sequence stop: 342.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
144 bp mRNA EST 14 *FEB-1996
LOCUS N46203.1 Soares melanocyte 2NbHM Homo sapiens CDNA clone
DEFINITION y938f03.11 Soares melanocyte 50.2356253_rnal CATION-DEPENDENT
MAGE:273533 $' stimilar to 90.2356253_rnal CATION-DEPENDENT
MANNOSE-6-PHOSPHATE RECEPTOR PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherfa; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 434;
Hillier,L., Clark,N.; Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Raikhni,L., Rohlfing,T., Soares,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1995)
On May 18, 1995 this sequence version replaced gi:811021.
Contact: Wilson University School of Medicine
Washington University School of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares melanocyte 2NbHM"
/sex="Male"
Length: 9
Gaps: 0
Percent Identity: 88.889
                                                                                                                                                                         to: 433

    .434
    /organism="Homo sapiens"
    /db_xref="GDB:3883175"

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/clone="IMAGE:27353"
                                                                                                                                                                                                                                                                    242 TACCICCICCICATCAGACIGGAIGAG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilson, R.
The WashU-Merck EST Project
                                                                                                                                                                                                                      1 TyrArgLeuLeuIleArgLeuAspGlu 9
                                                                                                                                                                         from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N46203.1 GI:1187369
  37.00
4.625
88.889
                                                                                                                                                                      Align seg 1/1 to: AI849304
                                                                                               alignment_block:
US-08-653-294-15 x AI849304
                                                                                                                                                                                                                                                                                                                      seq_name: gb_est6:N46203
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alignment_scores:

Quality: 37.00 Length: 10
Ratio: 3.700 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 60.000

alignment_block: US-08-653-294-15 x N46203/rev

Align seg 1/1 to reverse of: N46203 from: 1 to: 434

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us-08-653-294-15.rst

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 8, 2000, 01:29:38; Run on:

Search time 122.56 Seconds (without alignments)
2.319 Million cell updates/sec

US-08-653-294-16 58 Perfect score:

1 YRLLIRRILLRY 12 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

188963 seqs, 23686106 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

A_Geneseq_36:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	LA-B2702 84-	٠	Immunomodulating d	ō	84-	nomodulati	receptor		taglandin	Prostaglandin-EP3-		Human prostaglandi	Human EP3-V recept	Polyprotein of att	ein	Sequence of gpM en	Yeast transcriptio	H-Delta-1 polypept	CREB binding prote	Cellular transcrip	Actinobacillus ple	Polyfunctional pro	=	neuronal	agland	x toll	d pepti	c	Surfactant peptide	ılaria	atfish	Protein with Oxeta	ORFIO thermally st	ORF10 glycosylase.
SUMMARIES	QI	9542	W33798	W33799	R92907	R95428	W33778	R42281	R42280	R69518	R69517	R69516	W57411	W57410	W06591	W06590	P70467	W13821	W11725	R79054	W40058	W41731	R21517	R22960	W44156	R21690	W86351	W81462	R30657	W88194	1203	618	202	W11703	73
	ngth DB	12	~	~	0	0	20	61	65	65	88	90	93	02	91	391	63	44	099	41	441	36	61	61	04	66	04	2	,	_	40	80	16	221 1	21
d	Query Match Lengt	2.8	'n.	ď	ω.	ω.	ω.	ω.	ω.	ω.	8	φ.	ά.	&	6.9	6.9	ď.	5	5.2	5.2	5.2	m.	ω.	ά.	ω.	ω.	m	51.7	ä	ä	Η.	٦.	51.7		51.7
	Score	48	48	48	34	34	34	34	34	34	34	34	34	34	33	33	32	32	32	32	32	31	31	31	31	31	31	30	30	30	30	30	30	30	30
	Result No.	1	7	m	4	Ŋ	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58	30	31	32	33	34

Thymine DNA glycos Neuronal nicotinic Curvularia verrucu Chloroperoxidase. Rat VRRP-1 (VR2) c Human transient re Virulence gene clu Immunomodulatory p Immunomodulatory p Peptide #3 used in	
W81465 W09022 W12042 R82249 W99790 W55961 R97246 W47264 W47262 W33783	
папапапапапа	
221 504 600 640 761 720 472 472 6	
51.7 51.7 51.7 51.7 51.7 50.0 50.0	
33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	

ALIGNMENTS

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Whis 92-19402/725.

Tomposns. comparising lymphoid surface membrane proteins - which may finhibit cytolytic activity and differentiation of CTLS.

Example 12, 29pp; English.

Example 12, 29pp; English.

R95413, and R95415-R9543 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the protein associated with T-cell activation in mammalian T-cells, and is protein associated with T-cell activation in mammalian T-cells, and is a lise immunologically cross reactive with the heat shock protein Hsc70.

Top 14 is found in a limited number of cell types, but is particularly compositions of an anticell types, but is particularly colly with an amphoteric detergent, and then passed through an affinity colly min containing a covalently bound HLA-B2702 palindromic peptide.

Column containing a covalently bound HLA-B2702 palindromic peptide.

Column containing a covalently bound HLA-B2702 palindromic peptide.

Compositions comprising the extracellular fragment of p74 combined with the AB2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of determining the amount of binding between the candidate compound and p74.

Containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74 in an amount sufficient to compete with p74 for the binding of the p74 ligand.
                                        Nove-1996 (first entry)
HLA-B2702 84-79-84 palindrome.
HLA-B2702 84-79-84 palindrome.
HLA-B2702 84-79-84 palindrome.
Tecell lysate, membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
Synthetic.
W09513288-A1.
                                                                                                                                                                                                                                                              18-MAX-1995.
10-NOV-1994, UL2985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
R95429 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                              Clayberger C, Krensky AM; WPI; 95-194027/25.
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Gaps ; 0 Score 48; DB 1; Length 12; Pred. No. 0.0038; 0; Mismatches 2; Indels 82.8%; Query Match 82.8 Best Local Similarity 83.3 Matches 10; Conservative

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12

1 YRLLIRRILLRY 12

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W33798 standard; peptide; 12 AA. W33798; RESULT 2 W33798 ID W33798 AC W33798; ~

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New immunomodulating dimer peptide(s) - based on a Class I HiA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases.

Per treating activity, including the N-terminal acylated and/or corporate compruse the formune is claimed which has a for the advisor.

Per treating amidated or esterified forms of up to 60 amino acids, where the formula; A-B, where A, B = corp.

Per son N; aa39 = R or G; aa80 = 1 or N; aa81, aa84 = a hydrophobic or caid. The sequence in the brackets may optionally be absent or truncated at my peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HiA-B alphal domain (positions or any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HIA-B alphal domain (positions or 17e4). They can be used to inhibit cytocoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CDS. The peptide can be used for preventing rejection consument diseases, e.g. diabetes, the common of the compound or treating autoimmune diseases, e.g. diabetes, consumence the manner of the compound or the consumence of transplants or for treating autoimmune diseases, e.g. diabetes, consumence the consumence of the consumence o
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This sequence represents a specifically claimed immunomodulating
dimer peptide of the invention. A peptide-type compound or variant is
19-JUN-1998 (first entry)
Peptide B2702.84-79/79-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autodimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUN-1998 (first entry)
Immunomodulating dimer peptide #3.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New immunomodulating dimer peptide(s) - based on a Class I HLA-1 alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases
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Pred. No. 0.0038;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                 24-MAY-1996, US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-MAY-1997; U08689.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                          Beulow R, Clayberger C, Krensky AM; WPI; 98-086530/08.
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                                                                                                                                                                                                                                                                                                                22-MAY-1997; U08689
                                                                                                                                                                                                             Homo sapiens.
WO.9744351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
WO9744351-A1.
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                                                                                                                                               rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rejection.
                                                                                                                                                                            Synthetic
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claimed which has immunomodulating activity, including the N-terminal activity activity and the control amidated or esterified forms of up to 60 mino acids, where the peptide-type compound comprises the formula: A-B, where A, B = (R aa76-77L) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a represents amino acid; aa82 = R or L; aa83 = G or R; and as represents amino acid; are sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proteins of interest to activate CTLs. They can also inhibit the consequently rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus errythematosis.
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R83061-R83085, R83090-R83096 and R82907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to abuther deriod of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.84-75/75-84)
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clayberger C, Krensky AM, Parham P; WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.8%; Score 48; DB 1; Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0.0038;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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50.0%; Pred. No. 2.4;
11ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R92907 standard; peptide; 20 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 83.3%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
WO9526979-A1.
                                                                                                                                                                                                                                                                                                                                                                                            The products
Sequence 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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R92907
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autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus.
                                                                                                                                                                                                                                                                                             The products
Sequence 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP-557966-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antagonist
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R42281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tompsis. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs.

Example; Page 12: 29pp; English.

Example; Page 12: 29pp; English.

R95413, and R95413-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the reprotein p74 from a T-cell lyaste. P74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein HS70.

P74 is found in a limited number of cell types, but is particularly expressed on B and T cells. P74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide.

Column containing a covalently bound HLA-B2702 palindromic peptide.

Column containing a covalently bound HLA-B2702 palindromic peptide.

Column containing a covalently bound HLA-B2702 palindromic peptide.

Column containing a covalently bound HLA-B2702 palindromic peptide.

Column containing a covalently bound HLA-B2702 palindromic peptide.

Column containing the extracellular fragment of p74 combined with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74.

Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete containing the binding of the p74 ligand.
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                                                    12-NOV-1996 (first entry)
HIA-B2702 84-75-84 paindrome.
HIA-B2702 84-75-84 paindrome.
HIA-B2702 84-75-84 paindrome.
HIA-P2702 84-75-84 paindrome.
HIA-P2702 84-75-84 paindrome.
HIA-P2703 84-75-84 paindrome.
HIA-P2703 84-75-84 paindrome.
B cell; calcium influx: cytotoxic I lymphocyte; CTL; differentiation; Syptolysis; antigen presenting cell.
W09513288-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUN-1998 (first entry)
Immunomodulating dimer peptide #1.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAY-1997.
22-MAY-1997.
22-MAY-1996; US-653294.
(STRD) UNIV LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
WHY: 98-086530/08.
New immunoamodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
6
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                                                                                                                                                                         18-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI; 95-194027/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                           R95428 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W33778 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YRLLIR-----RILLRY 12
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Best Local Similarity 50.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 AA;
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WO9744351-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                        R95428;
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            R95428
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Taling in 16, Page 35, 41pp; English.

This sequence represents a specifically claimed immunomodulating dimension. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal activity, including the N-terminal activity, including the N-terminal activity, including the N-terminal activity, where the peptide-type compound comprises the formula: A-B, where A, B = (R anf6-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a represents amino acid; The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid; sequences related to a class I HLA-B alphal domain (positions 78-84). They can be used to inhibit cycloxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in proteins of interest to activate CTLs. They can also inhibit the proteins of interest to activate CTLs. They can also inhibit the proflemation of T cells in response to anti-CD3, The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New prostaglandin E receptor protein and DNA encoding it - used to study prostaglandin binding, agonists and antagonists etc. Claim 5, 10; Figure 4; 22pp; English.
The prostaglandin E receptor can e used to clone other PGE receptor genes, to clarify the structure of PGE receptors, to elucidate the function of PGE and to identify PGE agonists/ antagonists. The receptor is produced by recombinant methods,
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Prostaglandin E receptor; prostaglandin; binding; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.6%; Score 34; DB 1; Length 20; 50.0%; Pred. No. 2.4; tive 0; Mismatches 2; Indels
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/label- Transmembrane domain 3.
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/label- Transmembrane domain 6.
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/label= Transmembrane domain 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .55
|abel= Transmembrane domain 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label = Transmembrane domain 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R42281 standard; Protein; 361 AA. R42281;
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24-FEB-1993; 102873.
24-FEB-1992; JP-036580.
23-MAR-1992; JP-064889.
(TAKE ) TAKEDA CHEM IND LTD.
IChikawa A, Narumiya S;
WPI; 93-274435/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YRLLIR-----RILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YRLAIRLNERRENLRIALRY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-1994 (first entry)
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Best Local Similarity 50.0
Matches 10; Conservative
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                                                                                                                                            Gaps
transforming a host cell, culturing the cell and retrieving the recombinant protein from the culture medium. This PGE2 receptor is a derivative of the clone MP600 (Q66124) having 99 base pairs deleted from the coding sequence resulting in replacement of 30 C-terminal amino acids with a different sequence of 26 amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label- Phosphorylation site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New prostagiand in Erceptor protein and DNA encoding it - used to study prostaglandin binding, agonists and antagonists etc. Claim 10; Figure 1: 22pp; English.

The prostaglandin Erceptor can be used to clone other FGE receptor genes, to clarify the structure of PGE receptors, to elucidate the function of PGE and to identify FGE agonists/ antagonists. The receptor is produced by recombinant methods, transforming a host cell, culturing the cell and retrieving the recombinant protein from the culture medium.
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                                                                                                                Query Match 58.6%; Score 34; DB 1; Length 361; Best Local Similarity 77.8%; Pred. No. 46; Matches 7; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                             21-FEB-1994 (first entry)
PGE2 receptor coding sequence (Clone MP660).
Prostaglandin E receptor; prostaglandin; binding; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Phosphorylation site.
/note= Phosphorylation is by cAMP
                                                                                                                                                                                                                                                                                                                                                                                               Tabel- N-glycosylation site.
11. .55
| Transmembrane domain 1.
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/label= Transmembrane domain 6.
304. .325
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/label- Transmembrane domain 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label = Transmembrane domain 2.
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/label= Transmembrane domain 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label ■ N-glycosylation site.
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                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                      R42280 standard; Protein; 365 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-SEP-1993.
24-FEB-1993; 102873.
24-FEB-1992; JP-036580.
23-MAR-1992; JP-064889.
                                                                                                                                                                                       323 LLLRKILLR 331
                                                                                                                                                                     3 LLIRRILLR 11
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DB 1; Length 365;

58.6%; Score 34;

Query Match

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Tractment of diseases.

Claim 2: Page 43-45: 64pp: English.

The sequence represents a human uterus prostaglandin-EP3-9

Treceptor (mol. wt. 40,507). The sequence contains 4 conserved receptor (R69515) in transmembrane region-vii common to cher EP3 receptors. Conserved Cys residues are found in exofacial loops 1 and 2, and a conserved Arg found in all ecosanoid receptors is found in transmembrane region-vii. The receptor-antagonists, for use in therapy of e.g. glaucoma, side-effects of non-steroidal antinflammatories, cancer, metastasis, renal vasoconstriction, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                       338. .345 / Note= "conserved sequence in EP3 receptors"
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Pred. No. 46;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JUN-1994; CA0320.
25-JUN-1993; US-083746.
(MERI ) MERCK FROSST CANADA INC.
Abramovitz M, Adam M, Boie Y, Metters K, Rushmore TH;
WPI; 95-052012/07.
N-PSDB; Q81951.
                         Indels
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                                                                                                                                                                                                                                                                                                    'note- "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                             'note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                        /note- "N-glycosylation site"
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Prostaglandin-EF3-21 receptor.
Human uterus prostaglandin-EF3-21 receptor;
prostaglandin-EF3 receptor-agonist;
prostaglandin-EF3 receptor-agonist;
            Pred. No. 46;
                                                                                                                                                                      R69518;
02-SEP-1995 (first entry)
Prostaglandin-EP3-9 receptor.
Human uterus prostaglandin-EP3-9 receptor;
prostaglandin-EP3 receptor-agonist;
prostaglandin-EP3 receptor-agonist.
                                                                                                                                                                                                                                                                                                                                /note= "N-glycosylation
                                                                                                                                                                                                                                                                         Location/Qualifiers
77.88; Pic. 2;
                                                                                                                                                         R69518 standard; Protein; 365 AA.
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R69517;
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77.8%;
          Best Local Similarity 77.8
Matches 7; Conservative
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Matches 7; Conserv
                                                                     ||:|:||||
323 LLLRKILLR 331
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347 LLLRKILLR 355
                                                      3 LLIRRILLR 11
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                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                          region
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                                                                                                                            R69517
ID AC BR
DT OOT OOT KW
KW HI
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New human prostaglandin EP3 receptor(s) - useful for treatment and prevention of, e.g. inflammation claim 8; Pages 20-21; 27pp; Japanese.

This represents a human EP3-VI receptor. A replication or expression vector comprising cDNA sequences encoding EP-3V or EP3-3VI can be used to transform a host cell. The host cell is cultured and the polypeptides can be recovered from the culture medium. The polypeptides combine specifically with a prostaglandin PGE2 receptor and can be used as a preventive and treating agent for inflammation.
                                                                            New prostaglandin EP3 receptors and DNA - used partic. to identify modulators of prostaglandin receptor activity for treatment of diseases.

Treatment of diseases.

Claim 2: Page 40-41: 64pp: English.

The sequence represents a human kidney prostaglandin-EP3-alpha receptor (moll-Wt. 43.315). The sequence contains 4 conserved region (R69515) in transmembrane region-VII which has conserved region (R69515) in transmembrane region-VII which has conserved region (R69515) in transmembrane region-VII which has genes. Conserved Arg found in all eicosanoid receptor genes. Conserved Arg found in all eicosanoid receptors is found in transmembrane region-VII. The receptor may be used to identify receptor-agonists and receptor-antagonists, for use in therapy of e.g. glaucoma, side-effects of non-steroidal antiinflammatories,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-AUG-1998 (first entry)
Human prostaglandin EP3-VI receptor.
Prostaglandin E2 receptor; EP3-V receptor; human; treatment; inflammation; EP3-VI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.6%; Score 34; DB 1; Length 393; 77.8%; Pred. No. 50; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.6%; Score 34; DB 1; Length 390; 77.8%; Pred. No. 49; 1. Mismatches 0; Indels
(MERI ) MERCK FROSSI CANADA INC.
Abramovitz M, Adam M, Boie Y, Metters K, Rushmore TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W57410 standard; Protein; 402 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W57411 standard; Protein; 393 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-1998.
14-OCT-1996; 291150.
14-OCT-1996; JP-291150.
(ONOY) ONO PHARM CO LTD.
WPI: 98-315474/28.
N-PSDB; V29611.
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19-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 77.8
Matches 7: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 58.6
Best Local Similarity 77.8
Matches 7; Conservative
                      Abramovitz M, Adam
WPI; 95-052012/07.
N-PSDB; Q81949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||:|:||||
347 LLLRKILLR 355
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347 LLLRKILLR 355
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J10113185-A.
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19-AUG-1998
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W57410
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The sequence represents a human uterus prostaglandin-EP3-21
receptor (mol.wt. 42,688). The sequence contains 4 conserved
N-glycosylation sites in putative extracellular regions, and a
conserved region (R69515) in transmembrane region-VII common to
other EP3 receptors. Conserved Cys residues are found in
exceptors is found in transmembrane region-VII.
eicosanoid receptors is found in transmembrane region-VII. The
receptor may be used to identify receptor agoinists and
receptor antagonists, for use in therapy of e.g. glaucoma,
side-effects of non-steroidal antiinflammatories, cancer,
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                                                                                                                                                                                                                                      /note= "conserved sequence in EP3 receptors"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 New prostaglandin EP3 receptors and DNA - used partic. to identify modulators of prostaglandin receptor activity for treatment of diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.6%; Score 34; DB 1; Length 388; 77.8%; Pred. No. 49; ive 2; Mismatches 0; Indels
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/note= "conserved seguence (R69515) used
                                                                                                                                                                                                                                                                                                                                                                    Abramovitz M, Adam M, Boie Y, Metters K, Rushmore TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prostaglandin-EP3-alpha receptor.
Human Kidney prostaglandin-EP3-alpha receptor;
prostaglandin-EP3 receptor-agonist;
prostaglandin-EP3 receptor-antagonist.
                                                                                       /note= "N-glycosylation site"
217
                                                               /note= "N-glycosylation site"
                                                                                                                                                /note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "N-glycosylation site"
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                                                                                                                                                                           /note= "N-glycosylation 338. .345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          metastasis, renal vasoconstriction, etc.
Sequence 388 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
338. .345
                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R69516 standard; Protein; 390 AA.
                                                                                                                                                                                                                                                                                                                       25-JUN-1993; US-083746.
(MERI ) MERCK FROSST CANADA INC.
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Best Local Similarity 77.8
Matches 7; Conservative
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09-JUN-1994; CA0320.
25-JUN-1993; US-083746.
                                                                                                                                                                                                                                                                                                     09-JUN-1994; CA0320
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N-PSDB; Q81950.
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    Homo sapiens.
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W06590
AC W06590,
DD 11-SEP-
DE POUPER
KW DARA: 1
KW MS4A: 1
KW DHF: DX
OS DOUGE
FT POUPER
FT POOLEII
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                                                                                                                   New human prostaglandin EP3 receptor(s) - useful for treatment and prevention of, e.g. inflammation (claim 2) Pages 16-17; 27pp; Japanese.

This represents a human EP3-V receptor. A replication or expression vector comprising cDNA sequences encoding EP-3V or EP3-3VI can be used to transform a host cell. The host cell is cultured and the polypeptides can be recovered from the culture medium. The polypeptides specifically with a prostaglandin PGE2 receptor and can be used as a preventive and treating agent for inflammation.
                                                                                                                                                                                                                                                                                                                                                                                   12-SEP-1997 (first entry)
POLYprotean of attenuated DEN-2 virus, strain 16681, PDK-53.
Dengue 2 virus; polyprotean; capsid; prM; M; E; NS1; NS2A; NS2B; NS3; NS4A: NS4B: NS5: PDK-53; quadravalent vaccine; immunity; serotype; chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus; dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome; DEN-2/5 NESS.
                                                                                                                                                                                                                                                                               Gaps
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382
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Human EP3-V receptor.
Prostaglandin E2 receptor; EP3-V receptor; human; treatment; inflammation; EP3-VI.
                                                                                                                                                                                                                                                       Query Match 58.5%; Score 34; DB 1; Length 402; Best Local Similarity 77.8%; Pred. No. 51; Matches 7; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "N-linked glycosylation site, 776. .1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ?. .114
/label=_Capsid_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               W06591 standard; Protein; 3391 AA.
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/label= NS2A
1346. .1475
/label= NS2B
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/label- NS3
2094. .2242
/label- NS4A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                strain 16681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115. .205
/label- prM
                                                    06-MAY-1998.
14-OCT-1996; 291150.
14-OCT-1996; JP-291150.
(ONOX) ONO HARM CO LTD.
WPI; 98-315474/28.
N-PSDB: V29610.
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/label= M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          281. .775
/label= E
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                                Homo sapiens.
J10113185-A.
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N-PSDB; 749304.

N-PSDB; 749304.

PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681

The also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a quadravalent vaccine for protecting against Dengue virus infection claim 27; page 122-136; Sclipp; English.

Claim 27; page 122-136; Sclipp; English.

Claim 27; page 122-136; Sclipp; English.

Claim 16681. The attenuated virus is designated DEN-53. The polyprotein comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, NS4A, NS4B and NS5 proteins. A clone of this wildtype viral sequence, PDK-53, may be used in the production of a quadravalent vaccine which provides immunity against all four serotypes of dengue virus. The vaccine also comprises a chimeric DEN-2/1 virus, a chimeric DEN-2/3 virus, and/or a chimeric DEN-2/4 virus. The new quadravalent vaccines are used to protect against infection by all four serotypes of dengue virus, DEN-1, DEN-3 and DEN-4, which can lead to dengue fever or fatal dengue hemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are used to produce the recombinant protein products of the DNA constructs of common and the vaccines.
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Polyprotein of DEN-2 virus, strain 16681.
Polyprotein of DEN-2 virus, strain 16681.
Dengue 2 virus; polyprotein; capsid; prm; M; E; NS1; NS2B; NS3; NS4A; NS4B; NS5; PDR-53; quadravalent vaccine; immunity; serotype; chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus; dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
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54.5%; Pred. No. 6.8e+02;
.ive 2; Mismatches 3; Indels
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206. .280
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776. .1127
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06-JUN-1995; U09209.
07-JUN-1995; US-483292.
(UTMA-) UNIV MAHIDOL AT SALAYA.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Bhamarapravati N, Butrapet S, Chang J, Gl
Halstead SB, Kinney R, Trent DW;
WPI: 97-052330/05.
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/label= Capsid_protein
115. .205
/label= prM
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Key Location/Qualifiers
                                                                                                                                                                  /note- "Encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W06590 standard; Protein; 3391 AA.
2243. .2491
/label= NS4B
2492. .3391
/label= NS5
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281. .775
/label- E
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                   misc_difference
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PEC-1996.

PP (0-50-1996.)

PP (10SH) 10 SDEP HEALTH & HUMAN SERVICES.)

PA (UXMA-) UNIV MAHIDOL AT SALAYA.

PA (UXMA-) UNIV MAHIDOL AT SALAYA.

PA (UXMA-) UNIV MAHIDOL AT SALAYA.

PA (USMA-) UNIV MAHIDOL AT SALAYA.

PA (USBA) UNIV MAHIDOL AT S
                                           note= "N-linked glycosylation site"
                                                                                        note- "N-linked glycosylation site"
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                                                                                                           2243. .2491
/label- NS4B
2492. .3391
/label- NS5
/label= NS1
905
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Search completed: February 8, 2000, 01:29:39

2 RLLIRRILLRY 12 |:|| | :|| 2728 RMLINRFTMRY 2738

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0; Gaps

Query Match 56.9%; Score 33; DB 1; Length 3391; Best Local Similarity 54.5%; Pred. No. 6.8e+02; Matches 6; Conservative 2; Mismatches 3; Indels

Search completed: February 8, 2000, 01:29:39 Job time: 1751 sec THIS PAGE BLANK (USPTO)

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                                                                                                                                                                                                                                                                                                                                     142080
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                 142080 segs, 47169319 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                            summaries
                                                                   - protein search, using sw model
                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
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S29990

S29990

F641140

S48776

S53849

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S53849

S64876

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S65899

B55995

B55995

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B7887
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Listing first 45
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58
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Query
Match Length DB
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2: pir2:*
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4: pir4:*
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Perfect score:
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Maximum DB
                                                                     OM protein
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prostaglandin E2 r protaglandin recep prostaglandin E re protaglandin recep prostaglandin E re hypothetical prote hypothetical prote hypothetical prote genome polyprotein	ALIGNMENTS ifex aeolicus on 08-May-1998 #text_change 20-Aug-1999 land, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;	1998 470300; MUID:98196666 470300; MUID:98196666 17; nucleic acid sequence not shown; translation not shown NGP> GB:AE000705; NID:92983310; PIDN:AAC06902.1; PID:92983312; GB:AE0001010	re 37; DB 2; Length 408; d. No. 14; Mismatches 2; Indels 0; Gaps 0;	rhesus macaque -Feb-1995 #text_change 23-Jul-1999 ary 1993 ary 1993 68; PIDN:CAA79885.1; PID:g38569 antigen; immunoglobulin homology
JC2056 138747 551317 138750 551315 5531316 84375 853313 853216 853216 853319 853216 853319 853216 85319 853210	ALIGNN C - Aquifex a Lrevision 08 Gaasterland,	the hyperthe. D:98196666 acid sequence , NID:9298331 F5	Score 3 Pred. N 1; Mism	mulatta (Thesus macaque) 5 #sequence_revision 20-Fe 0 LMBL Data Library, February 1: \$29990 ary RNA GBON> 1: EABL: 221819; NID: 938568; ss I histocompatibility an immunoglobulin homology <i< td=""></i<>
ппппппппппппппппппппппппппппппппппппппп	c - Lrev Gaas	of t UID: c ac 05; VF5		, HLA-F- (rhesus nce_revi Library 21819; N toccompat protein
367 374 374 388 388 388 393 393 3434 133 133	protein PilC aeolicus 8 #sequence_1 ren, P.V.; Gē	1998 A70300; MUID A70300; MUID Y; nucleic at AE> GB:AE000705; GB: strain VF:	63 72 rativ	antigen, HLA-F- ulatta (rhesus ; #sequence_revi BL Data Library S29990 .rry .RA BON> EMBL: 221819; N s I histocompat mbrane protein
ϕ			rit LR DSe	anti mulati 5 #se 0 12 #se 0 13 #se 14 #se 15 #se 16 #s 16 #s
	ly prot fex aeo 11998 #s 0365 Warren,	353-358, 1999 complete ges number: A7031 b70365 b70365 complete brown a 1-408 cAQF> rences: GB:Al al source: s¹ 1	# # H	ity an ca mul 11995 # 1995 # 1995 # 1990 me EMBL cher: S pher:
	RESULT 1 D70365 fimbrial assembly pr C.Species: Aquifex of C.Cate: 08-May-1998 C.Catession: D70365 R.Deckert, G.; Warr	transpired to the control of the con	atcl	RESULT 2 S29990 histocompatibility antigen Cispecies: Macaca mulatta Cispecies: Macaca mulatta Cipate: 20-Feb-1995 #seque Cibate: 20-Feb-1995 #seque Algerence number: S29990 Algerence number: S29990 Algerence number: S29990 Algerence preiminary Algerence type: mRNA Algerence type: mRNA Algerence: Experiminary Cisuperfamily: class I his Cisuperfamily: class I his Cisuperfamily: class I his Cisuperfamily: class I his
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Gaps

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62.1%; Score 36; DB 2; Length 348; llarity 54.5%; Pred. No. 19; Conservative 4; Mismatches 1; Indels

Query Match Best Local Similarity Matches 6; Conserval

EP3-alpha receptor

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Accession: S467/o

A; Residues: 1-278 < COS>
A; Cross-references: EMBL: X82086; NID:9558241; PID:9558260

B; Richards, C.; Harris, D.E.
A; Reference number: 349842
A; Molecule type: DNA
A; Residues: 1-278 < CRIC.
A; Cross-references: EMBL: 246796; NID:9577794; PID:9577814
A; Residues: 1-279 < CRIC.
A; Cross-references: EMBL: 246796; NID:9577794; PID:9577814
A; Residues: 1-273 < CRIC.
A; Cross-references: EMBL: 246796; NID:9403890
A; Title: The yeast SSS1 gene is essential for secretory protein translocation and enc A; Reference number: S39583; MUID:9403890
A; Residues: 146-278 < CRIC.
A; Molecule type: DNA
A; Residues: 146-278 < CRIC.
A; Molecule type: DNA
A; Residues: 146-278 < CRIC.
A; Cross-references: EMBL: X74499; NID:9414690; PID:9414691
B; Coster, F; Jonniaux, J.L; Goffeau, A.
A; Cross-references: EMBL: X7499; MUID:96093910
A; Reference number: S55819; MUID:96093910
A; Reference number: S58819; MUID:96093910
A; Reference number: S58819; MUID:96093910
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J. Mol. Biol. 245, 522-537, 1995
A;Title: The mitochondrial DNA of the amoeboid protozoon, Acanthamoeba castellanii: c
A;Reference number: S53825; MUID:95147275
A;Reference number: Gray acid sequence not shown; translation not shown
A;Recule type: DNA
A;Residues: 1-298 ABUR>
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A;Residudes: 1-278 <FOUS
A;Cross-references: EMBL:274383; NID:91431562; PID:e253404; PID:91431563; MIPS:YDR087
A;Experimental source: strain S288C
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A; References: EMBL: X82086; NID:9558241; PID:9558260
A; Cross-references: EMBL: X82086; NID:9558241; PID:9558260
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994
B; Foury, F.; Jonniaux, J.L.; Purnelle, B.; Coster, F.; Goffeau, A.
A; Reference number: S67889
A; Accession: S67904
hypothetical protein YDR087c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein D4478; hypothetical protein YD8554.20c
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-May-1999
C;Accession: S48776; S49642; S39583; S55836; S67904
R;Coster, F.; Jonniaux, J.L.; Goffeau, A.
submitted to the EMBL Data Library, October 1994
A;Reference number: S48758
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C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Feb-1999
C;Accession: S53849
R;Burger, G; Plante, I.; Lonergan, K.M.; Gray, M.W.
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ribosomal protein S3 - Acanthamoeba castellanii mitochondrion (SGC6)
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Pred. No. 19;
2; Mismatches
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60.0%;
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121 YLLLIRRVLFSQLKY 135
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                               probable efflux protein - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Species: Chlamydia trachomatis
C;Species: C;Species: Chlamydia trachomatis
C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C;Species: C
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C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 29-Sep-1999
C;Accession: F64114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P. Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A; Reference number: A64000; MUID:95350630
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1055 < TIGR>
A;Cross-references: GB:U32808; GB:L42023; NID:g1574739; PID:g1574743; TIGR:HI1285
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C;Genetics:
A.Gene: hisdR
C:Superfamily: unassigned DEAD/H box helicases; DEAD/H box helicase homology
C:Superfamily: unassigned DEAD/H box helicases; P-loop; restriction modification system
F:300-665/Domain: DEAD/H box helicase homology <DEAD>
F:404-409/Region: nucleotide-binding motif B
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A:Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: ygeD
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Pred. No. 56;
2; Mismatches 2; Indels
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Pred. No.
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63.6%;
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63.68;
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Best Local Similarity 63.0°
". 7; Conservative
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Matches 7; Conservative
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98 RVALRKLLLRY 108
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                                                2 RLLIRRILLRY 12
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A:Molecule type: DNA
A:Residues: 1-559 <ARN>
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ô g Query Match

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RESULT S48776

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C. Accession: D5595
B.An. S.; Yang, J.; So, S.W.; Zeng, L.; Goetzl, E.J.
Blochemistry 33, 14496-14502, 1994
A.Title: Isoforms of the EP3 subtype of human prostaglandin E-2 receptor transduce bo A.Reference number: A55995; MUID:95072021
A.Accession: D55995
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-48 < ANA.A.
A.Residues: 1-48 < ANA.A.
A.Residues: GB:L32662
C. Superfamily: prostaglandin E receptor EP1
C. Keywords: alternative splicing
                                                                                                                                                                                                                                                                                     C;Accession: C55995
R;An, S:; Yang, J; So, S.W.; Zeng, L.; Goetzl, E.J.
B;ochmistry 33, 14496-14502, 1994
A;Tille: Isoforms of the EP3 subtype of human prostaglandin E-2 receptor transduce bo A;Reference number: A55995; MUID:95072021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prostaglandin E2 receptor, subtype EP3 splice form II - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: 19-dan-1996 #sequence_revision 19-Jan-1996 #text_change 17-Mar-1999
C; Accession: B55995
R; An, S; Yang, J; So, S.W.; Zeng, L.; Goetzl, E.J.
Blochemistry 33, 14496-14502, 1394
A; Title: Isoforms of the EP3 subtype of human prostaglandin E-2 receptor transduce bo
A; Reference number: A55995; MUID:95072021
                                                                                                                                                                                                                prostaglandin E2 receptor, subtype EP3 splice form III - human (fragment) C;Species: Homo sapiens (man) C;Species: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 17-Mar-1999
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5.2;
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Pred. No. 5.2;
2; Mismatches
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Pred. No. 6.4;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           A.Accession: C55995
A.Status: preliminary
A.Molecule type: MRNA
A.Residues: 1-39 <ANA>
A.Cross-references: GB-L12661
C.Superfamily: prostaglandin E receptor
C.Keywords: alternative splicing
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77.8%;
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Best Local Similarity 77.8%;
Matches 7; Conservative
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                                                               Query Match
Best Local Similarity
Matches 7; Conserv
                                1 YRLLIRRILLRY
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22 LLLRKILLR 30
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R; Vysotskala, V.S.; Osborne, B.I.; Schwartz, J.R.; Toriumi, M.; Kwan, A.; Yu, G.; Oji, C
K.; Feng, J.; Kim, C.; Kurtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.;
submitted to the EMBL Data Library, May 1998
A; Description: Arabidopsis thaliana chromosome 1 BAC F20D22 complete sequence.
A; Reference number: Z14214
A; Accession: T00953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:AC002411; NID:g2570223; PID:g3142290; GSPDB:GN0059; ATSP:F20D22
C;Genetics:
A;Gene: ATSP:F20D22.3
A;Map position: 1
A;Introns: 64/1; 144/1; 239/3; 304/1; 386/1; 415/2; 473/3; 516/3; 554/3; 594/2; 624/3; 6
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A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743
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A;Cross-references: GB:AE001386; GB:AE001362; NID:g3845148; PID:g3845151; TIGR:PFB0315w
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0315w
A;Cross-references: GB:U12386; NID:9562028; PID:9562053 A;Experimental source: strain Neff; ATCC 30010 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F20D22.3 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein PFB0315w - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C:Species: Plasmodium falciparum C:Date: 13. Nov-1998 #sequence_revision 13.Nov-1998 #text_change 07-May-1999 C;Accession: C71618
                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                            Length 298
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Pred. No. 25;
4; Mismatches 2
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A;Molecule type: DNA
A;Residues: 1-814 <VYS>
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60.0%; Pred. No. 67;
iive 3; Mismatches
                                                                                                                                                                                                                                            60.3%;
50.0%;
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Matches 6; Conservative
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Best Local Similarity 50.0
Matches 6; Conservative
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126 FMLLKKRVILRY 137
                                                                                                        A:Genome: mitochondrion
A:Genetic code: SGC6
C:Keywords: mitochondrion
                                                                                                                                                                                                                                                                                                                                               1 YRLLIRRILLRY 12
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263 LVVRRLLLNY 272
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les 6; Conserv
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Best Local S
Matches 6
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NAN-directed RNA polymerase (EC 2.7.7.6) 22K chain - vaccinia virus (strains WR and C C) Species vaccinia virus

Nilternate names: J4R protein
C;Species: vaccinia virus
A;Note: host Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 11-Jun-1999
C;Accession: A25734; I23092; G42513
R;Broyles, S.S.; Moss, B.
Proc. Natl. Acad. Sci. U.S.A. 83, 3141-3145, 1986
A;Title: Homology between RNA polymerases of poxviruses, prokaryotes; and eukaryotes: A;Reference number: A25734; MUID:86205852
A;Recission: A25734
A;Molecule type: DNA
A;Residues: 1-185 CBRO>
A;Cross-references: GB:M13209; GB:M14122; NID:9335739; PIDN:AAB59833.1; PID:9335740
A;Cross-references: GB:M13209; GB:M14122; NID:9335739; PIDN:AAB59833.1; PID:9335740
A;Cross-references: GB:M13209; GB:M14122; NID:9335739; PIDN:AAB59833.1; PID:9335740
A;Cross-references: GB:M13209; GB:M1521527
A;Accession: 123092
A;Accession: G.P.; Perkus, M.E.; Davis, S.W.; Winslow, J.P.; Paoletti, E.V.
Viclogy 179, 517-563; 1990
A;Reference number: A42501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R:Goebel, S.J.; Johnson, G.P.; Perkus, M.E.; Davis, S.W.; Winslow, J.P.; Paoletti, Virology 179, 247-266, 1990
A:Title: The complete DNA sequence of vaccinia virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A42531; MUID:91021027
A; Contents: annotation; possible protein coding frames
A; Note: neither amino acid nor nucleotide sequence is given
C; Superfamily: vaccinia virus DNA-directed RNA polymerase 22K polypeptide
C; Keywords: early protein; nucleotidyltransferase; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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A; Residuce: 1:15 < GGD:
A; Cross-references: GB: M35027; NID: 9335317; PIDN: AAA48084.1; PID: 9335432
A; Experimental source: strain Copenhagen
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Pred. No. 24;
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A; Reference number: A36859
A; Accession: F36845
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Best Local Similarity
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 23-Jul-1999
C;Accession: C53216
R;Breyer, R.M.; Emeson, R.B.; Tarng, J.L.; Breyer, M.D.; Davis, L.S.; Abromson, R.M.; Fe
A;Title: Alternative splicing generates multiple isoforms of a rabbit prostaglandin E-2
A;Reference number: A53216; MUID:94164982
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C;Superfamily: prostaglandin E receptor EP1
C;Keywords: alternative splicing; transmembrane protein
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C;Superfamily: DNA-directed RNA polymerase chain E
C;Keywords: nucleotidyltransferase; transcription
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10;
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Pred. No. 1
                                                                             A.Cross-references: GB.L32660
C.Superfamily: prostaglandin E receptor EP1
C.Keywords: alternative splicing
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A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-62 <ANA>
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A:Status: preliminary
A:Molecule type: mRNA
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A; Molecule type: DNA
A; Residues: 1-185 <abrack section 1.185 <a href="https://doi.org/10.185/10.185">https://doi.org/10.185/10.185</a>
A; Shchelkunov, S.N.; Blinov, V.M.; Totmenin, A.V.; Marennikova, S.S.; Kolykhalov, A.A.; databaridae, O.G.; Sandakhchiev, L.S.

Virus Res. 27, 25-35, 1993
A; Fitle: Nucleotide sequence analysis of variola virus HindIII M, L, I genome fragments. A; Recreace number: S33069; MUID: 93190624
A; Recreace number: S33069; MUID: 93190624
A; Accession: S33095
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-185 <abra>A; Coss-references: ENBL: X67119; NID: 962330; PIDN: CAA47580.1; PID: 962357
A; Cross-references: ENBL: X67119; NID: 962330; PIDN: CAA47580.1; PID: 962357
A; Cross-references: Expain India-1967, isolate Ind3
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1992
C; Superfamily: vaccinia virus DNA-directed RNA polymerase 22K polypeptide
C; Keywords: nucleotidyltransferase; transcription
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Search completed: February 7, 2000, 11:54:27 Job time: 24337 sec

1 YRLLIRRILERY 12 | :: | :|||| 24 YAVINRNVLLRY 35

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

8, 2000, 00:59:54; Search time 63.71 Seconds (without alignments) 5.625 Million cell updates/sec February Run on:

US-08-653-294-16 58 1 YRLLIRRILLRY 12 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

82229 segs, 29864866 residues

Searched:

82229 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

SwissProt_38:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	g	macaca mul			meth		vaccini		Q9zcs6 rickettsia	P36151 saccharomyc	P30557 mus musculu	P34980 rattus norv								-		076090 homo sapien		P29990 d genome po		methanc	herpes	herpes	mycopla		S	ഗ	nays (P12091 oryza sativ
SUMMARIES	ΩI		HLAF_MACMU	YD87_YEAST	RT03_ACACA	RPOH_METJA	DP1_MOUSE			KAD_RICPR	YK50_YEAST	PE23_MOUSE	PE23_RAT	PE23_HUMAN	PE23_RABIT	YRAM_HAEIN	PTP3_YEAST	POLG_MVEV	CBIQ_SALTY	LICA_MYCCA	OPPB_LACLA	OPPB_LACLC	VMD2_HUMAN	CRTI_CERNC	POLG_DEN26	POLG_DEN27	Y290_METJA	VGLM_HSV6U		SYD_MYCGE	- 1	ı	YEAS	RPOB_MAIZE	RPOB_ORYSA
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P38717 saccharomyc P33174 cricetulus P34241 saccharomyc P54241 saccharomyc P45481 mus musculu P47760 chlamydia t P66796 mus musculu P25789 homo sapien P21670 rattus norv P19390 haemophilus P22235 haemophilus	TRESULT 1 YHS5_CAREL ID YHS5_CAREL STANDARD; PRT; 411 AA. 10 18304; DT 15-JUL-1999 (Rel. 38, Created) DT 15-JUL-1999 (Rel. 38, Last sequence update) DT 15-JUL-1999 (Rel. 38, Last annotation update) DT 15-JUL-1999 (Rel. 38, Last annotation update) MX 15-JUL-1999 (Rel. 38, Last annotation update) DT 15-JUL-1999 (Rel. 38, Last sequence update) MX 200-1999 (Rel. 38, Last sequence update) DT 15-JUL-1999 (Rel. 38, Last sequence update) ON XR849.5. ON XR849.5. ON ZR849.5. ON ZRAGOSA, Nematoda; Secernentea; Rhabditida; ON SHABDILINA; Rhabditidae; Rhabditidae; Caenorhabditis.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE TO N.2. SUBMITTED N.2. SUBMITTED N.2. SUBMITTED N.2. SUBMITTED N.2. This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). EMBL: 282095; CAB05028.1; WORMMERP: XR849.5; CEL6750. BYPRAM: PFO1062; Worm_family_8; 1. Hypothetical protein. SEQUENCE 411 AA; 48236 MW; B5736F70 CRC32;	DB 1; Length 411; 5.8; ches 1; Indels 0; Gaps 0;	STANDARD; PRT; 348 AA. (Rel. 28, Created) (Rel. 28, Last sequence update) (Rel. 28, Last annotation update) LS. (WOCYTE ANTIGEN F). (Expected to the conference) (Rhesus maccaque). (Expected to the conference) (Releases) Chordate; Craniate; Vertebrate; Mammalia; (Hates; Catarrhini; Cercopithecidae; Cercopithecinae;
SIP3_YEAST MDR3_CRIGR YKB4_YEAST CBP_MOUSE RL17_COUSE PRC9_HUMAN PRC9_RAT PRC9_RAT BEX1_HAEIN BEX2_HAEIN BEX2_HAEIN BEX3_HAEIN	ttion 19.5 II	/Genbar ESTROPP FILL Tht. Bhoin It Shoin It Stute. S as lo S a lo S as lo S a lo S a lo S a lo S a lo S a lo S a lo S as lo S a	37; No.	; 34 ce upo tition TIGEN TIGEN TIGEN
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ESNAULT Y., BLONDEL M.-O., DESHAIES R.J., SCHEKMAN R., KEPES F.;
"The yeast SSS1 gene is essential for secretory protein translocation
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HIA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN F.

EXTRACELULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

EXTRACELLULAR ALPHA-3.

CONNECTING PEPTIDE.
                                                             OTTING N., BONTROP R.E.; "Characterization of the rhesus macaque (Macaca mulatta) equivalent
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Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                   -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL 33.2 KD PROTEIN IN SSS1-SLU7 INTERGENIC REGION.
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Pred. No. 7.6;
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COSTER F., JONNIAUX J.-L., GOFFEAU A.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
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3A375142 CRC32;
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PFAM; PF00129; MHC_I; i.
MHC I; Transmembrane; Glycoprotein; Signal.
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HSSP; P03989; 1HSA.
PROSITE; PS00290; IG_MHC; 1.
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SEQUENCE FROM N.A.
MEDLINE; 93246295.
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348 AA;
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YD87_YEAST
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organization.";
J. Mol. Biol. 245:522-537(1995).
-: SUBCELLULAR LOCATION: MITOCHONDRIAL.
-: SUBCELLULAR ELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
and encodes a conserved protein of the endoplasmic reticulum."; EMBO J. 12:4083-4093(1993).
-i- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-i- SIMILARITY: BELONGS TO THE NNP-1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ë,
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SERAINS-ATCC 30010 / NEFF;
MEDLINE; 9514/7275.
BURGER G., PLANTE I., LONERGAN K.M., GRAY M.W.;
"The mitochondrial DNA of the amoeboid protozoon, Acanthamoeba castellanii: complete sequence, gene content and genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35.5; DB 1;
Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278 AA; 33202 MW; FAD7CAC9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7BA48AD7 CRC32;
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01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
TATCCHONDRALAL RIBOSOMAL PROTEIN 83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 AA.
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PFAM; PF00189; Ribosomal_S3_C; 1.
PFAM; PF00417; Ribosomal_S3_N; 1.
Ribosomal_Drotein; Mitochondiion.
SEQUENCE 298 AA; 36060 MW; 7BA48AD7 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Acanthamoebidae; Acanthamoeba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR: S48776; S48776.
Hypothetical protein; Nuclear protein.
DOMAIN 266 274 POLY-GLU.
SEQUENCE 278 AA; 33202 MW; FAD7CACS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acanthamoeba castellanii (Amoeba).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.2%;
60.0%;
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Best Local Similarity
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P46754;
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Length 298;

DB 1;

60.3%; Score 35;

us-08-653-294-16.rsp

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10 YRLVIKRII 78
                                                                                                                                                            DP1_MOUSE
Q60870;
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TRANSMEM
SEQUENCE
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DP1_MOUSE
DD 1.NOV.
DT 01-NOV.
DT 15-DEC.
DE POLIPOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "RNA polymerase subunit H features a beta-ribbon motif within a novel fold that is present in archaea and eukaryotes.";
J. Mol. biol. 287:753-760(1999).
-: FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE: 96337999.

BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,

SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCANNE J.D.,

SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GCOANNE J.D.,

SCOTT J.L., GEOGHAGENT B.A., TOMB J.F., ADAMS M.D.,

SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,

UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,

COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORDOVSKY M.,

KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;

"COMPLETE GENOME SEQUENCE Of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01110; RNA_POL_H_23KD; 1.
PFAM; PF01191; RNA_Pol_H; 1.
Transferase; Transcription; DNA-directed RNA polymerase; 3D-structure.
SEQUENCE 78 AA; 9001 MW; 9F10C0F3 CRC32;
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 99208760.
THIRU A., HODACH M., ELORANTA J.J., KOSTOUROU V., WEINZIERL R.O.,
MATTHEWS S.;
                              ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
DNA-DIRECTED RNA POLYMERASE SUBUNIT H (EC 2.7.7.6).
                              ;;
                                                                                                                                                                                                                                                                            78 AA
  Pred. No. 10;
4; Mismatches
                                                                                                                                                                                                                                                                            PRT;
  50.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U67546; AAB99042.1; -.
PDB; 1HMJ; 05-APR-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 273:1058-1073(1996)
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methanococcus jannaschii.
                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                1 YRLLIRRILLRY 12
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ID RPOH_METJA
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ID RPO6_VACCY

ID RPO6_VACCY

ID 01-APR-1988 (Rel. 07, Created)

DT 01-APR-1988 (Rel. 37, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DT 15-DEC-1998 (Rel. 37, and viruse (Strain Copenhagen).

GN RPO22 OR J4R OR F10.

OS Vaccinia virus (strain WR), and Vaccinia virus (strain Copenhagen).

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 96194804.
PRIESCHL B.E., PENDL G.G., HARRER N.E., BAUMRUKER T.;
"The murine homolog of TB2/DP1, a gene of the familial adenomatous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polyposis (FAP) locus.";
Gene 169:215-218(1996).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: TO C.ELEGANS T19C3.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=WR;
MDLLINE; 86205852.
BROXLES S.S., MOSS B.;
HOMOLOGY between RNA polymerases of poxviruses, prokaryotes, an eukaryotes: nucleotide sequence and transcriptional analysis of vaccinia virus genes encoding 147-RDa and 22-KDa subunits.";
Proc. Natl. Acad. Sci. U.S.A. 83:3141-3145(1986).
                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 185;
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185 AA; 21050 MW; FC5BA4A2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 1;
Pred. No. 9.5;
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185 AA
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PRT;
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58.38;
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STANDARD;
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133 YRKIIRPIFLRH 144
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Best Local Similarity
7; Conserve
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01-NOV-1997
15-DEC-1998
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Query Match Best Local Similarity Matches 6; Conserv

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Gaps

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58.6%; Score 34; DB 1; Length 78; 66.7%; Pred. No. 3.8; live 3; Mismatches 0; Indels

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'Nucleotide sequence analysis of variola virus HindIII M, L, I genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YRLLIRRILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 AA;
                                                 COMPLETE GENOME.
STRAIN-INDIA-1967 /
MEDLINE; 93202281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-MADRID E;
MEDLINE; 99039499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADK OR RP638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAD_RICPR
Q9ZCS6;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAD_RICPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                               VICOLOGY 179:517-563(1990).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE . N PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                             STRAIN-COPENHAGEN;
GOEBEL S.J., JOHNSON G.P., PERKUS M.E., DAVIS S.W., WINSLOW J.P.,
                                                                                                                                    SOEBEL S.J., JOHNSON G.P., PERKUS M.E., DAVIS S.W., WINSLOW J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHCHELKUNOV S.N., BLINOV V.M., TOTMENIN A.V., MARENNIKOVA S.S., KOLYKHALOV A.A., FROLOVI I.V., CHIZHIKOV V.E., GYTOROV V.V., GASHIKOV P.V., BELANOV E.F., BELAVIN P.A., RESENCHUK S.M., ANDZHAPARIDZE O.G., SANDAKHCHIEV L.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                   MEDLINE: #5215527.

PLUCIENNICZAK A., SCHROEDER E., ZETTLMEISSL G., STREECK R.E.;

"Nucleotide sequence of a cluster of early and late genes in a conserved segment of the vaccinia virus genome.";

Nucleic Acids Res. 13:985-998(1985).
                                                                                                                                                                                                                                                                                                                          SUBUNIT: THIS ENZYME CONSISTS OF AT LEAST EIGHT SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1993 (Rel. 27, Created)
10-OCT-1993 (Rel. 27, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DNA-DIRECTED RNA POLYMERASE 22 KD POLYPEPTIDE (EC 2.7.7.6).
RPO22 OR J4R OR L4R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB 1; Length 185; Pred. No. 9.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL: M35027; AAA48084.1; -...
PIR; I23092; RNYZ22.
Transferase: DNA-directed RNA polymerase; Transcription.
SEQUENCE 185 AA; 21342 WW; 2947E2C5 CRC32;
                                                                                                                                                              "The complete DNA sequence of vaccinia virus."; Virology 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-INDIA-1967 / ISOLATE IND3;
MEDLINE; 93190624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M13209; AAB59833.1; -. EMBL; X01978; CAA26018.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.6%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 :: | :|||||
24 YAVINRNVLLRY 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YRLLIRRILLRY 12
SEQUENCE FROM N.A.
                                                                                                SEQUENCE FROM N.A
                                                                                                              STRAIN-COPENHAGEN
                                                                                                                        MEDLINE; 91021027
                                                                                                                                                                                                    COMPLETE GENOME
                                                                                                                                                                                                                                                                                     SUBSTRATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Variola virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Orthopoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPO6_VARV
P33054;
                                                                                                                                                                                                                                                                                                                 RNA(N)
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                                                                  SHCHELKUNOV S.N., BLINOV V.M., SANDAKHCHIEV L.S.;
"Genes of variola and vaccinia viruses necessary to overcome the host protective mechanisms.";
FEBS Lett. 319:80-83(1993).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                           -1 - SUBUNIT: THIS ENZYME CONSISTS OF AT LEAST EIGHT SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 396:133-140(1998).

-!- FUNCTION: THIS SMALL UBIOUITOUS ENZYME IS ESSENTIAL FOR MAINTENANCE AND CELL GROWTH.

-!- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.

-!- SUBGELLIAR (BY SIMILARITY).

-!- SUBCELLIAR LOCATION: CYTOPLASHIC.

-!- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1999 (Rel. 39, Created)
15-DEC-1999 (Rel. 39, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
ADENYLATE KINASE (EC 2.7.4.3) (AIP-AMP TRANSPHOSPHORYLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.6%; Score 34; DB 1; Length 185; larity 50.0%; Pred. No. 9.5; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-directed RNA polymerase; Transcription.
35 AA; 21354 MW; 547A4AC2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
/ ISOLATE IND3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rickettsia prowazekii.
Bacteria; Proteobacteria; alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X67119; CAA47580.1; -.
EMBL; S55844; AAB24677.1; -.
EMBL; X69198; CAA49022.1; -.
PIR; F56845; F36845.
PIR; S33095; S33095.
Transferase; DNA-directed RNA p
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EMBL; D10204; BAA01051.1; -. EMBL; D13321; BAA02578.1; -.
                                                                                                                                                                                                                                                                      MEDLINE; 94039052.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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(Rel. 25, Last sequence update)
(Rel. 39, Last annotation update)
IN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                            01-JUN-1994 (Rel. 29, Created)
1-JUN-1994 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 39.4 KD PROTEIN IN METI-SIS2 INTERGENIC REGION.
                                                                                                                                                                 Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 352;
                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
POHL T.M., POHL F.M.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                     P (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                 Score 34; DB 1;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 1;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39406 MW; F5B1BB2A CRC32;
                                                                                                                                                                                                                                                                                          352 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365 AA
                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                   EMBL; AJ235272; CAA15078.1; -. PROSITE; PS00113; ADENYLATE_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetaceae; Saccharomyces.
                                                                                                PROSITE; PSUOLLS, ALL. Transferase; Kinase; ATP-binding.
                                                                                                                                  213 AA; 24503 MW;
                                                                                                                                                                 58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.6%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 228295; CAA82149.1; -.
                                                                                                                                                                                       7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1993 (Rel. 25, La
15-DEC-1999 (Rel. 39, La
PROSTAGLANDIN E2 RECEPTO
RECEPTOR, EP3 SUBTYPE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l protein.
352 AA; 3
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|116 LLIKRVLGRY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S38147; S38147
Hypothetical protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|||:||: |
223 FRLLVRRLYL 232
                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                             3 LLIRRILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YRLLIRRILL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1993
                                                                                                                                                                                                                                                                                         YK50_YEAST
P36151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PE23_MOUSE
P30557;
                                                                                                                                SEQUENCE
                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                       Matches
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A HASEGAM H., NEGISHI M., ICHIKAMA A.;
ITWO isoforms of the prostaglandin E receptor EP3 subtype different in agonist independent constitutive activity.";
J. Biol. Chem. 271:1857-1860[1996].

J. Biol. Chem. 271:1857-1860[1996].

I. Biol. Chem. 271:1857-1860[1996].

MAY BE INVOLVED IN INHIBITION OF GASTRIC ACID SECRETION, MODULATION OF NEUROTRANSMITTER RELEASE IN CENTRAL AND PERIPHERAL NEURONS, INHIBITION OF SODIUM AND WATER REABSORPTION IN KIDNEY THIS RECEPTOR CAN COUPLE TO BOTH THE INHIBITION OF ADENYLATE C CYCLASS MEDIATED BY G-I PROTEINS, AND TO AN ELEVATION OF ADENYLATE C CYCLASS MEDIATED BY G-I PROTEINS, AND TO AN ELEVATION OF DIFFERENT SECOND MESSENGER SYSTEMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

ALTERNATIVE PRODUCTS: AT LEAST THREE ISOFORMS; ALPHA (SHOWN HERE),
BETA AND GAMMA; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY HAVE
IDENTICAL LIGAM BINDING PROPERTIES BUT DIFFERENT COUPLING
PROPERTIES WITH G PROTEINS; ALPHA AND BETA COUPLE TO G-I PROTEINS,
WHEREAS GAMMA COUPLES TO WULTIPLE G-PROTEINS, G-I AND G-S. ALPHA
SHOWS HIGH AGONIST-INDEPENDENT CONSTITUTIVE INHIBITION OF
ADENYLATE CYCLASE, WHILE BETA HAS NO AGONIST INDEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IRIE A., SUGIMOTO Y., NAMBA T., HARAZONO A., HONDA A., WATABE A., NEGISHI M., NARUMIYA S., ICHIKAWA A.;
"Third isoform of the prostaglandin-E-receptor EP3 subtype with different C-ferminal tail coupling to both stimulation and inhibition of adenylate cyclase.";
Eur. J. Blochem. 217:313-318(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: LIGAND BINDING IS AFFECTED BY CAMP-DEPENDENT PHOSPHORYLATION
                                                                                                                                                                                                                                           MEDLINE; 92202182.
SUGIMOTO Y., NAMBA T., HONDA A., HAYASHI Y., NEGISHI M.,
ICHIKAWA A., NAKUMIYA S.;
"Cloning and expression of a cDNA for mouse prostaglandin E receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIRATA M., NARUMIYA S., ICHIKAWA A.; "Two isoforms of the EP3 receptor with different carboxyl-terminal domains. Identical ligand binding properties and different coupling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 93155085.
SUGIMOTO Y., NEGISHI M., HAYASHI Y., NAMBA T., HONDA A., WATABE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: KIDNEY, UTERUS, AND MASTOCYNOMA CELLS, IN A LESSER AMOUNT IN BRAIN, THYMUS, LUNG, HEART, STOMACH,
                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARACTERIZATION (ALPHA AND BETA FORMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                        EP3 subtype.";
J. Biol. Chem. 267:6463-6466(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    properties with Gi proteins.";
J. Biol. Chem. 268:2712-2718(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (GAMMA FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (BETA FORM). MEDLINE; 93155085.
                                                                                                                                                                FROM N.A. (ALPHA FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BRAIN MEMBRANES
musculus (Mouse).
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GCRDB; GCR_0762;
GCRDB; GCR_1006;
GCRDB; GCR_1158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCRDB; GCR_1467
                                                            PUESCHEL G.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCRDB;
ö
                                                                                                                                                                                                                                                            IRDHTNYASSSTSLPCPGSSALMWSDQLER -> MMNNLKM
TRANVVSLGLRISSPREG (IN ISOFORM BETA).
IRDHTNYASSSTSLPCPGSSALMWSDQLER -> VANAVSS
CSSDGQKGQAISLSNEVVQPGP (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                          P34980; 063194; 064376;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
FIS-DEC-1999 (Rel. 39, Last annotation update)
PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
MEDLINE; 93343951.
MEDLINE; 93343951.
TAKEUCHI K., ABE T., TAKAHASHI N., ABE K.;
"Molecular cloning and intrarenal localization of rat prostaglandin E2 receptor EP3 subtype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-SPRAGUE DAWLEY: TISSUE KIDNEY;
MEDLINE; 94183265.
TAKEUCHI K., TAKHASHI N., ABE T., ABE K.;
TWO ISOFORMS of the rat kidney EP3 receptor derived by alternative
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                           G-protein coupled receptor; Transmembrane; Glycoprotein;
Lipoprotein; Palmitate; Phosphorylation; Alternative splicing.
DOMAIN 130 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                  Score 34; DB 1; Length 365;
Pred. No. 19;
2; Mismatches 0; Indels
                                                                                                                                                                            S (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                        2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                           4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                        1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                      GCRDB: GCR_0367; --
GCRDB: GCR_0549; --
GCRDB: GCR_0944; --
MGD: WGI: 97795; PTGEREP3.
PROSITE: PS00237; G_PROTEIN_RECEPTOR; FALSE_NEG.
PFAM; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                          91CB103C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                    365 AA.
                                                                                                                                                                                                                                                     BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ALPHA AND GAMMA FORMS).
                                                                                                                                                                                                                                                                                                          365 AA; 40077 MW;
                                                                                                                                                                                                                                                                                                                                   58.68;
77.88;
EMBL; D17406; BAA04229.1;
                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 77.8-
                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                ||:|:||||
| 323 LLLRKILLR 331
                                                                                                                                                                                                                                                                                                                                                                     3 LLIRRILLR 11
                                                                                                DOMAIN
TRANSMEM
                                                                                                                DOMAIN
TRANSMEM
                                                                                                                                                           TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                           RANSMEM
                                                                                                                                                                              FRANSMEM
                                                                                                                                                                                               PRANSMEM
                                                                                                                                                                                                                  RANSMEM
                                                                                                                                                                                                                                    CARBOHYD
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                                                                                                                                                                                                                                                     DISULFID
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                                                                                                                                                                                        DOMAIN
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RE BIOLOGY EN A. (ALPHA AND BETA FORMS).

RE SIGNER HORDAY.

RE SIGNER PROME A. (ALPHA AND BETA FORMS).

RE SIGNER PROME A. (ALPHA AND BETA FORMS).

RESIDENCE PROME A. (ALPHA AND BETA FORMS).

RESIDENCE PROME A. (BETA SIGNER).

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us-08-653-294-16.rsp

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ö
 IRDHTNYASSSTSLPCPGSSVLMWSDQLER -> MMNNLKR
SFIALPASLSMRISSPREG (IN ISOFORM BETA).
IRDHTNYASSSTSLPCPGSSVLMWSDQLER -> VANAVSS
CSSDQCKGQAISLSNEVVHPGP (IN ISOFORM
GAMMA).
 SEQUENCE FROM N.A.
MEDLINE; 94139918.
ADAM M., BOIE Y., RUSHWORE T.H., MULLER G., BASTIEN L., MCKEE K.T.,
METTERS K.M., ABRAMOVITZ M.;
"Cloning and expression of three isoforms of the human EP3 prostanoid
receptor.";
 PE23_HUMAN STANDARD; PRT; 390 AA.
P43115; Q12943; Q12944; Q12945; Q16546;
01-NOY-1995 (Rel. 32, Created)
11-NOY-1995 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PROSTAGLANDIN E2 RECEPTOR, EP3 SUBIYPE (PROSTANOID EP3 RECEPTOR) (PGE
 Gaps
 SCHWID A., THIERAUCH K.H., SCHLEUNING W.D., DINTER H.; "Splice variants of the human EP3 receptor for prostaglandin E2."; Eur. J. Biochem. 228:23-30(1995).
 YANG J., XIA M., GOETZL E.J., AN S.;
Tcloning and expression of the EP3-subtype of human receptors for
prostaglandin E2.";
Biochem. Biophys. Res. Commun. 198:999-1006(1994).
 ö
 SEQUENCE FROM N.A.
MEDILINE; 94183149.
WINNPULI S.P., FEN MAO G., BASTEPE M., LIU-CHEN L.-Y., LI S.,
CHEUNG P.P., DERIEL J.K., ASHBY B.;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Score 34; DB 1; Length 365;
Pred. No. 19;
 Indels
 EXTRACELLULAR (POTENTIAL).
 6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
 P -> RA.
V -> S (IN REF. 3 AND 4).
S -> F (IN REF. 3).
F302B36A CRC32;
CYTOPLASMIC (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
 ö
 BY SIMILARITY.
 2; Mismatches
 5 (POTENTIAL)
 POTENTIAL. POTENTIAL.
 152 P
51 V
354 S
39942 MW;
 FEBS Lett. 338:170-174(1994).
 Ouery Match 58.6%;
Best Local Similarity 77.8%;
Matches 7; Conservative
 RECEPTOR, EP3 SUBIYPE).
365
 Homo sapiens (Human)
 152 1
51
354 3
365 AA;
 ||:|:||||
323 LLLRKILLR 331
 SEQUENCE FROM N.A.
 TISSUE-UTERUS;
MEDLINE; 95188908.
 SEQUENCE FROM N.A.
 TISSUE-KIDNEY;
MEDLINE; 94161771.
 3 LLIRRILLR 11
131
152
174
204
204
208
304
304
103
310
336
336
 336
DOMAIN
TRANSMEM
DOMAIN
TRANSMEM
 DOMAIN
TRANSMEM
DOMAIN
 DISULFID
 VARIANT
CONFLICT
CONFLICT
SEQUENCE
 FRANSMEM
 CARBOHYD
 CARBOHYD
 VARSPLIC
 DOMAIN
 PTGER3
 RESULT 13
PE23_HUMAN
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 "Molecular cloning and expression of human EP3 receptors: evidence of three variants with differing carboxyl termini."; Br. J. Pharmacol. 112:377-385(1994).
 SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. CAUTION: IN REF. 7 EP3B IS KNOWN AS EP3E, EP3C AS EP3D AND EP3D AS
 AS EP3-I, EP3A, OR EP3A1.
-!- TISSUE SPECIFICITY: EXPRESSED AT LEAST IN SMALL INTESTINE, HEART,
 REGAN J.W., BALLEY T.J., DONELLO J.E., PIERCE K.L., PEPPERL D.J., ZHANG D., KEDZIE K.M., FAIRBAIRN C.E., BOGARDUS A.M., WOODWARD D.F.,
'Cloning and expression of a prostaglandin E receptor EP3 subtype irom human erythroleukaemia cells."; 31ochem. J. 298:263-267(1994).
 MEDLINE; 96074809.

KOTANI M., TANKA I., OGAWA Y., USUI T., MORI K., ICHIKAWA A., NARMONIA S., YOSHIMI T., NARMO K.;

"Molecular cloning and expression of multiple isoforms of human prostaglandin E receptor EP3 subtype generated by alternative messenger RNA spliding: multiple second messenger systems and tissue-specific distributions.";

Mol. Pharmacol. 48:869-879(1995).
 AN S., YANG J., SO S.W., ZENG L., GOETZL E.J.; Isoforms of the EP3 subtype of human prostaglandin E2 receptor transduce both intracellular calcium and cAMP signals."; Biochemistry 33:14496-14502(1994).
 EMBL; 569200; AAB29854.1; -. EMBL; L27490; AAC13374.1; -. EMBL; L27488; AAC13372.1; -. EMBL; L27489; AAC13373.1; -.
 SEQUENCE FROM N.A.
TISSUE-SMALL INTESTINE;
MEDLINE; 94356288.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A. MEDLINE; 97230456.
 SEQUENCE FROM N.A.
 95072021
 AND PANCREAS.
 TISSUE-UTERUS;
MEDLINE: 9507;
 IISSUE-KIDNEY
 from
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Gaps ö

Indels

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 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE SEQUENCE FROM N.A.

SEQUENCE STRAIN-NEW ZEALAND WHITE; TISSUE-KIDNEY CORTEX;

MEDILINE; 94164982.

BREYER R.M., EMESON R.B., TARNG J.L., BREYER M.D., DAVIS L.S.,

ABROMSON R.M., FERRENBACH S.M.;

Theoretaglandin E2 receptor.";

J. Biol. Chem. 269:6163-6169(1994).

THIS RECEPTOR ROR PROSTAGLANDIN E2 (PGE2). THE ACTIVITY OF

THIS RECEPTOR CAN COUPLE TO BOTH THE INHIBITION OF ADENYLATE

CYCLASE MEDIATED BY G-I PROTEINS, AND TO AN ELEVATION OF

INTRACELLULAR CALCIUM. THE VARIOUS FORMS CAN INTERACT WITH

DIFFERENT SECOND MESSENGER SYSTEMS (BY SIMILARITY).

CHORDING RECEPTOR THE SECOND MESSENGER SYSTEMS (BY SIMILARITY).

TERMINUS ARE PRODUCTS: AT LEAST FOUR FORMS THAT DIFFERS AT THE C-ITERNATIVE PRODUCTS: A LEAST FOUR FORMS THAT DIFFERS AT CREED TO THE SEQUENCE OF CLONE 77A IS
 EP3C/EP3-II).
IRYHTNNYASSTSLPCQCSSTLMMSDHLER -> EEFWGN
IN ISOFORM EP3B/EP3-II).
IRYHTNNYASSSTSLPCQCSSTLMMSDHLER -> MRKRRL
REQEEFWGN (IN ISOFORM EP3D).
 IRYHTNNYASSSTSLPCQCSSTLMWSDHLER -> VANAVS
SCSNDGQKGQPISLSNEIIQTEA (IN ISOFORM
 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PROSTAGLANDIN E2 RECEPTOR, EP3 SUBIYPE (PROSTANOID EP3 RECEPTOR) (PGE
 TISSUE SPECIFICITY: IN THE KIDNEY, HIGH LEVELS OF EXPRESSION ARE SEEN IN MEDULLARY THICK ASCENDING LIMB, AND LOWER LEVELS IN THE CORTICAL AND MEDULLARY COLLECTING DUCTS.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPPORS.
 Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 DB 1; Length 390;
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
 7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
 Score 34; DB 1
Pred. No. 21;
2; Mismatches
 411 AA.
 POTENTIAL. POTENTIAL.
 EMBL; U04274; AAA17413.1; -. EMBL; U04273; AAA17412.1; -.
 58.6%;
77.8%;
 Query Match
Best Local Similarity 77.0
 STANDARD;
 390
 390
 253
283
307
327
349
390
390
390
390
 347 LLLRKILLR 355
 3 LLIRRILLR 11
 2228
2284
3288
328
350
360
360
360
 360
 PE23_RABIT
P46069;
 DOMAIN
TRANSMEM
DOMAIN
 TRANSMEM
DOMAIN
TRANSMEM
 CARBOHYD
VARSPLIC
 CARBOHYD
 VARSPLIC
 VARSPLIC
 PTGER3
 RESULT 14
PE23_RABIT
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G
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 1111111111111
 PROJECTION (1) 1. G. Protein coupled receptor; Transmembrane; Glycoprotein; G. Protein coupled receptor; Transmembrane; Glycoprotein; Dipoprotein; Palmitate; Phosphorylation; Alternative splicing. EXTRACELLULAR (POIENTIAL).
 1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUTAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLUTAR. (POTENTIAL).
 G_PROTEIN_RECEPTOR; FALSE_NEG.
 5; BAA19951.1;
7; BAA19951.1;
8; BAA19951.1;
 CAA58741.1;
CAA58742.1;
CAA58743.1;
 AAA21133.1;
AAA21134.1;
 AAA68191.1;
AAA68192.1;
 AAA68193.1;
BAA07416.1;
 AAA60076.1;
 CAA58740.1
 AAA21130.1
 AAA21132.1
 53
78
91
1112
131
153
174
197
 BAA07417
 BAA07418
 PS00237;
 GCR_2667;
GCR_2668;
 Lipoprotein, F
DOMAIN
TRANSMEM 5
DOMAIN 7
TRANSMEM 9
 x83861;
 X83862;
 X83863;
 D38298;
 013214;
 D86087;
D86088;
 D86096
 DOMAIN
TRANSMEM
DOMAIN
 DOMAIN
TRANSMEM
 PROSITE;
 EMBL; U EMBL; U EMBL; U EMBL; D EMBL; D EMBL; D EMBL; D GCRDB; GCRDB; GCRDB;
 GCRDB;
GCRDB;
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VENTER J.C.; "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";

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 BY SIMILARITY.

T -> A (IN CLONE 72A).

WIHENN -> EEFWEK (IN CLONE 72A).

WIHENNEQKDEIORENRNYSHS -> IRYHTNNYASSSTSL

THQCSST (IN CLONE 74A).

THGCSST (IN CLONE 74A).

WIESING (IN CLONE 74A).
 VIHENNEÇKDEIQRENRNVSHSGQHEEARDSEKS -> HSP
ANIGOLQISTHISKINKYFEGLMKTFHSLAYL (IN CLONE
 Gaps
 STRAINED / KW20:
MEDLINE: 95350630.

PELSICKHANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
FLEISCHMANN R.D., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
WITERBACK T.R., HANNA M.C., NGOYEN D.T., GEOGHAGEN D.M., BRANDON R.C.,
FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
GNEHM C.L., MCDONALD D.A., SMALL K.V., FRASER C.M., SMITH H.O.,
 ö
 Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
 DB 1; Length 411;
 4 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
5 (POTENTIAL).
7 (POTENTIAL).
EMBL: U04275; AAA17414.1; -.
EMBL: U04276; AAA17415.1; -.
GCRDB: GCR_0954; -.
GCRDB: GCR_0955; -.
PROSITE: PS00237; G_PROTEIN_RECEPTOR; FALSE_NEG.
PFAM: PF00001; 7Tm_1; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Alternative splicing.
 0; Indels
 EXTRACELLULAR (POTENTIAL).
 7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
POTENTIAL.
 EXTRACELLULAR (POTENTIAL)
 3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
 (POTENTIAL).
 MISSING (IN CLONE 80A)
 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
NOV-1995 (Rel. 32, Last annotation update)
HYPOTHETICAL PROTEIN HI1655.
 1 (POTENTIAL).
CYTOPLASMIC (PC
2 (POTENTIAL).
 575 AA.
 (POTENTIAL).
 Score 34; DB :
Pred. No. 22;
2; Mismatches
 PRT;
 45600 MW;
 58.6%;
77.8%;
 Query Match 58.6
Best Local Similarity 77.8
Matches 7; Conservative
 STANDARD;
 390 411 AA;
 ||:|:||||
| 343 LLLRKILLR 351
 SEQUENCE FROM N.A.
 3 LLIRRILLR 11
 RESULT 15
YRAM_HAEIN
ID YRAM_HAEIN
 TRANSMEM
DOMAIN
TRANSMEM
 DOMAIN
TRANSMEM
DOMAIN
 VARSPLIC
SEQUENCE
 DOMAIN
TRANSMEM
 DOMAIN
TRANSMEM
 DOMAIN
 VARSPLIC
VARSPLIC
 PRANSMEM
 CARBOHYD
 VARSPLIC
 FRANSMEM
 CARBOHYD
 DISULFID
 VARSPLIC
 DOMAIN
 VARIANT
 P45299;
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                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 1; Length 575;
Pred. No. 31;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                         TIGR; H11655; -. PROKAR_LIPOPROTEIN; UNKNOWN_1
                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEOUENCE 575 AA; 63436 MW; 90038AEB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: February 8, 2000, 00:59:55 Job time: 3784 sec
                                                 Science 269:496-512(1995).
-!- SIMILARITY: STRONG, TO E.COLI YRAM.
                                                                                                                                                                                                                                                                                                                                                                                 58.68;
54.58;
                                                                                                                                                                                                                                                      EMBL; U32838; AAC23299.1; -.
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Best Local Similarity 54.5
Matches 6; Conservative
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65 YKLLAARVLIR 75
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SYNTHANDOCCOCKENTS
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09yw71 melanoplus
066951 aquifex aeo
084647 chlamydia t
084887 homo sapien
005052 haemophilus
027591 drosophilus
024487 arabidopsis
064487 arabidopsis
06450 plasmodium
P94495 caenorihabdi
085331 vaccinia vi
085333 variola vir
P97213 clostridium
09xb05 myxococcus
000326 homo sapien
                                                                           8, 2000, 13:17:42; Search time 209.03 Seconds (without alignments) 3.980 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                      225878
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                             225878 seqs, 69334122 residues
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                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                      OM protein - protein search, using sw model
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0096160
P91495
085331
085383
085383
085383
085383
097805
000325
000325
015191
0971162
076912
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Gapop 10.0 , Gapext 0.5
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005052
027591
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_fung1:*
sp_human:*
sp_novertebrate:*
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sp_organele:*
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58
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Match Length DB
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Maximum DB seq length: 1000000
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                                                                                 February
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                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                  Database :
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                                                                                  Run on:
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P70780 anabaena sp 092903 chlamydia p 026858 methanobact 045433 bacillus st 09x9y3 streptomyce p97084 salmonella 026797 methanobact P72007 mycobacteri 0922063 caenorhabdi 092365 tolypocladi 059744 schizosacch 011875 denque viru 009234 unidentifie 09x378 bacillus an 004336 cryza sativ 094336 prizobium m 006790 saccharomyc 060503 cricetulus 060503 cricetulus 060503 cricetulus 060503 cricetulus 086179 sanopheles g 056779 sanothabdil 045795 caenorhabdil 019771 caenorhabdil			date) update)	e; Entomopoxvirinae;	G.F., ROCK D.L.; virus.";	G.F., ROCK D.L.; atabases.	Length 260; ; Indels 0; Gaps 0;
2 P70780 2 Q92903 2 Q92903 2 Q9x9x3 2 Q9x9x3 2 Q9x9x3 2 Q9x9x3 3 Q92385 3 Q92385 3 Q92385 3 Q92385 3 Q92385 3 Q92385 3 Q92385 3 Q92385 2 Q9x378 2 Q9x378 2 Q9x378 2 Q9x378 2 Q9x378 2 Q9x378 2 Q9x378 2 Q9x378 2 Q9x378 5 Q9x378	ALIGNMENTS	PRT; 260 AA.	0, Created) 0, Last sequence up 0, Last annotation FAMILY PROTEIN.	entomopoxvirus. no RNA stage; Poxviridae;	, LU Z., OMA E., KUTISH G.F.s sanguinipes entomopoxviru	R., LU Z., OMA E., KUTISH to the EMBL/GenBank/DDBJ d 150.1; - AB880E14 CRC32;	5%; Score 38; DB 12; 7%; Pred. No. 14; a 1; Mismatches 3
33 56.9 33 56.9 34 56.9 35 56.9 36 56.9 37 56.9 38		1 471 PRELIMINARY;	O9YW71; 01-MAY-1999 (TrEMBLrel. 1 01-MAY-1999 (TrEMBLrel. 1 01-MAY-1999 (TrEMBLrel. 1	MSV021. Melanoplus sanguinipes e Viruses; dsDNA viruses, Entomopoxvirus B.	SEQUENCE FROM N.A. STRAIN=TUCSON; MEDLINE; 99102612. AFONSO C.L., TULMAN E.R., "The genome of Melanoplu J. Virol. 73:533-552(1999)	JENCE FROM N.A. AIN-TUCSON; SOC C.L., TULMAN E. INTEG (MAY-1998) t L; AF063866; AAC978 UENCE 260 AA; 31	Match Local Similarity 66.7% es 8; Conservative 1 YRLIRRILER 12
222222222222222222222222222222222222		EW.	AC OOY DT OOI-			RN (2) RC SEQ RC STR RA AFO DR EMB	Query Matc Best Local Matches Qy 1 YR

066951 PRELIMINARY; PRT; 408 AA. 066951, 01-806-1998 (TrEMBLrel. 07, Created) 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)

RESULT 066951 ID 06 AC 06 DT 01

043162 homo saplen Q9zvc8 arabidopsis 015191 homo sapien 09y136 drosophila 076912 drosophila 043162 homo sapien homo sapien drosophila

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us-08-653-294-16.rspt

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NAGASE T., ISHIKAWA K., SUYAMA M., KIKUNO R., MIYAJIMA N., TANAKA A., KOTANI H., NOMURA N., OHARA O.; "Preddiction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; Pfor large proteins in vitro.";
                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [3]
SEQUENCE OF 1-754 FROM N.A.
SEQUENCE OF 1-754 FROM T., LANGSTON Y., LAPLANT Y.;
SUN H., STONEKING T., LANGSTON Y., LAPLANT Y.;
"The sequence of Homo sapiens BAC clone RG442F18.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WATERSTON R.H.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases EMBL, AB018336; BAA34513.1; -. BMBL; AD01504; ABD12224.1; -. HSSP; P08567; 1PLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
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01-JUL-1997 (TIEMBLIE). 04, Last sequence update)
01-NOV-1998 (TIEMBLIE). 08, Last annotation update)
TYPE I RESTRICTION ENZYME ECOR124/3 R PROTEIN (HSDR).
                                                                                                                             Created)
Last sequence update)
Last annotation update)
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Pred. No. 1.2e+02;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3BA89171 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE OF 1-754 FROM N.A.
MEDLINE: 99063792.
SULSTON J.E., WATERSTON R.;
"Toward a complete human genome sequence.";
Genome Res. 8:1097-1108(1998).
                                                                                                 1054 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1055 AA.
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58.3%;
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                                                                                              PRELIMINARY;
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Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                         01-MAY-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
          409 YRLLLTRVLKR 419
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                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                MEDLINE; 99087487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WATERSTON R.;
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005052;
01-JUL-1997 (
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094887
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STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-D/UW-3/CX;
STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
                                                                                                                                  MEDLINE; 98196666.

DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                  "Genome Sequence of an Obligate Intracellular Pathogen of Humans: Chlamydia trachomatis.";
Science 0:0-0(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.8%; Score 37; DB 2; Length 408; llarity 72.7%; Pred. No. 33; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 62.1%; Score 36; DB 2; Length 559; Best Local Similarity 63.6%; Pred. No. 68; Matches 7; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAVIS R.W.;
DAVIS R.W.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AEO01334; AAC68245.1; -.
SEQUENCE 559 AA: 61931 MW; 618B74E1 CRC32;
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
FIMBRIAL ASSEMBLY PROTEIN PILC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
                                                  Aquifex aeolicus.
Bacteria: Aquificales; Aquificaceae; Aquifex.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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08,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
EFFLUX PROTEIN.
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250 FRALIHRILLR 260
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Best Local Similarity
Matches 8; Conserv
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                                                                                                 SEQUENCE FROM N.A.
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STRAIN-CV. COLUMBIA,
VYSOTSAIA V.S., OSBORNE B.I., SCHWARTZ J.R., TORIUMI M., KWAN A.,
VYSOTSAIA V.S., OSBORNE B.I., SCHWARTZ J.R., TORIUMI M., BRENDEL V.,
BUCHLER E., CONWAY A.B., CONWAY A.R., DEWAR K., FENG J., KIM C.,
KURTZ D., LI Y., PALM C.J., SHINN P., SUN H., DAVIS R.W., ECKER J.R.,
SUDMITTED N.A., THEOLOGIS A.,
SUDMITTED (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                        -:- FUNCTION: INTEGRINS ARE A LARGE FAMILY OF CELL SURFACE GLYCOPROTEINS THAT MEDIATE CELL TO CELL & CELL TO MATRIX ADHESION.
-:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-:- SINILARITY: WITH OTHER BETA CHAINS FROM THE INTEGRIN FAMILY OF CELL-SURFACE RECEPTOR.
EMBL; L13305; AAC37169.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Makaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermarophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
tissue-specific integrin subunit, beta nu, expressed in
                                                                                                                                                                                                                 FLYBASE; FBGN0010395; beta-Int-nu.
PROSTIE; PS00243; INPEGRIN.BETA; 1.
PFAM; PF00362; integrin.B. 1.
Integrin; Cell adhesion; Transmembrane; Glycoprotein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                            Length 799;
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Pred. No. 1.5e+02;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AC002411; AAC16741.1; --
SEQUENCE 814 AA; 92446 MW; AE8AF982 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the EMBL/GenBank/DDBJ databases
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 5; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                 0F909972 CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0: Mismatches
    "A novel, tissue-specific integrin su
midgut of Drosophila melanogaster.";
Development 118:845-858(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                 90741 MW;
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60.0%;
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07,
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Best Local Similarity 66...
18. Conservative
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Best Local Similarity
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Submitted (OCT-1997)
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THEOLOGIS A.;
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STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                               799 AA;
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SEQUENCE
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064487
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                                                                                                                                                                                                                                                                                                         "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                            KERLAYAGE A.R., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERLAYAGE A.R., BULT C.J., TOMB J.F., DOUGHERTY B.A., MERRICK J.M., MERRICK J.M., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIRLEY R., LIU L.I., GLODER A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERRACK T.R., HANNIA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
FLEISCHAMN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
KERLAVAGE A.R., BULT C.J., TOMB J.F., DOUGHERTY B.A., MERRICK J.M.,
MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCANNE J.D.,
SCOTT J.D., SHIRLEY R., LUT L., GLODEK A., KELLEY J.M.,
WHIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOW E., COTTON M.D.,
UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
FINE L.D., FRITCHMAN J.L., FUHRWANN J.L., GEOGHAGEN N.S.M.,
VENTER J.C.,
VENTER J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

BADLINES 95398784.

L TARUSOV R., MUSHEGIAN A.R., BORK P., BROWN N.P., HAYES W.S.,

BORODOVSKY M., RUDD K.E., KOONIN E.V.;

BORODOVSKY M., RUDD K.E., RODIN E.V.;

BORODOVSKY M., RUDD K.E., KOONIN E.V.;

BORODOVSKY M., RUDD K.E., KOONIN E.V.;

BORODOVSKY M., RUDD K.E., KOONIN E.V.;

CULT. BIOL. 6:279-291(1996).
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WHITE O., CLAYTON R.A., KERLAVAGE A.R., FLEISCHMANN R.D.; Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases. EMBL; U32808; AAC22934.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1055 AA; 120709 MW; 9F1C0713 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 2; I
Pred. No. 1.2e+02;
2; Mismatches 2;
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Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTEGRIN BETA SUBUNIT (FRAGMENT).
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63.6%;
                                                                                                                                                                                                                                                                                                                                                        Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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TISSUE-MIDGUT ENDODERM;
MEDLINE; 94357079.
YEE G.H., HYNES R.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||:|| | :|
|1017 RLLVRRALQKY 1027
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                                                                        SEQUENCE FROM N.A. MEDLINE; 95350630.
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                                                                                                                                                                                                                                                                                                VENTER J.C.;
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Gaps

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Length 814;

Q27591 Q27591; 9

RESULT Q27591

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Variola virus.
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Orthopoxvirus.
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01-NOV-1996 (
01-NOV-1998 (
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Q85383;
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085383
AC 085383
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BONFIELD J., BURTON J., CONNELL M., COPSET T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURRIN R., FAVELLO A., FULTON L.,
JONES M., KERSHAW J., KIRSTEN J., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCWIRKARY A., MORTHWORE B., O'CALLAGHAN M.,
PRAKSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAM K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINGON-SPROAT J., WOHLDMAN F.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDILINE; 99021743.
MEDILINE; 99021743.
MEDILINE; 99021743.
KOONIN E.V., FETTELIN H., CARUCCI D.J., CUMMINGS L.M., ARAVIND L., KOONIN E.V., SHALLOM S., MASON T., YU K., FUJII C., PEDERSON J., SHING J., ASTON C., LAI Z., SCHWARTZ D.C., PERTEA M., SALZBERG S., ZHOU I., SUTTON G.G., CLAYTON R., WHITE O., SMITH H.O., FRASER C.M., ADAMS M.D., VENTER J.C., HOFFMAN S.L.;
"Chiconosome 2 sequence of the human malaria parasite Plasmodium fallobarum.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
SIMILARITY TO RAT INTEGRAL MEMBRANE GLYCOPROTEIN GP120 PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMEL; AE001386; AAC71852.1; -.
Hypothetical protein.
SEQUENCE 1712 AA; 204013 MW; E8B0BD71 CRC32;
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                                                                                                                                                                                               1712 AA
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01-MAY-1999 (TrEMBLrel. 10, Last seq
01-MAY-1999 (TrEMBLrel. 10, Last ann
HYPOTHETICAL 204.0 KD PROTEIN.
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01-WAY-1997 (TrEMBLrel. 03, Last seq
01-NOV-1998 (TrEMBLrel. 08, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 282:1126-1132(1998).
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Best Local Similarity 50...
6: Conservative
                                                                                                                                                                                                     PRELIMINARY;
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Caenorhabditis elegans.
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1316 YKIYLRRILFGY 1327
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SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
MEDLINE; 94150718.
                             |::||:|| |
263 LVVRRLLLNY 272
3 LLIRRILLRY 12
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P91495;
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MEDLINE: 89094998.
THOMPSON C.L., HOODA-DHINGRA U., CONDIT R.C.;
"Fine structure mapping of five temperature-sensitive mutants in the 22-and 147-kilodalton subunits of vaccinia virus DNA-dependent RNA
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccinia virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MASSURG R.F., ESPOSITO J.J., LIU L.I., QI J., UTTERBACK T.R., KNICHT J.C., AUBIN L., YURAN T.E., PARSONS J.M., LOPAREV V.N.; "Potential virulence determinants in terminal regions of variola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                               Length 1847;
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                                                                                                                                               Score 35; DB 5; Length 184
Pred. No. 3.2e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
STRAIN-BRISTOL N2;
WAMSLEY P., BRADSHAW H.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U80033; AAC48199.1; -.
SEQUENCE 1847 AA; 199637 WW; BOA25E0F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TremBirel. 01, Created)
(TremBirel. 01, Last sequence update)
(TremBirel. 08, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
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54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 smallpox virus genome.";
Nature 366:748-751(1993).
EMBL; L22579; AAA60829.1; -.
SEQUENCE 185 AA; 21355 MW; 3B9F48DE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 179
179 AA; 20757 MW; 7E103F8D CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
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Pred. No. !
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-NOV-1998 (TrEMBLrel. 08, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMOLOG OF VACCINIA VIRUS CDS J4R
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                                                                                                                                                    60.3%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polymerase.";
J. Virol. 63:705-713(1989).
EMBL; M24216; AAA48277.1; -.
NON_TER 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 50.0.
                                                                                                                                                 Query Match 60.3
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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SEQUENCE FROM N.A.
STRAIN-BANGLADESH-1975;
MEDLINE; 9400874747.
                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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19 YRLNVPRVLLPY 30
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P97213 P97213;

RESULT 12 P97213

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TISSUE-UTERUS;
MEDLINE: 97230456.
KOTANI M., TANARA I., OGAWA Y., USUI T., TAMURA N., MORI K.,
NARUMIYA S., YOSHIMI T., NARAO K.;
"Structural organization of the human prostaglandin EP3 receptor
subtype gene (PTGRR3).";
Genomics 40:425-434(1997).
EMBL: D86098; BAA19959.1; -.
EMBL: D86098; PROMO428; PROSTAGLIDDR.
PRINTS; PROMO428; PROSTAGLIDDR.
PRINTS; PROMO482; PRSTNOIDEP3R.
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KOTANI M., TANNKA I., OGAWA Y., USUI T., TAMURA N., MORI K., NARUMIYA S., YOSHIMI T., NAKAO K.;
"Structural organization of the human prostaglandin EP3 receptor
                                                                                                                                      01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 12, Last annotation update)
PROSTAGLANDIN EP3 RECEPTOR SUBTYPE ISOFORM.
Homo sapiens (Human).
Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.6%; Score 34; DB 4; Length 393; 77.8%; Pred. No. 1.1e+02; Live 2; Mismatches 0; Indels
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PROSTAGLANDIN EP3 RECEPTOR SUBTYPE ISOFORM.
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                                                                                      PRT;
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Genomics 40.425-434(1997).
Genomics 40.425-434(1997).
FPMBL. D86097; BAA1995B.1; -.
FPRM, PF00001; 7tm_1; 1.
PRINTS; PR00428; PRSTNOIDEP3R.
PRINTS; PR00584; PRSTNOIDEP3R.
SEQUENCE 402 AA; 44937 MW; 6
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                      PRELIMINARY;
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SEQUENCE FROM N.A.
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347 LLLRKILLR 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. TISSUE-UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||:|:||||
347 LLLRKILLR 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            000325;
01-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                   000326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
000325
AC 000325;
DT 01-JUL-
DT 01-JUL-
DT 01-NUL-
DE PROSTAK
DE PR
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PAITAN Y., ORR E., RON E.2., ROSENBERG E.;
PAITAN Y., ORR E. RON E.2., ROSENBERG E.;
"Genetic and functional analysis of genes required for the post-
modification of the Polyketide antibiotic TA of Myxococcus xanthus.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ132503; CAB46503.1; -..
SEQUENCE 325 AA; 35985 MW; 4CC64E85 CRC32;
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-1997 (TrEMBLrel. 03, Last annotation update)
CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4
GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium difficile.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 58.6%; Score 34; DB 2; Length 313; Best Local Similarity 41.7%; Pred. No. 92; Matches 5; Conservative 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 2; Length 325;
Pred. No. 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIM-VPI10463;
VON EICHEL-STREIBER C.:
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; X92982; CAA63559.1; -
EMBL; X92982; CAA63558.1; -
EMBL; X92982; ARA63558.1; -
SEQUENCE 313 AA; 33380 MW; 4F20347A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MEMBRANE ASSOCIATED PROTEIN.
                             Score 34; DB 12;
Pred. No. 56;
3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                    313 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                    PRT;
                       58.6%;
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58.3%;
Ouery Match
Best Local Similarity 50.0
The 6; Conservative
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259 YRVVARRLSIKY 270
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202 YRLTVDRFPLRY 213
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24 YAVINRNVLLRY 35
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Best Local Similarity
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Q9XB05; **Q9XB05**

RESULT Q9XB05

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Gaps

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Matches

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Search completed: February 8, 2000, 13:17:44 Job time: 32493 sec

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http://webace.sanger.ac.uk/cgi-
bin/display?db-wormace&class=Sequence &object=F14B6
current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is NOT necessarily the entire insert of
the specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a small
impoRTANT: This sequence is not the entire insert of clone F14B6.
It may be shorter because we only sequence
overlapping sections.
It may be shorter because we arrange for a small once, or longer because we only sequence
neighbouring submissions.
The true left end of clone F41D3 is at 29177 in this sequence. The
true right end of clone F41D3 is at 19221 in this sequence. The
start of this sequence (1. .109) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota, Metazaa; Nematoda; Secernentea; Rhabditida;
Bukaryota, Matazaa; Nabditidae; Peloderinae; Caenorhabditis.
Rhabditina; Rhabditiodea; Rhabditidae; Peloderinae; Caenorhabditis.
Caenor, Rhabditina; Rhabditidae; Peloderinae; Caenorhabditis.
Caenor, Rainscough, R., Anderson, K., Baynes, C., Berks, M.,
Bonfledd, J., Burton, J., Conneal, M., Copsey, T., Cooper, J.,
Coulson, A., Caraton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,
Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,
Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,
Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A.,
Saunders, D., Shownkeen, R., Sanldon, N., Smith, A., Sonnhammer, E.,
Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vaughan, K., Waterston, R., Watson, A., Weinstock, L.,
Wilkinson-Sproat, J. and Wohldman, P.,
Caenoriguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The end of this sequence (29177. ,29283) overlaps with the start of sequence 281537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submission
Submitted (06-NOV-1996) Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rw@nematode.wustl.edu
on Jan 28, 1998 this sequence version replaced gi:1665918.
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             For a graphical representation of this sequence and its analysis
                                                                                                                                                                                          Caenorhabditis elegans cosmid F14B6, complete sequence. 281502.1 G1:2814053
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/gene="F14B6.1"
complement(join(947. .1390,1835. .2063,2114. .2169))
  901
902
1296
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  114.88
115.02
169.89
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/chromosome="1"
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120.09
120.08
117.04
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  39.00
39.00
39.00
                                                                                                                                                                     seq_documentation_block:
LOCUS CEF14B6
                                                                                                              seq_name: gb_in1:CEF14B6
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  gb_ba2:AF134389
gb_ba2:AF134390
gb_ba1:UAR133622
                                                                                                                                                                                                                    DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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REFERENCE
AUTHORS
TITLE
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4 uncultured euryarchaec
5 uncultured euryarchaec
6 uncultured euryarchaec
7 uncultured euryarchaec
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AC011085 Homo sapiens chrome
AC006377 Homo sapiens clone
AC016259 Homo sapiens chrome
AL132800 Homo sapiens chrome
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AC008413 Homo sapiens chromos
AC002453 Human BAC clone 6S44
AC006300 Arabidopsis thaliana
AC004368 Drosophila melanogas
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AF165139 Homo sapiens chromo
                                                                                                                                                                                                                    -MODEL-frame-p21.model -DEV=x1p
-Q=/Cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15779/app_query.fasta.1
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-QGAPEXT-0.000 -YGAPOP-10.000 -XGAPEXT-0.500 -FGAPOP-6.000
-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-LIST-45 -DOCALIGN=200 -THR_SCORE-pct -ALIGN=15 -MODE-LOCAL
-UIST-45 -DOCALIGN=200 -THR_SCORE-pct -ALIGN=15 -MODE-LOCAL
-OUTFWT-pfs -NORM-ext -MINLERN-0 -MAXIEXT-1000000 -USER-US08653294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ! Documentation
                                                                                                              About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130435
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3.8e+03
6.2e+03
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.5e+03
.4e+03
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1e+04
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53.93
53.98
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79.99
79.99
79.38
79.22
78.69
122.34
120.44
120.44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database sequences: 821193
Database length: -1518192014
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                                                             Ā
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                                                                                                                                                                                                Command line parameters:
                                                          Date: Feb 8, 2000 4:41
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Query length: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database: GenEmbl:*
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Wed Feb

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EIRGDEEEDDDDESYVEGEEEDSSDEDLDDEDQEGESSIEPRLSETFKKSEARESLSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-"MEISLOKKLIFLFLFANASSVSGCGSFDYYLLKSISGLLNYQID
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ETNOKSAMRALLFVSNAPKSVODDYFTMLARAVDIFTHTWSLSVEVOFYFLVPFIFLE
AIKLGGLLSYAFFFFFSNTSFNSYFRINOFLIGMIYFLLSSHSKKSPEABKNIEBE
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INSTENDELLIGNKILTYTODISYSLYILHWPITAYWKLAFDGDVNLLISSLLSSILLAI
IVFEFFEKNYLKLSSTSIGLLIVFLFFLNVILINKDELIPDREENNNHNSSMNTDDAI
                                                                                                                                                                                                                          SETSDSELGODSPNPNLSEALNNCIENFDQLVDEVVRHKDFHERSQLLRVLEECLGNM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   jóin(23603. 23727,23784. 24048,24104. 24209,24287. 34
24425. 24635,24799. 24965,25030. 25343,25388. 25514,
25566. 25680,25729. 25933,25988. 26251)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HRINLGQEKGTDLVFAWHSPLNDPEYKDLYYKTWSSQQFKEKLRLQEINVT"
20434. .22684
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Gaps: 0
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                     ELDDDSNGKEEEELELDVTQEDSEDDEQFFSL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start-1
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4.091
91.667
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US-08-653-294-16 x CEF14B6
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Ratio:
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LKKAKKLTEAEKLLNNSTSTSVIPDTAVSRKPKGKGLKKSKKLNQKPKSDEEVTKQPR
HLVGKSSSLSPTTPRPKSSWMNGVLDPQDPNFSNQGQIRGYPWQKASRKPSATTASPS
                                                                                                                                                                                                                                                                                                                                                                                                                                        LIEIDSSGRVQPFVSIVEEGSKPYFSPHVGCAECAQWWDVYGEQPHRVEETEDQDTDE
GVEEESEIEDSDFDDQIIFVKPTTPAPLSPETENFIEDKMKFHFQATDIINEYLGKGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RKIDSNHIPAVPPYEPDDDLPMTTMVTLTNTQIVQLSGEETGVVKMKTIRNRVEKVGS
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PMLKETFEEATTSTEKPLPGGMSKDQWEKKKEAFEAYIPPISLSDLQPSHSSHSGPAQ
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/Adde="cond EST yk242e8.5 comes from this gene; cDNA EST yk242e8.3 comes from this gene; cDNA EST yk4714b10.5 comes from this gene; cDNA EST yk477b2.3 comes from this gene; cDNA EST yk477b2.5 comes from this gene; cDNA EST yk608e9.3 comes from this gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGHLESTTKSYDPLHLEVSFESFECGGGLLCHFVFDP,
MGHLESTTKSYDPLHLEVSFESFECGGGLLCHFVFDP,
Complement(9869..9940)

fogne="Flab6.t2"

preliminary prediction; similar to tRNA-Met"

complement(9869..9940)

fogne="Flab6.t2"
13752..13823
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L SUBMITTER (26-NOV-1999) Sanger Centre, Hinxton, Cambridgeshire, Cabonalitted (26-NOV-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerquest@sanger.ac.uk
On Nov 27, 1999 this sequence version replaced gi:6066017.
IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate contig_ID: 00009 Length: 1968bp Contig_ID: 00039 Length: 1518bp Contig_ID: 00039 Length: 1840bp Contig_ID: 00039 Length: 1840bp Contig_ID: 00039 Length: 1840bp
                     Submission
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                                                                                                                                                                                                                                        Contig_ID:
Contig_ID:
 AUTHORS
TITLE
JOURNAL
                                                                                      COMMENT
                                                                                                                                                                                                                                                                                   McLay.K.

Direct Submission

Submitted (07-52E-1999) Nematode Sequencing Project, Sanger Centre,
Blincton, Cambridge CB10 1RQ, UK and Department of Genetics,
Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics,
Washington University, St. Louis, MO 63110, USA. E-mail:
jes(sanger.ac.uk or refenemence wustl.edu
on Aug 10, 1999 this sequence version replaced g1:4938508.

Order of segments is not known; 800 n's separate segments.
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct, sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                    07-SEP-1999
*** SEQUENCING IN
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Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 296589)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 306999)
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This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                               2401 others
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Percent Identity: 66.667

    1. .296589
/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"

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295311.10 GT:5725202
HTG: HTGS_PHASE1.
Caenorhabditis elegans.
Caenorhabditis elegans.
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AL121956.2 GI:6469398
HTG; HTGS_PHASE1.
human.
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* be preserved
                                                   seq_name: gb_htg1:CEY47H10
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1781bp 10365bp

dq06,

158bp

.96bp

86bp

901bp

506bp

1722bp 260bp 1606bp .648bp

299bp

1742bp .888bp

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2 (sites)
Seki,N., Ohira,M., Nagase,T., Ishikawa,K., Miyajima,N.,
Nakajima,D., Nomura,N. and Ohara,O.
Characterization of cDNA clones in size-fractionated cDNA libraries
from human brain
DNA Res. 4 (5), 345-349 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (08-001-1997) to the DDBJ/EMBL/GenBank databases. Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913, Fax:+81-438-52-3914)
                    Direct Submission

Direct Submission

Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,

Rockville, MD, USA

This sequence was identified as CDM:10210882 by the submitter.

For further information on this sequence e-mail to fly@celera.com.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location_Qualifiers
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HOMO Sapiens mRNA for KIAA0462 protein, partial cds.
AB007931 1 G1:3413885
KIAA0462 protein.
HOMO Sapiens male brain cDNA to mRNA, clone_lib:pBluescriptII SK plus clone:HG0891.
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/db_xref="taxon:7227"
16683 a 13092 c 13361 g 16729 t
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Gaps: 0
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/clone_lib="pBluescriptii SK plus"
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/gene="KIAA0462"
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     Adams, M. and Venter, J.C.
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LOCUS AC014422 59865 bp DNA HTG 16-NOV-1999
DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydoidea; Drosophilidae; Drosophila.
1 (bases 1 to 59865)
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the accession number will
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/clone="RP4-65505"
/clone="RP4-65505"
/dlone="RP4-65505"
/dlone="6" 46393 g 68867 t 71293 others
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Gaps: 0
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* This record will be updated with
* as soon as it is available and th
* be preserved.
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AC014422.1 GI:6436913
HTG; HTGS_PHASE2.
fruit fly.
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us-08-653-294-16.rge

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source
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AUTHORS
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LDGEDEKDKGALDNLLSQLIAELGMDKKDVSKKNERSALNEVHLVVMRLLSVFMSRTK
SGSKSSICESSSLISSATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLL
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EMENKPRKQOGYSTVSHFNIVHYDCHLAAVRLARGREEWESAALQNANTKCNGLLPVW
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VLALHILPPEOWRATRVEILRRLLVTSOARAVAPGGATRLTDKAVKDYSAYRSSLLFW
ALVDLIYNMFKKVPTSNTEGGWSCSLAEYIRHDMPIYEAADKALKTFOEEFMPVETF
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KLEOVSSDEGIGTLAENLLEALREHPDVNKKIDAARRETRAEKKRMAMAMROKALGTL
                                                                                                                                            KPHTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLPYQIKKITDTNSRIPF
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/translation="EHSVSGRSSAYGDATAEGHPAGPGSVSSS]
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3.818 Gaps: 0
91.667 Percent Identity: 58.333
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Submitted (13-NOV-1999) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
3 (Dases 1 to 82875)
Direct Submission
Direct Submission
Submitted (30-NOV-1999) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
4 (bases 1 to 82875)
E Shinn,P., Brooks,S., Buehler,E., Chao,Q., Johnson-Hopson,C.,
Khan,S., Kim,C., Altafi,H., Bei,B., Chin,C., Chiou,J., Choi,E.,
Conn,L., Conway,A., Gonzalez,A., Hansen,N., Howing,B., Koo,T.,
Lam,B., Lee,J., Lenz,C., Li,J., Liu,A., Liu,J., Liu,S.,
Mukharsky,N., Nguyen,M., Palm,C., Pham,P., Sakano,H., Schwartz,J.,
Southwick,A., Thaveri,A., Toriumi,M., Vaysberg,M., Yu,G., Davis,R.,
Federspiel,M., Theologis,A. and Ecker,J.
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RCIPHILITIKLIKDAHKFGKGVELPLALSGMAGMNILNVGLGLDLFHAFRRERSHRR
NQENGNLHDHGE"
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LOQINUKEGORSLQGTTSSTEIDLMDDFLEMERLVALLPTTGAKNSKOGYELSLAMEK
LEKIQAEKDDLEREYKCERAARELEDERAVVGDKMELEDWLKRVBAEKAEKTSFD
VLKDKYQESRVCFQEVDTKLEKLQAEKDELDSEVICCKEAEKRFSLELEAVVGDKIEM
                                                                                                                                                                                                                    Shinn, P., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., Shinn, P., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., Khan, S., Klin, C., Altafi, H., Bei, Q., Chin, C., Chiou, J., Choi, E., Cona, L., Conway, A., Gonzales, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Federspiel, N.A., Theologis, A. and Ecker, J. R.
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                                                   euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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      Embryophyta; Tracheophyta
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/note="hypothetical protein"
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join(140. 398,676. 953,1145. 1474)
/note="unknown: similar to EST gb|H74506"
/evidence=not_experimental
/product="T26F17.1"
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/^Organism="Arabidopsis thaliana"
//db_xref="taxon:3702"
/chromosome="1"
      Streptophyta;
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/db_xref="G1:6552748"
Eukaryota; Viridiplantae;
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2 (bases 1 to 82875)
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CDS

CDS

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. .24104,24201. .24450,24546. .24753,24936. .25167,
DYTLLVGDMYKTNHKDLKAQLDNGGKLPLPDGILINGRSGGATLNIEPGKTYRLRISN
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VSSRTSKILTTTGVLHYSNVAPVSCPIPDGPIKLSWFSNGARAIRTNLTASGPRPN
POGGYRYGYLNITTRLANNLGHIEGKQRYAVNSASFYPADTPLKLVDGYYK
PGSISDQPTNGAIFPTTSVMQADFRAFVEVIFENSEDIVQSWHLDGYSFYVVGMELGK
                                                                                                                                     WSPASEKTVRILNDALLECTIONY PREWTAITIALDNVGMWNRSEIWERQYLGGOFFW
RVITTSTSLRDEYLIPKNALLCGRASSSHR"
RVITTSTSLRDEYLIPKNALLCGRASSSHR"
Anote—"hypothetical protein"
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FECAALEGCLATSTKTILESELLHGYKTBOSITHVYTWARFATMYLIGHEAFLLERNGI
LDWFFRAHSEWSALIIFNSSYLAFCLHFSIFYVOSTTAVTFNVAGNLKVAVVFVS
WAIFRNPISPWNAVGCGITLVGCTFYGYVRHMLSOOOPGIPRTPRTPRNKMELIPLVN
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GYRKSYSTHYKTRESDNLGSTADSVYGGLVSARQIQEANSVNDPSLLDVGTSLVIPLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(23991. .24104,24201. .24450,24540. .44755,25259. .25480)
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Gaps: 0
Percent Identity: 66.667
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ACCESSION AC005365 GI:3367509 VERSION AC005365.1 GI:3367509
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US-08-653-294-16 x AC013482/rev
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KEYWORDS
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TCPIPPGKNYTYALQVKDQIGSFYFPSLGFHKAAGGFGAIRISSRRRIPVEPRAPAG
TCPIPPGKNYTTNHKDLRAQLDNGGKLPFDGILLINGRGSGATLNIEPGKTYRLRISN
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VSSRFTSKILITAGALHYSNSAGPYSGPIPEAPIQLRMSFDQARAIKTNLAASGPRPN
PQGTYHYGKIKVTRTIKLASSAGNINGKQRYAVNSASFYPTDTPLKLADYFKIAGVYN
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WSAASRKVYNLNDAVSRCTVQVYPRSWTAIYVSLDNVGMWNLRSELWERQYLGQQFYM
RVYTPSTSLRDEYLIPKNALLCGRATGHHTTTPGPLSEGSERF"
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SYTRARGAEVSKERIVSDGLKEKCEFFEBERE IBEKTMIKREKVEPKIKQEDTATAA
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NGRSLEFLAIONSNNKTSPPCSSSDSTTVSLIMSSNRGSSEKNRNGFATVFTRSRNS
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ESQRAXLFYULRDVLSAATRLNIVGPMGASVMQHRIAIVTETVLEKWNNREAGEACQ
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COMPLEMENT ( JOIN (13586 . . 13828, 13930 . . 14008, 14146 . . 14511,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(13586. .13828,13930. .14008,14146. .14511,
14642. .14984,15072. .15171,15388. .15658,15975. .16084,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MEVKSVNTTAMILGLFFLISFVAAEDPYKFFEWHVTYGNISPLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(16811. 17014,17112. 17190,17407. 17772, 18036. 18378,18463. 18562,18737. 19007,19646. 19755,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16170. .16313))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KHSSSSPIISLPKIFALSSLLSRLDLRHRKFHPSSDLDVSTSQEGTVFL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESTs gb/T21171 and
                                                                                                                                                                                          EST gb|AA586241"
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                                                                                                                                                            complement(7212. .7601)
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CDS

CDS

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Eutheria: Primates; Catarrhini; Hominidae; Homo. AUTHORS Ricke, D.O., Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Goodwin, L., Bryant, J., Tesmer, J., Chasteen, L., Thompson, S., White, S., Ueng, S., Tatum, O., Campbell, C., Fawcett, J., Maitble, M., Maitble, M., and Deaven, L., Campbell, C., Fawcett, J., Maitble, M., and Deaven, D., De	AL RS	JOURNAL Unpublished REFERENCE 3 (bases 1 to 86130) AUTHORS Ricke, D.O., Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., RODINGON, D., Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L., Bryant, J., Tesmer, J., Maincke, L., Longmire, J., White, S., Ueng, S., Tatum, O., Campbell, C., Fawcett, J., Maltble, M.,	Misra,M. and Deaven,L. TITLE Direct Submission JOURNAL Submitted (01-AUG-1998) Center for Human Genome Studies, DOE Joint Genome Institute, Los Alamos National Laboratory, MS M888, Los Alamos, NM 87545, USA	FEATURES Location/Qualifiers Source 186130 /organism="Homo sapiens"	/db_xref="taxon:9606" /clone="79-2A" misc_feature 2000. 2142 //nrte="fpat: 2 evrellent evon frame 2"	repeat_region 9717. 10001 /rpt_family="Alu"	repear_region 1094210303 /note="(T)22" /rpt_type=tandem	c	аше			/rpt_family="MER33" repeat_region complement(18481874) reneat_region 10/Rz 10.773		/rpt_type=tandem /rpt_unit=A repeat_region 2030720329 /note="[T]23"	/rpt_type=tandem /rpt_unit=T misc_feature 20836. 21048	.22428)	/rpt_ramily="Alu" repeat_region 2756827837 /rpt_family="Alu"

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(bases 1 to 97906)
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LOCUS HSJ1112h6 1
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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ACCESSION AL109912
ACCESSION AL109912
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Gaps: 0
Percent Identity: 58.333
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complement(72760. .72985)
/rpt_family="MER46"
complement(73181. .73243)
/rpt_family="MIR"
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complement(63604. .63875)
/rpt_family="Alu"
                                                                           complement(63894. .64098)
/rpt_family="MER1"
64463. .64588
                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(69213. .69456)
/rpt_family="Alu"
70077. .70906
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rpt_family="Alu"
4601. .74899
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71602. .7201
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/rpt_family="L1"
75843. .76122
/rpt_family="Alu"
/6105. .7614
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/2758. .7207
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57741. .68036
/rpt_family="Alu"
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4915. .75035
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76635. .76655
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/rpt_unit=A
76163. .76652
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US-08-653-294-16 x AC005365
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Ratio:
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Direct Submission

Submitted (10-SEP-1999) Wellcome Trust Genome Campus, Hinxton,
Cambridgeshire, CB10 15A, UK. E-mail enquires:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Sep 12, 1999 this sequence version replaced gi:5777438.
IMPORTANT: This sequence version replaced gi:5777438.
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of segments is not known; 800 n's separate
segments. Unfinished: dJ1141E20 Contig_ID: 00340 acc-AL109912
Length: 64235 bp Unfinished: dJ1141E20 Contig_ID: 00679
acc-AL109912 Length: 13869 bp Unfinished: dJ1141E20 Contig_ID:
00679. acc-AL109912 Length: 13869 bp Unfinished: dJ1141E20 Contig_ID:
00679. acc-AL109912 Length: 13202 bp.
* NOTE: This is a 'working draft' sequence
* as soon as it is available and the accession number will
* be preserved:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (09-SEP-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clonerequest@sanger.ac.uk clonerequest@sanger.ac.uk clones.com com Sep 6, 1999 this sequence version replaced gi:5791529.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with the following abbreviations are used to associate primary accession
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryoia; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 135305)
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Gaps: 0
Percent Identity: 58.333
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18298 c 18016 g 29795 t
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/db_xref="taxon:9606"
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1. .97906
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Human DNA sequence from
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HTG; CpG Island.
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/clone="RP11-7024"
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US-08-653-294-16 x AC013772/rev
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                                                                   TITLE
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                                                                                                                                                     COMMENT
numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_legans/wormpep This sequence is
the entire insert of clone 1112D6. This sequence has been finished
according to sequence map criteria as follows. An attempt is made
to resolve all sequencing problems, such as compressions and
repeats, but not necessarily within known annotated human repeat
sequence elements (e.g. Alu). Where the sequence is ambiguous,
there is an annotation using the 'unsure' feature key.
This sequence was generated from part of bacterial clone contigs of
human chromosome 6, constructed by the Sanger Centre Chromosome 6
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6
1112D6 is from the library RPCI-5 constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong. For further
cancer Institute by the group of Pieter de Jong. For further
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS AC013772 142796 bp DNA HTG 09-DEC-1999
DEFINITION Homo sapiens clone RP11-7024, WORKING DRAFT SEQUENCE, 6 unordered
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 142796)
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Percent Identity: 58.333
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/clone="RP5-1112D6"
26002 c 26091 g 42041 t
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/db_xref="taxon:9606"
/chromosome="6"
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AC013772.2 GI:6553994
HTG: HTGS_PHASE1; HTGS_DRAFT.
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1. .135305
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TITLE
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REFERENCE
AUTHORS
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KEYWORDS
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Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

Subract Subhission

Submitted (15.00v-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Dec 10, 1999 this sequence version replaced gi:6425750.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatWasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 138000; agarose-fp
Insert size: 142796; sum-of-contigs
Quality coverage: 5.7 in 020 bases; agarose-fp
Quality coverage: 5.5 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vectors. M13, M77815; 100% of reads Sequenciaty: Dye-terminator B19 Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 126649 bases at least 040 Consensus quality: 137112 bases at least 020 Consensus quality: 140758 bases at least 020
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4834: contig of 2692 bp in length
gap of unknown length
gap of unknown length
9211: contig of 4377 bp in length
gap of unknown length
25157: contig of 15946 bp in length
gap of unknown length
gap of unknown length
contig of 15946 bp in length
66208: contig of 41051 bp in length
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/db_xref="taxon:9606"
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1. .142796
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cDNA library; nitrogen deprivation
                                  Botryotinia fuckeliana.
Botryotinia fuckeliana
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Glas,A.M., Nottenburg,C. and Milner,E.C.B.
Direct Submission
Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
1000 Seneca Street, Seattle, WA 98101, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /map="14q32-q33"
/note="CD19+ peripheral blood B cells obtained from a bone
marrow transplant recipient 1 year post transplant; clone
59 in reference 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="immunoglobulin heavy chain variable region"
/protein_id="AAC51049.1"
//db_xref="G1:1791111"
//tb_xref="G1:1791111"
//tb_xref="G1:1791111"
//tb_xref="G1:1791111"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 375)
Glas,A.M., Nottenburg,C. and Milner,E.C.
Analysis of rearranged immunoglobulin heavy chain variable region genes obtained from a bone marrow transplant (BMT) recipient
Clin. Exp. Immunol. 107 (2), 372-380 (1997)
                            HSU80134 375 bp DNA PRI 19-FEB-1997
Human immunoglobulin heavy chain variable region (V4-34) gene,
partial cds.
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Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation.
ALL15310 GI:5829929
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Percent Identity: 58.333
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/db_xref="taxon:9606"
/cell_type="CD19+ B cells"
/tissue_type="peripheral blood"
/clone="312a3"
/chromosome="14"
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/note="Ig VH4 heavy chain"
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/gene="V4-34"
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US-08-653-294-16 x HSU80134
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                            seq_documentation_block:
LOCUS HSU80134
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Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage: CP 5706 91057 EVRZ cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
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The CDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal
Eukaryota; Fungl: Ascomycota; Euascomycetes; Discomycetes; Leotiales; Sclerotinaceae; Botryotinia.

1 (bases 1 to 650)
Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.
Direct Submission
Submitted (01-SP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
2 (bases 1 to 710)
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LOCUS CNS01CBB 710 bp mRNA PLN 02-SEP-1999
DEFINITION BOLTYLIS cinerea strain T4 cDNA library under conditions of nitrogen deprivation.
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AL5311
AL5311
G1:5829930
CDNA library, introgen deprivation.
Botryotinia fuckeliana.
Botryotinia fuckeliana.
Botryotinia fuckeliana
Eukaryota; Fundi, Ascomycota; Euascomycetes; Discomycetes;
Leotiales; Sclerotiniaceae; Botryotinia.
I (bases 1 to 710)
Bitton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Genoscope sequence ID : W60E121"
121 c 169 g 167 t
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Gaps: 0
Percent Identity: 50.000
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/db_xref="taxon:40559"
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US-08-653-294-16 x CNSOICBA/rev
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Percent Similarity: 100.000
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situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
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Lurgens, G.N., Glokner, F.O., Saano, A., Amann, R. and Munster, U. Freshwater Archaeal diversity and FISH in boreal forest lake in Finland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea; Euryarchaeota; unclassified Euryarchaeota; environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="From surface water of freshwater Finnish forest lake Valkea Kotinen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 .865
/organism="uncultured euryarchaeote VAL147"
/db xref="taxon:85395"
/clone="VAL147"
                                                                                  /organism="Botryotinia fuckeliana"
/strain="r4"
/db_xref="taxon:40559"
/note="Genoscope sequence ID : W60E122"
135 c 178 g 181 t 1 others
                                                                                                                                                                                                                                                                                                                                                                               to: 710
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Ratio: 3.417 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 50.000
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Percent Identity: 50.000
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/product="16S ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                               from: 1
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AJ131275.1 GI:3955079
AJ131275.1 GI:3955079
I6S ribosomal RNA: 16S rRNA gene.
uncultured euryarchaeote VAL147.
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178 c 271
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US-08-653-294-16 x CNS01CBB/rev
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Jurgens, G.N.
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Percent Similarity: 100.000
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AUTHORS
TITLE
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uncultured archaeon BURTON20_A.
uncultured archaeon BURTON20_A
Archaea; Buryarchaeota; Thermoplasmales; environmental samples.
[ (bases 1 to 910)
Bowman, J.P., McCammon, S.A. and McMeekin, T.A.
Diversity and community structure of Antarctic maritime lake and flord benthic zones
                                                                                                                                                                                                                                                                                       LOCUS AF142982 910 bp DNA BCT 06-JUL-1999
DEFINITION Uncultured archaeon BURTON20_A 16S ribosomal RNA gene, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="uncultured archaeon BURTON20_A"
/db_xref="taxon:97847"
/clone="BURTON20_A"
                                                                         to: 865
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Gaps: 0
Percent Identity: 50.000
                                                                      Align seg 1/1 to reverse of: UEU131275 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <1. .>910
/product="16s ribosomal RNA"
185 c 287 g 204 t
                                                                                                                                               229 TACAACCTGATAGTCCGCAGACTCATCCTAAGGCAC 194
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AF142982.1 GI:5359964
alignment_block:
US-08-653-294-16 x UEU131275/rev
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US-08-653-294-16 x AF142982/rev
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Ratio: 3.417
Percent Similarity: 100.000
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LOCUS AF142982
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Streptococcus pneumoniae gen
Sequence for a synthetic la
1941 HIV envelope protein c
Synthetic p41 gene with p12
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For sequences, used as insecticides also in inducible gene therapy systems and for recombinant protein production

Example 2: Fig 4: 50pp: English.

This nucleotide sequence has an open reading frame (ORF) that codes from third instart. Cuprina larvae and converted to converted from third instart. L. outsina larvae and converted to converted from third instart. L. outsina larvae and converted to converted from third instart. L. outsina larvae and converted to convert by the fragment was isolated from third instart. See V60307-09) based on conserved DNA and how to design further primers (see V60307-08) for 3'-RACE to produce a containing the complete ORF. Also claimed are peptides containing the complete ORF. Also claimed are peptides containing the containing the complete of the A/B, C, D, E or F (especially C or E) domains of the edysteroid receptor, nucleic acid encoding them, expression vectors, an inducible expression system, ligands able to bind the receptor or its peptides, and a vector encoding antisense RNA.

The edysteroid receptor, or its C or E domains, vectors ontaining antisense sequences, and vectors in which a gene encoding the edysteroid receptor is inactivated are used as insecticides, particularly against files and specifically. L. cuprima (Australian blowfly, a vector of human and animal diseases)

C particularly used in baits for adult files. Also contemplated is germine transformation of files using a transposon encoding the receptor or its C or E domains. Host cells are used to produce recombinant receptor, and inducible expression systems are used for steroid-responsive expression of other genes, e.g. in gene therapy (where expression will be induced by administration of insect steroid-responsive expression of other genes. e.g. in gene encodin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Lucilia cuprina ecdysteroid receptor, its fragments and related
                                                                                                                                                                                                                                                             0.2-FEB-1999 (first entry)
Lucilia cuprina ecdysteroid receptor cDNA.
Ecdysteroid receptor; insecticide; biological control;
gode therapy; Australian blowfly; ds.
Lucilia cuprina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 2812
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Gaps: 0
Percent Identity: 72.727
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16-FEB-1998; NZ0018.
14-FEB-1997; NZ-314239.
(NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD.
(NZWO-) NEW ZEALAND WOOL BOARD.
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US-08-653-294-16 x V60302/rev
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WPI; 98-520754/44.
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Ratio:
N_Geneseq_36:X30865
N_Geneseq_36:Q55183
N_Geneseq_36:Q62660
N_Geneseq_36:N90797
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2812 : Lucilia cuppina ecdysteroid re
119 : Human gene signature HUMGS00405
1332 : Enterococcus faecalis genome c
2966 : Human secreted protein gene 3
2379 : Sequence encoding protein L. N
3279 : Sequence encoding protein L. N
3279 : Sequence encoding protein L. N
5892 : BRCA2 cancer susceptibility ge
7240 : Partial BRCA2 cancer susceptibility ge
7240 : Partial BRCA2 cancer susceptibility ge
7240 : Partial BRCA2 (omi2) encoding
7240 : Ruman BRCA2 (omi2) encoding
7248 : Human BRCA2 (omi1) encoding
7248 : Human BRCA2 (omi1) encoding
7248 : Human BRCA2 (omi1) encoding
7249 : Human breast and ovarian can
7251 : Est clone AQ2 . New polynucleoti
7262 : N meningitidis strain M990 L
7262 : N meningitidis strain M990 L
7262 : N meningitidis strain M990 L
7262 : N meningitidis seaurls gene. Ne
7240 : Aureobasidin sensitivity gene
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BARI barrier protease gene. Pu
Recombinant heat-resistant tre
Drosophila para voltage-activa
Calcium permeable voltage sens
| Total base sequence of rice
| Oyster derived CDNA encoding E
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Sequence of BAR 1 gene contg.
Nucleotide sequence of the S.
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                                                                                                                                                                                                        software, version 4.5,
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  OM of: US-08-653-294-16 to: N_Geneseq_36:*
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102.43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 590.520000
                                                       Date: Feb 8, 2000 1:28 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search information block:
Query: US-08-653-294-16
Query length: 12
                                                                                                                                                                                  Command line parameters:
                                                                                                        About: Results were
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N_Geneseq_36:V52245
N_Geneseq_36:Q79140
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_Geneseq_36:Q50946
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N_Geneseq_36:V74278
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_Geneseq_36:T79680
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N_Geneseq_36:Q04525
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N_Geneseq_36:X30742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genesed_36:T09355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N_Geneseq_36:V82467
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N_Geneseq_36:X30257
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N_Geneseq_36
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Sequence
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HUMA-) HUMAN GENOME SCI INC.

Barash Sc, Dillon PJ, Kunsch CA;

WHP1: 99-045111/04.

WHP1: 99-045111/04.

Why: 99-04511/04.

Why: 99-041/04.

Why: 99-041/04.

Why: 99-041/04.

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Why: 99-04
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Human secreted protein gene 30 clone HTLAB25.

Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foctal deficiency; blood; allergy; renal; immune system; asthms; lymphocytic disease; brain; hepatic; lymphoma; inflammation; isothemia; shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 12
Gaps: 0
Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           801 TATCGTATTATATGAAGAAAATACTTATTAAGGTAT 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: X13394 from: 1 to: 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID X04340 standard; DNA; 1966 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  479 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: N_Geneseq_36:X04340
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US-049608.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1332 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUN-1998; U12125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
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13-JUN-1997; 1
13-JUN-1997; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 372; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp.

double-stranded DNA) which comprises one of the 7837 "GS" sequences
given in T19001-T26837 and which is able to hybridise to part of
human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
sequences were obtained from 3'-directed CDNA libraries prepared
from various human tissues; synthesis of cDNA was initiated from the
3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
untranslated sequence is unique to a particular mRNA species,
all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
is constructed so as to reflect accurately the relative abundance of
different mRNAs in the particular tissue from which it was derived.
The appearance frequency of a given GS in a cDNA library can be
determined (esp. using primers and probes derived from the GS
sequences) as a means of diagnosing abnormal cell function or for
recognising different cell types.
Sequence 119 BP; 37 A; 34 C; 24 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                T19381;
04-JUL-1996 (first entry)
Human gene signature HUMG500405.
Gene signature; messenger RNA; mRNA; relative abundance; frequency human; cloning; mapping; non-biased library; diagnosis; detection; human; cloning; abnormal cell function; ss.
Homo sapiens.
WOOSTLATA2-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis genome contig SEQ ID NO:457.

Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.

Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 11
Gaps: 0
Percent Identity: 72.727
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            76 AGGITACIICIGAGGAGGAIICIICIAACAIII 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ArgLeuLeuIleArgArglleLeuLeuArgTyr 12
                                                                                                                                                          I19381 standard; cDNA to mRNA; 119 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
11D X13394 standard; DNA; 1332 BP.
AC X13394;
DT 19-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-08-653-294-16 x T19381/rev
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3.800
90.909
                                                                  seq_name: N_Geneseq_36:T19381
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                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matsubara K, Okubo K;
WPI; 95-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-NOV-1998.
04-MAY-1998; U08985.
14-NOV-1997; US-066009.
06-MAY-1997; US-044031.
                                                                                                                               seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (OKUB/) OKUBO K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9850555-A2.
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227 G;

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Disclosure: Figure 1: 28pp; English.

Disclosure: Figure 1: 28pp; English.

Lomprise repeated sequences from protein L which bind

Lomprise repeated sequences from protein L which bind

Lomprise repeated sequences from protein L which bind

Immunoglobulin Kappa 1ight chains. They can be used in protein

analysis, purification procedures and other biochemical processes e.

9. ELISA. The synthetic molecules are of particular advantage if

they are free of regions in protein L which exhibit albumin and cell

wall binding (The repeat regions commencing at nucleotide numbers 1045, 1261, 1483 and 1705).

Sequence 3279 BP; 1505 A; 481 C; 625 G; 668 T;
                                                        /*tag= c
/note= "Repeat units are not adjacent, repetitions
of this sequence are not 100% homologous and
begin at nucleotide position 757"
                                                                                                                                                                                                                                                  1045. .1158
//tag= e
/note= "Repeat units are not adjacent, repetitions
of this sequence are not 100% homologous and
begin at nucleotide positions 1261, 1483
                                                                                                                                                     /*tag- d
/note- "Repeat units are not adjacent, repetitions
of this sequence are not 100% homologous and
begin at nucleotide positions 1162, 1375
and 1597"
                                                                                                                                                                                                                                                                                                                                                                                                          /note- "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 2347, 2545 and 2731"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New immunoglobulin binding proteins derived from Protein {\tt L} -which bind immunoglobulin kappa light chains but not albumin or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= g
/note= "Repeat units are adjacent, repetitions
of this sequence are not 100% homologous and
begin at nucleotide positions 2935, 2953,
2968, 2986, 3001, 3019 and 3034"
of this sequence are not 100% homologous and begin at nucleotide positions 673 and 856" 574. .672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: Q50946 from: 1 to: 3279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trowern AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TyrArgLeuLeuIleArgArgIleLeuLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-NOV-1993

07-MAY-1993; G00950.

07-MAY-1992; GB-009804.

24-DEC-1992; GB-026928.

(PUBL-) PUBLIC HEALTH LAB SERVICE BOARD.

Atkinson A. Duggleby CJ, Murphy JP, Tro-

WPI: 93-368798/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID Q51556 standard; cDNA; 3279
                                                                                                                                                                                                                                                                                                                                                                         1822. .1938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-16 x Q50946/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouality: 38.00
Ratio: 3.167
Percent Similarity: 100.000
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                                          repeat_unit
                                                                                                                                       repeat_unit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_unit
                                                                                                                                                                                                                                                                                                                                                                           repeat_unit
    New isolated human genes and the secreted polypeptides they encode -

"Seful for diagnosis and treatment of e.g. cancers, neurological

"Gasorders, immune diseases, inflammation or blood disorders

"Inflammation or blood disorders

"Claim 1; Page 195-196; 380pp; English.

"This sequence represents a nucleic acid molecule which encodes a secreted

"This sequence represents a nucleic acid molecule which encodes a secreted

"This sequence represents a nucleic acid molecule which encodes a secreted

"This sequence represents a nucleic acid molecule which encodes a secreted

"This sequence represents to the gene to a human immunoglobulin Fc portion

"The invention relates to 86 novel genes and their fragments (nucleic acid

"The invention relates to 86 novel genes and their fragments (nucleic acid

"Sequences: X04311-X04410; amino acid sequences W78126-W78225) which

"The invention relates to 86 novel genes and their fragments (nucleic acid

"Sequences: X04311-X04410; amino acid sequences W78126-W78225) which

"The invention of gene therapy. Also, pathological conditions

"The invention of gene therapy. Also, pathological conditions are useful for preventing, treating or ameliocating medical conditions

"The invention of gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Based on which tissues are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed in (see X04311 for described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag* b
/note= "Repeat units are not adjacent, repetitions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q50946;
18-MAY-1994 (first entry)
Sequence encoding protein L.
Peptide; immunoglobulin; binding; analysis; purification; ELISA;
enzyme linked immunoabsorbant assay; ss.
                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
Brewer LA, Ebner R, Ferrie AM, Feng P, Greene JM, Lafleur DW,
Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Young P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 1966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 0
Percent Identity: 72.727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  584 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: X04340 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ArgLeuLeulleArgArglleLeuLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  545 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a /product= Protein L. 490. .573 /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
103. .3185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID Q50946 standard; cDNA; 3279 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                440 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-16 x X04340/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.800
90.909
                                                    12-SEP-1997; US-058668.
12-SEP-1997; US-058669.
12-SEP-1997; US-058697.
12-SEP-1997; US-058972.
12-SEP-1997; US-058975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: N_Geneseq_36:Q50946
                                                                                                                                                                       02-OCT-1997; US-060834.
02-OCT-1997; US-060841.
02-OCT-1997; US-060844.
02-OCT-1997; US-060865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 1966 BP;
                                                                                                                                                                                                                                                                                                                                                   WPI; 99-080881/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptococcus magnus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; W78155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uses).
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It

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alignment_scores:
                                                                                                                                                                                                                                                   8000
                                                                                                                               /note- "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 673 and 856"
                                                                                                                                                                               /*tag= c
/note= "Repeat units are not adjacent, repetitions
of this sequence are not 100% homologous and
begin at nucleotide position 757"
/*tag= d
                                                                                                                                                                                                                                              /note- "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 1162, 1375 and 1597"
                                                                                                                                                                                                                                                                                                         /*tag= e
//note= "Repeat units are not adjacent, repetitions
of this sequence are not 100% homologous and
begin at nucleotide positions 1261, 1483
and 1705"
                                                                                                                                                                                                                                                                                                                                                            1822. .1938
//tag- f
//otbe= "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 2347 and 2545"
1939. .2007
                                                                                                                                                                                                                                                                                                                                                                                                                                       /note- "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 2479, 2665 and 2851"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag- h
/note= "Repeat units are not adjacent, repetitions
of this sequence are not 100% homologous and
begin at nucleotide position 2209"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repetitions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin binding polypeptide, protein L - used for prodn. of pharmaceuticals and for immobilising antibodies e.g. on columns, in diagnostic tests and in assays bisclosure; Figure 1; 29pp; English. Protein L forms a complex with immunoglobulin Kappa light chain. Purified protein can be used as a reagent for immobilising
         18-MAY-1994 (first entry)
Sequence encoding protein L.
Protein; immunoglobulin; binding; immobilisation; light chains; antibodies; diagnosis; pharmaceutical; ss.
Peptococcus magnus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Repeat units are adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 2935, 2953, 2968, 2986, 3001, 3019 and 3034"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               force "Repeat units are not adjacent, repet. of this sequence are not 100% homologous and begin at nucleotide positions 2269"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-NOV-1993: 000949. 07-MAY-1993: G00949. 07-MAY-1992; GB-009804. (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD. 47-Kinson A. Duggleby CJ. Murphy JP. Trowern AR; P-PSDB: R436997/46.
                                                                                                  'product- Protein L.
                                                                 Location/Qualifiers 103. .3185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 2094
                                                                                                                                                                                                                                                                                            1045. .1158
                                                                                                            490. .573
/*tag= b
                                                                                      /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
Q51556;
18-MAY-1994
                                                                                                              repeat_unit
                                                                                                                                                                   repeat_unit
                                                                                                                                                                                                                            repeat_unit
                                                                                                                                                                                                                                                                                              repeat_unit
                                                                                                                                                                                                                                                                                                                                                               repeat_unit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9322438-A
                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_unit
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PT New isolated plant glycosyltransferase nucleic acids - used to transform plants to alter the properties or composition of cell walls, e.g. for modifying foodstuffs or wood pulp products Claim 8: Fig 1A-C; 66pp; English.

CC This is the nucleotide sequence of clone gt16, which encodes a convel glycosyltransferase (see W90188) of Arabidopsis thallana.

CC novel glycosyltransferase pendentified i.e. gt11 (gma twelve-like and 5 different genes were identified, i.e. gt11 (gma twelve-like constitution obtain the full-length clone. The predicted truncated truncated protein, and 5/RACE was performed using RNA from A. thaliana callus cells to obtain the full-length clone. The predicted protein has the characteristics of a Golgi glycosyltransferase, i.e. a short cytosolic N-terminus, single transmembrane domain, and a larger cytosolic N-terminal domain with conserved cysteines. The plant cytosyltransferases of the invention (see W90188-94) can catalyse cone or more steps in the blosynthasis of complex non-cellulosic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plant cell wall polysaccharides. They may also catalyse the glycosylation of plant cell wall protein and/or the transfer of saccharide moteties from nucleotide sugar precursors to oligosaccharide precursors. Nucleic acids encoding the glycosyltransferases can be used to transform plants to alter the properties or composition of the cell wall. The plants produced can be used in the preparation of e.g. food or wood pulp products
antibodies e.g. on columns, in diagnostic tests and in assays. may also be used in the production of pharmaceuticals. Sequence 3279 BP; 1505 A; 480~\rm C; 626~\rm G; 668~\rm T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; W90188.
New isolated plant glycosyltransferase nucleic acids - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis Golgi glycosýltransferase clone gtl6.
Glycosyltransferase; Golgi, gtl6 gene; transgenic plant;
glycosylation; plant cell wall; paper; pulp; food; ss.
Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: Q51556 from: 1 to: 3279
                                                                                                                                                                                                                             Length: 12
Gaps: 0
Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2746 TITGCCTGGTTTTTCAGCGTGTGCTTTTAAGATT 2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TyrArgLeuLeulleArgArglleLeuLeuArgTyr 12 :::||||||||||:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-1997; GB-013852.
(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
Dupree P. Mogelsvang S;
WPI; 99-106058/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
100.1449
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V74278 standard; cDNA; 1564 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        per or cardboard
1564 BP; 474
                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-16 x Q51556/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: N_Geneseq_36:V74278
                                                                                                                                                                                                                                                                      Ratio: 3.167
Percent Similarity: 100.000
                                                                                                                                                                                                                                 38.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-1998; G01911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                 Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            such as paper
                                                                                                                                                                                            alignment_scores:
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10

Length:

37.00

Quality:

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BRCA2 cancer susceptibility gene exon 11 and intron boundaries. RCA2 cancer susceptibility gene; breast cancer; ovarian cancer; gene therapy; prostate cancer; colorectal cancer; ocular melanoma; leukaemia; human; ss.
                                                                                                                                                                                                                 5413. .5892
/*tag= c
                                                                                                                                                                                   /*tag= b
/number= 11
                                                                                                                    ៧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.00
3.700
90.909
                                                                                                 1. .480
/*tag=
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                                                                                                                                                                                                                                                                                                                                    28-AUG-1996; GB-017961.
23-NOV-1995; GB-023959.
14-DEC-1995; GB-025555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: T79680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-16 x T79680
                                                                                                                                                                                                                                                                                                    28-MAY-1997.
25-NOV-1996; 024453
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Quality:
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                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Align seg 1/1
                                                                                                 intron
                                                                                                                                                                                                                    intron
                                                                                                                                                                     exon
 Claim 1: Page 813-816; 2084pp; English.

A computer readable medium has been developed which has recorded on it
Computer readable medium has been developed which has recorded on it
X12938 to X13919 represent these nucleotide sequences which are primary
nucleotide sequences; also known as contigs. The computer-based system
can identify fragments of the Enterococcus faecalis genome with
commercial importance. The products can be used to detect the presence
of Enterococcus faecalis in samples. They can also be used for
configuration of disease, and for identifying agents which can be used to
modulate the growth or pathogenicity of Enterococcus faecalis, or
conclusted organism, in vivo or in vitro. In particular the
polypeptides encoded by the Enterococcus faecalis nucleotide sequences
can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI: 99-045171/04.

New isolated Enterococcus faecalis polynucleotides and polypeptides

- used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                   Enterococcus faecalis genome contig SEQ ID NO:137.
Enterococcus faecalis; contig; detection; Enterococcal infection;
vaccine; attenuation; computer readable medium; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1041 G;
 Gaps: 0
Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: X13074 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TyrArgLeuLeulleArgArglleLeuLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80e C;
                                                                                                 Align seg 1/1 to: V74278 from: 1 to: 1564
                                                                                                                               04-MAY-1998; U08985.
14-NOV-1997; US-066009.
06-MAY-1997; US-044031.
16-MAY-1997; US-046655.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC. Dillon PJ, Kunsch CA;
                                                                                                                                                                                                                               seq_documentation_block:
ID X13074 standard; DNA; 5550 BP.
AC X13074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1940 A;
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T79680 standard; DNA; 5892
T79680;
                                                                                                                                                                                                                                                                                     19-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.00
3.364
91.667
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US-08-653-294-16 x X13074/rev
Ratio: 3.700
Percent Similarity: 100.000
                                                                                                                                                                                                 seq_name: N_Geneseq_36:X13074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: N_Geneseq_36:T79680
                                                                                                                                                                                                                                                                                                                                                       Enterococcus faecalis. WO9850555-A2.
                                               alignment_block:
US-08-653-294-16 x V74278
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                 12-NOV-1998.
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DA E

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RANCECTIONS, GB-02555.

PA (CANCE) 1987, GB-02555.

A (UTDU-) UNIV DUKE.

PASH STATE OF THE STAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide, which can be used as cancer therapeutics. Sequence 5892 BP; 2146 A; 967 C; 1046 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dercent Identity: 54.545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /number= 11
/note= "Start of intron 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /number- 10
/note= "End of intron 10"
481. .5412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ArgLeuLeulleArgArglleLeuLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1 to: 5892
Location/Qualifiers
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The unchase

Claim 1; page 814-819; 1409pp; English.

The present invention describes a computer readable medium which has

The present invention describes a computer readable medium which has

the nucleotide sequences SEO ID No:1 to 391 (V52134 to V52524) recorded

on it, or a representative fragment or a sequence at jeast 95% identical

to SEO ID No: 1 to 391. The nucleotide sequences depicted in SEO ID No:1

to 391 (V52134 to V52524) are genomic fragments from Streptococcus

pneumoniae. The present invention also describes an isolated nucleic acid

molecule encoding a homologue of any of the fragments of the Spneumoniae

comprising; (a) screening a genomic DNA library using as a

probe a target sequence defined by any of the sequences in SEO ID No:1

to 391, identifying members of the library which contain sequences

that hybridise to the target sequence and isolating the nucleic acid

molecules from the members; or (b) isolating mRNA, DNA or CDNA produced

from an organism, amplifying nucleic acid molecules whose nucleotide

sequence is homologous to amplification primers derived from the

sequence is homologous to amplification primers derived from the

isolating the amplified sequences. The computer readable medium can be

sequence of commercial importance, or expression modulating

fragment of the sequences or expression modulating

fragments of the sequences or expression modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fragments of the S. pneumoniae genome. Products from the present
invention can be used in diagnosis kits and assays, and pharmaceutical
compositions and vaccines for S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                             Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                                   Streptococcus pneumoniae genome fragment SEQ ID No:112.
Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
computer readable medium; vaccine; pharmaceutical composition; ds.
                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Chol GH, Dillon PJ, Dougherty BA, Fannon
Kunsch CA, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              079140 standard; cDNA; 9487 BP. 079140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2482 A;
                                 entry)
                                                                                                                                               Streptococcus pneumoniae WO9818931-A2.
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                                                                                                                                                                                                                                  30-OCT-1997; U19588.
31-OCT-1996; US-029960.
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                              (first
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                                                                                                                                                                                                                                                                                                                                                                                       WPI; 98-272225/24.
                                                                                                                                                                                                         07-MAY-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                              23-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
Cancer susceptibility gene. The nucleic acid molecule can be used to construct probes for screening cDNA or genomic libraries, sequencing construct probes for screening cDNA or genomic libraries, sequencing construct probes for screening cDNA or genomic libraries, sequencing construct probes for screening cDNA or genomic libraries, sequencing construct probes for screening cDNA or genomic libraries, sequencing construct probes for caid molecules and proteins are useful in a method of medical treatment, preferably gene therapy, especially for treating cancer, where the cancer is female or male breast cancer, ovarian, prostate or colorectal cancer, ocular melanoma or latekaemia. In particular antisense oligonucleotides capable of bybridising to the BRCA2 nucleic acid, pre-mRNA or mature mRNA are used to that the expression of the BRCA2 nucleic acid is reduced or prevented. The nucleic acid molecules are also useful in a method for nucleic acid molecules are used to design probes or primers for PCR to determine or detect the presence of mutations in a sample of nucleic caid molecules are used to design probes or primers for PCR to determine or detect the BRCA2 promoter region is useful for screening for substances which modulate the expression of nucleic acid under control of the promoter. Antibodies are used to determine the presence of mutations or properties are used to screen for binding partners, these are used to screen for binding partners, these are used to screen for binding partners, these are used to substances which mimic the activity of BRCA2 customer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; W25038.
Nucleic acid molecules comprising part or all of the BRCA2 cancer
susceptibility gene - useful for diagnosis, prognosis or therapeutic
                                                                                                                 Partial BRCA2 cancer susceptibility gene. RECA2 cancer susceptibility gene; breast cancer; ovarian cancer; gene therapy; prostate cancer; colorectal cancer; ocular melanoma; leukeemia; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1995 T;
                                                                                                                                                                                                                                                                                                                                                   /product= BRCA2_fragment
/transl_except= (pos:3800. .3801,aa:Glu)
/transl_except= (pos:3802. .3803,aa:Lys)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        can be used as cancer therapeutics. 2735 A; 1188 C; 1322 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ashworth A, Futreal PA, Stratton MR, Wooster RF; WPI; 97-261854/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.00 Length: 11
3.700 Gaps: 0
90.909 Percent Identity: 54.545
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28-AUG-1996; GB-011961.
23-NOV-1995; GB-023959.
14-DEC-1995; GB-025555.
(CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
(UVDU-) UNIV DUKE.
                                                                                                                                                                                                                                                                Location/Qualifiers
2. .6989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treatment of cancer
Claim 3; Fig 4; 124pp; English.
seq_documentation_block:
ID T79668 standard; cDNA; 7240 BP.
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                                                                                     02-FEB-1998 (first entry)
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US-08-653-294-16 x T79668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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Ratio:
                                                                                                                                                                                                                                        Homo sapiens.
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1634 G;

1307 C;

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aa:Glu
aa:Glu
aa:Ala
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Hepatitis C virus gene HC-G9 cDNA.
Hepatitis C virus; HCV; non-A non-B; HC-G9; treatment;
Hepatitis C virus.
Ouality: 37.00 Length: 10 Ratio: 3.700 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              342. .937
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/transl_except= pos:7950. .7952,
/transl_except= pos:7953. .7955,
                                                                                                                                              to: 7902
                                                                                                                                                                                                               1 TyrArgLeuLeuIleArgArgIleLeuLeu 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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seq_documentation_block:
ID V52245 standard; DNA; 7902 BP.

seq_name: N_Geneseq_36:V52245

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(ONCO-) ONCORMED INC
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     F 13-MAY-1993; 147133.
F 13-MAY-1994; 147133.
F 13-MAY-1995; 147133.
A (IMMO) IMMUNO JAPAN KK.
R PP-SDB; R67588.
T A hepatitis C virus gene and oligo-nucleotide(s) - used for the ratment of hepatitis C (Jaim 1: Pages 10-15; 41pp; Japanese.
Claim 1: Pages 10-15; 41pp; Japanese.
C (J79140 is the hepatitis C virus (HCV) gene HC-G9 cDNA, it encodes the protein described in R67588. Both the cDNA and protein can be used in the treatment of HCV infection
Sequence 9487 BP; 1905 A; 2798 C; 2687 G; 2097 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUN-1999 (first entry)

Human BRCA2 (omi2) encoding cDNA.

Human BRCA2; genetic testing; protein therapy; haplotype; detection; genet therapy; breast cancer; ovarian cancer; ds.

Homo sapiens.
                                                                     aa:Pro
aa:Pro
aa:His
aa:Ser
aa:Ala
                                                                                                                                                           aa:Arg
aa:Ser
aa:Lys
aa:Tyr
aa:Asp
aa:Val
aa:Val
aa:Lys
                                                                                                                                                                                                                                                                                                                      aa:Leu
aa:Pro
                                                                                                                                                                                                                                                                                                                                                           aa:Ile
                                                                                                                                                                                                                                                                                                                                                                           aa:Ala
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Gaps: 0
Percent Identity: 58.333
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                                                                                                                                                                                                                                                                                    .8006,
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                                                                                                                                                                                                                                                                   .8003,
                                                                                                                                                                                                                                                                                                                      .8012,
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   pos : 7956.
pos : 7959.
pos : 7965.
pos : 7968.
pos : 7974.
pos : 7977.
pos : 7980.
pos : 7980.
pos : 7980.
pos : 7980.
                                                                                                                                                                                                                                pos:7995.
pos:7998.
pos:8001.
pos:8004.
pos:8017.
pos:8010.
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pos:8019.
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229. .10485
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/transl_except=
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ID X30256 standard; cDNA; 10485 BP.
AC X30256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 37.00
Ratio: 3.700
Percent Similarity: 83.333
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US-08-653-294-16 x Q79140/rev
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14-AUG-1998; U16905.
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PT We coding sequence haplotypes of the human BRCA2 gene - used to develop products for determining susceptibility to, detection and treatment of breast or ovarian cancer and the products for determining susceptibility to, detection and treatment of breast or ovarian cancer.

The present invention describes genomic DNA which contains a BRCA2 gene where the first 12 nucleotides beginning exon 5 are 5'TCCTGTTGTTCT-3' as in sequence (I) (see X03249), where nucleotides numbers 5782-5790 are GTTGGTGT as in sequence (II) (see X03251), and where the isst 20 nucleotides encoding exon 15 are 5'-CTGGTGTTCTCARAACAG-3' as in sequence (II) (see X03251) and the first 20 nucleotides beginning exon 16 are 5'-CTGTARAGCTARGGGTTCT-3' as in sequence (III) (see X30253).

Products and methods from the present invention can be used for insequence intripying mutations in the BRCA2 gene leading to predisposition or higher susceptibility to breast or ovarian cancer. They can also be used in methods for monitoring disease progression, for determining be used in methods for monitoring disease progression, for determining between the presence or quantifying the amount of a tumour growth inhibitor following such therapy. The BRCA2 protein, polypeptides, their functional equivalents, antibodies, and PNS may also be useful in the study of the characteristics of BRCA2 proteins, such as structure and function of BRCA2 in oncogenesis or subcellular localisation of BRCA2 (omis).

Products in normal and cancerous cells. The present sequence encodes human BRCA2 (omis).
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Human BRCA2 (omi3) encoding cDNA.

Human BRCA2; genetic testing; protein therapy; haplotype; detection; agene therapy; breast cancer; ovarian cancer; ds.

Homo sapiens.
22-MAY-1998; US-084471.
15-MG-1997; US-055784.
07-NOV-1997; US-064926.
12-NOV-1997; US-065367.
01-MAY-1998; US-071715.
(ONCO-) ONCORMED INC.
ESKandari T, Jackson GM, Murphy PD, Olson SJ, Park M, Rablin MB, Schryer B, White MB, Yoshikawa M; WPI: 99-190163/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 11
Gaps: 0
Percent Identity: 54.545
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229. .10485
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID X30257 standard; cDNA; 10485 BP.
AC X30257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.00
3.700
90.909
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12-NOV-1997; US-065367
01-MAY-1998; US-071715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-16 x X30256
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14-AUG-1998; U16905.
22-MAY-1998; US-08447
15-AUG-1997; US-05578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
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PP-PSDB: Y04356.

PP-PSDB: Y04356.

PW coding sequence haplotypes of the human BRCA2 gene - used to develop products for determining susceptibility to, detection and treatment of breast or ovarian cancer.

PS Claim 13: Page 97-111; 226pp; English.

Claim 13: Page 97-111; 226pp; English.

Che present invention describes genomic DNA which contains a BRCA2 gene where the first 12 nucleotides beginning exon 5 are 5-TCCTGTTGTTGTT as 1n sequence (IV) (see X03249), where nucleotides numbers and where the first 20 nucleotides encoding exon 15 are 5-CTGCTGTTCTCATAAACAG-3' as in sequence (II) (see X03251) and the first 20 nucleotides beginning exon 15 are 5-CTGCTTTCTCATAAACAG-3' as in sequence (III) (see X03251) and the first 20 nucleotides beginning exon 16 are 5'CTGTATAGTAGTGTTGTTG-3' as in sequence (III) (see X03251) and the first 20 nucleotides beginning exon 16 are 5'CTGTATAGTAGTGTTGTTG-3' as in sequence (III) (see X0253).

Crompation and methods from the present invention can be used for identifying mutations in the BRCA2 gene leading to predisposition or confidentifying mutations in the BRCA2 gene leading to predisposition or for detection and gene therapy for breast and ovarian cancers. They can be used in methods for monitoring disease progression, for determining confeccing the presence or quantifying the amount of a tumour growth inhibitor following such therapy. The BRCA2 protein, polypeptides, their confinence or quantifying the amount of a tumour growth inhibitor all equivalents, antiboddes, and PNS may also be useful in the characteristics of BRCA2 proteins, such as structure and cunction of BRCA2 in oncogenesis or subcellular localisation of BRCA2 contains and contains and contains and concerns and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUN-1999 (first entry)
Human BRCA2 (om14) encoding cDNA.
Human BRCA2; genetic testing; protein therapy; haplotype; detection; gene therapy; breast cancer; ovarian cancer; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2870 T;
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Eskandari T, Jackson GM, Murphy PD, Olson SJ, Park M,
Rabin MB, Schryer B, White MB, Yoshikawa M;
WPI: 99-190163/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1965 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.00 Length: 11
3.700 Gaps: 0
90.909 Percent Identity: 54.545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1842 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: X30257 from: 1 to: 10485
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15-AUG-1997; US-055784.
07-NOV-1997; US-064926.
12-NOV-1997; US-065367.
01-MAY-1998; US-071715.
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numan BRCA2 (omi3).
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Claim 14; Page 119-133, 228pp; Begilsh.

The present invention describes genomic DNA which contains a BRCA2 gene where the first 12 nucleotides beginning exon 5 are 5'-TCCTGTTGTTCT-3' as in sequence (I) (see X03249), where nucleotides numbers 5782-5790 are GTTTGTTT as in sequence (IV) (see X30255), and where the last 20 nucleotides ancoding exon 15 are 5'-CTGTGTGTTCTGTAAACAG-3' as in sequence (II) (see X30251) and the first 20 nucleotides beginning exon 16 are 5'-CTGTATAGGTTTC-3' as in sequence (II) (see X30253).

Croducts and methods from the present invention can be used for identifying mutations in the BRCA2 gene leading to predisposition or higher susceptibility to breast or ovarian cancer. They can also be used for detection and gene thratapy for breast and ovarian cancers. They can be used in methods for monitoring disease progression, for determining patients suited for gene and protein replacement progression, or for detecting the presence or quantifying the amount of a tumour growth inhibitor following such therapy. The BRCA2 protein, polypeptides, their functional equivalents, antibodies, and PNS may also be useful in the study of the characteristics of BRCA2 proteins, such as structure and function of BRCA2 in oncogenesis or subcellular localisation of BRCA2 contains and sequence encodes buman BRCA2 (onl4).
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Gaps: 0
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treatment of breast or ovarian cancer
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US-08-653-294-16 x X30258
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A1927435 w075f12.x1 NCI_CGAP
AA591962 v150b07.r1 Beddingt
AQ632742 RPCI-11-475D13.TJ R
                                                                                                                                                                                                                                                                         Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis;
I (bases 1 to 300)
Kohara,Y., Shin 1,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H.,
Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A.,
Nomoto,H.
                                                                                                                seq_documentation_block:

LOCUS AV182651 300 bp mRNA EST 21-JUL-1999

DEFINITION AV182651 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans cDNA clone yk64097 3', mRNA sequence.

ACCESSION AV182651 GI:5562552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:6239"
/clone="yk64097"
/clone=lib="yuji Kohara unpublished cDNA:Strain N2
hermaphicodite embryo"
/sex="hermaphicodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi:3189500.
Contact: Yuji Kohara
Gene Library Lab
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Gaps: 0
Percent Identity: 66.667
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Location/Qualifiers
1. 300
/organism="caenorhabditis elegans"
  316
337
363
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Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
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AQ137850.1 GI:3528503
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US-08-653-294-16 x AV182651
                                                                             seq_name: gb_est36:AV182651
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gb_est36:AI927435
gb_est16:AA591962
gb_gss15:AQ632742
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A0311590 RPC111-1A13.TJ RPC1-11
A0311590 RPC111-1A13.TJ RPC1-11
A0311590 RPC111-1A13.TJ RPC1-11
A174609 EST255709 tomato resis
B70241 CTT-HSP-502812.TR CTT-H
A177548 EST255709 tomato resis
AN095409 EST285989 tomato mixed
A1162936 A0279320 Hybrid aspen
AV283447 AV283447 RIKEN full-1-6
A0097888 HS.3036 B2_A06_MF CIT-HSP-2013720 TRC CIT-HSP-201372
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AU006893 Schizosacchar
                                                                                                                                                       -MODEL-frame+_p2n.model -DEV-x1p
-Q-fcqn1_J/OSPTO_2001/OS08653294/runat_04022000_160700_15770/app_query.fasta.1
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-FGAPDP=6.000 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
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-LIST=45 -DOCALIGN=200 -THR_SCORE=PCt -ALIGN=15 -MODE=LOCAL
-OUTPWIT=pfs -NORM-ext -MINLEN=0 -MAXIEN=1000000 -USER=US08653294
-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1
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AA709270 a
AU006893 A
                                                                             About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Query length: 12
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 8553.360000
  OM of: US-08-653-294-16 to:
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                                      Date: Feb 8, 2000 4:03
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gb_gss11:AQ311590
gb_gss6:AQ869567
gb_est37:A1960153
gb_est33:A1774609
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gb_est24:Ai16206443
gb_est24:Ai161739
gb_est44:AN219466
gb_gss11:AQ328194
gb_gss11:AQ328194
gb_gss11:AQ328194
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9b_gss6.AQ835306
9b_est10:AA748739
9b_est20:AA748739
9b_est9.AA103036
9b_gss14:AQ569045
9b_gss11:AQ569045
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gb_gss1:AQ097888
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gb_est27:A1163552
gb_est24:A1163552
gb_est24:A1163545
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gb_est8:AA012276
gb_gss12:AQ339784
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gb_gss8:AQ055939
gb_est24:AI162058
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gb_est33:A1775248
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gb_est24:All62936
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gb_est36:AV182651
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AA748739 309 bp mRNA EST 22-JAN-1998 ny06e12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1270990 3',
Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallacedu washington.edu

Clones may be purchased from Research Genetics (info@resgen.com).

BAC end Web Server: http://www.htsc.washington.edu

Plate: 4815 row: G column: 23
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 309)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                    /clone_lib="CIT Approved Human Genomic Sperm Library D"
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DB108"
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Onpublished (1997)
On Jan 14, 1998 this sequence version replaced gi:1797612.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenth.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                               7 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 12
Gaps: 0
Percent Identity: 58.333
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 256.
Location/Qualifiers
1. 3309
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High quality sequence stop: 605.
Location/Qualifiers
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AA748739
AA748739.1 GI:2788697
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3.909
91.667
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US-08-653-294-16 x AQ835306
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LOCUS AA748739
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  Eutheria; Primates; Catarrhini; Hominidae; Homo.
I bases 1 to 4811
Mahairas, G.G., Walls
Mahairas, G.G., Walls
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 605)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

125 c 102 g 102 t
                                                                                         Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
LOCUS A0835306 605 bp DNA GSS 27-AUG-1999
DEFINITION HS.4815_A1_D12_T7A CIT Approved Human Genomic Sperm Library D
sapiens genomic clone Plate-4815 Col-23 Row-G, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
                                                                                                                                                                                                Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3058 row: F column: 18
Class: BAC ends
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High Throughput Sequencing Center
High Throughput Sequencing Center
Minversity of Washington North, Seattle, WA 98109, USA
401 Queen Anne Avenue North, Seattle, WA 98109, USA
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Gaps: 0
Percent Identity: 75.000
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Location/Qualifiers
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AQ835306.1 GI:5801368
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US-08-653-294-16 x AQ137850
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Sequencing Center Information can be

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Unpublished (1995) this sequence version replaced gi:801493.
On May 8, 1995 this sequence version replaced gi:801493.
Contact: Marra M/Mouse EST Project
WashD-HBHI Mouse EST Project
WashD-HBHI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fmail: mouseest@watson.wustl.edu
This clone is available royaltyfree through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:335021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 519)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
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DEFINITION mo21d11.rl Life Tech mouse embryo 13 5dpc 10666014 Mus musculus CDNA clone IMAGE:554229 5', mRNA sequence.
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                                                                                                                                     1 others
                                                                                                                                                                                                                                                                     Gaps: 0
Percent Identity: 80.000
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Location/Qualifiers
1. .519
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                                                                                                                                                                                                                                              Length:
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The WashU-HHMI Mouse EST Project
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Ratio: 4.200
Percent Similarity: 100.000
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US-08-653-294-16 x AQ253565
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                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 490)
Mahalras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
LOCUS AQ233565 490 bp DNA GSS 10-OCT-1998
DEFINITION HS.3026_A1_A07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=13 Row-A, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                 constructed by Bento Soares and M. Fatima Bonaldo." 52\ c 55\ g 107\ t
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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University of Washington
Voll Queen Anne Avenue North, Seattle, WA 98109, USA
4P1: (206) 616-3618
Fax: (206) 616-3887
                                  /clone="IMAGE:120990"
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Gaps: 0
Percent Identity: 66.667
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Sequence Tagged Connector
Plate: 3026 row: A column: 13
Class: BAC ends
High quality sequence stop: 490.
  /organism="Homo sapiens"
/db_xref="taxon:9606"
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AQ253565.1 GI:3724919
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US-08-653-294-16 x AA748739/rev
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Percent Similarity:
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/organism="crypta sativa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Poales; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.

1 (bases 1 to 685)

1 (bases 1 to 685)

A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS
LOCUS
AQ259553
DEFINITION nbxb0023E12r CUGI Rice BAC Library Oryza sativa genomic clone
nbxc0023E12r, genomic survey sequence.
                                                            to: 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                        210 TATAAGITAAIGGTITATAAGATACITITAAGATAT 175
                                                            to reverse of: AQ569045 from: 1
                                                                                                                        1 TyrArgLeuLeuIleArgArgIleLeuLeuArgTyr 12
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence start: 71
High quality sequence stop: 310.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: rwing@clemson.edu
Seg primer: GGAAACAGCTATGACCATG
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ259553.1 GI:3784035
US-08-653-294-16 x AQ569045/rev
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On Mar 23, 1999 this sequence version replaced g1:3324756.

Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Fax: (206) 616-3887
Email: jwallacedu washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library avallability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Seq primer: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 596)
Mahaharas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBACe3.6; Genomic sequence of BAC ends"
116 c 93 g 161 t 22 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ569045 596 bp DNA GSS 01-JUN-1999 HS_5344_A1_F08_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=920 Col=15 Row=K, genomic survey sequence.
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/clone_libb"RPCI-11 Human Male BAC Library"
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                                                                                     Length: 12
Gaps: 0
Percent Identity: 58.333
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Gaps: 0
Percent Identity: 58.333
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High quality sequence stop: 596.
Location/Qualifiers
1. .596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ569045.1 GI:4962265
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US-08-653-294-16 x AA103036/rev
                                                                                  42.00
3.818
91.667
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3.818
91.667
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Percent Similarity:
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Ratio:
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

MEDLINE COMMENT

JOURNAL

TITLE

BASE COUNT ORIGIN

FEATURES

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Eutheria: Primates: Catarrhin; Hominidae; Percentary, Panimania, Eutheria: Primates: Catarrhin; Hominidae; Homo.

1 (bases 1 to 420)

8 Adams, M.D., Rounsley, S.D., Zho, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Use of human BAC End Sequences for Sequence-Ready Map Building Other_GSSS: RPCIII-1A13.TWB

Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
The Institute for Genomic Research
Tel: 301 838 0200
Fax: 301 838 020
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bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Poaceae, Oryza
Foaceae, Oryza
Ming, R.A. and Dean, R.A.
Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cen-"---/sex-"Male"
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/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
RPCIII Human Male BAC Library"
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                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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LOCUS A0869567 438 bp DNA
DEFINITION nbeb0035D05f CUGI Rice BAC Library (ECORI) Or
ACCESSION A0869567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 10
Gaps: 0
Percent Identity: 80.000
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/clone="RRCI-11-1A13"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 420
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US-08-653-294-16 x AQ311590
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                                 Homo sapiens
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JOURNAL
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      SOURCE
                                                                                                                                                                                                                                                                                                                                                                                            D37193 360 bp mRNA EST 24-OCT-1994 CELKO41G6F Yuji Kohara unpublished cDNA Caenorhabditis elegans CDNA clone yk41g6 5', mRNA sequence.
D37193 GI:525575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Bukaryota, Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 360)
Kohaza,Y., Mitsuki,H., Nishigaki,A., Motohashi,T., Sugimoto,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:

LOCUS AQ311590 420 bp DNA GSS 04-MAY-1999
LOCUS AQ311590 420 bp DNA GSS 04-MAY-1999
DEFINITION RPCIII-1A13.T3 RPCII-11 Homo sapiens genomic clone RPCI-11-1A13,

GEDSION AD311590
ACCESSION AQ311590 1 GI:4043339
KERMORDS GSS 04-MAY-1999
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/clone=lib="yk1g6"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Toward an expression map of the C.elegans genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 12
Gaps: 0
Percent Identity: 58.333
Identity: 75.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
                                                                                                                                                                                                       /strain="CB1489 him-8(e1489)
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1994)
Contact: Yul Kohara
Gene Library Lab
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="varied"
76 c 80 q
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      Percent
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3.727
91.667
                                                                                                                                                   Align seg 1/1 to: AQ259553
      83.333
                                                               alignment_block:
US-08-653-294-16 x AQ259553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-16 x D37193
                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
LOCUS
                                                                                                                                                                                                                                                                                                                      seq_name: gb_est1:D37193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rabara, H.
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Ratio:
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      Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
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source

FEATURES

BASE COUNT ORIGIN

VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

DEFINITION

ACCESSION

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eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
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Percent Similarity:
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                                                                        REFERENCE
                                                                                                        AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db xref='taxon:4530"
/clone="nbeb0035D05f"
/clone="nbeb0035D05f"
/clone="lbebc015D05f"
/clone="lbebc015D05f"
/clone="lbebc015D05f"
/clone="lbebc015D05f"
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/clone="lbebc015D05f"
/clone="lbebc015D05f"
/clone="lbebc015D05f"
/closue_type="lbebc015D05f"
/closue_type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A1960153 457 bp mRNA EST 20-AUG-1999 sc39b09.x1 Gm-c1014 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1014-1458 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glýcine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 others
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Percent Identity: 90.000
                                                         Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwingeclemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
Contact: Wing RA
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Resource Center
c 65 g 10
                                                                                                                                                                                                                                                                                                       High quality sequence start: 24
High quality sequence stop: 397
Location/Qualifiers
1. 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="Japonica"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LeuLeulleArgArglleLeuLeuArgTyr 12
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
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E 1 (bases 1 to 457).

Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Shoemaker, R., Marra, M., Hiller, L., Kuchab, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.,
Public Soybean EST Project
Unpublished (1999)
Other_ESTs: sc39b09, yl
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anote—"Vector: pT713Pac (pT713, Pharmacia); Site_1: ECORI; Site_2: HindIII; This cDNA library was constructed from mRNA isolated from leaves of 2-3 week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a 3' anchored poly (dT) primer. ECORI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with ECORI and HindIII. The CDNA fragments were directionally cloned into the ECORI-HindIII restriction were transformed into the BCORI-HindIII restriction were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker and Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
This clone is available through: Genome Systems, Inc. 4633 World
This clone is available through: Genome Systems, Inc. 4633 World
Call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web_site: www.genomesystems.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Leaves, 2-3 week old seedlings, greenhouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCUS A1774609 578 bp mRNA EST 29-JUN-1999
DEFINITION EST25709 tomato resistant, Cornell Lycopersicon esculentum cDNA
CLONE CLERLIZHI2, mRNA sequence.
ACCESSION A1774609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Glycine max"
/db_xref="taxon:3847"
/clone="cENOME SYSTEMS CLONE ID: Gm-c1014-1458"
/clone_lib="Gm-c1014"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 10 Gaps: 0 Gaps: 0 Percent Identity: 80.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: primer name ambiguous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 364,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 CGCCTCCTCGTTCGACGACTTCTCCTCCGA 207
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106 c 1
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US-08-653-294-16 x AI960153/rev
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100 Jordan Hall, Člemson, SC 29634, USA
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ORIGIN
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JOURNAL
COMMENT
                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                       FEATURES
                       TITLE
                                                                                COMMENT
                                                                                                                                      Potatoe: Lycopersicon.

I (bases 1 to 578)

S D' Ascenzo, M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujil,C.Y.,
Bowman,C.L., Nierman, W., Fraser,C.M., Venter,J.C., Tanksley,S.D.,
Giovannoni,J.J. and Martin,G.B.
Generation of ESTs from Pseudomonas resistant tomato
Unpublished (1999)
On Dec 20, 1995 this sequence version replaced gi:1136039.
Other.ESTs: TYC2277
Contact: David Frisch
Clemson University
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 prime sequence.
Location/Qualifiers
1. 578
/organism="Lycopersicon esculentum"
/cultivar="711-12 (355::Pto in Rio Grande x Money Maker)"
/db_xref="taxon:4081"
/clone="cLRR12112"
/clone="cLRR12112"
/clone_type="tomato resistant, Cornell"
/dev stage="4"week old"
/lab_host="SOLR"
                                                             Lycopersicon esculentum Sukaryota, Embryophyta; Tracheophyta; bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophyta; Spermatchyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol; cLER - Tomato Pseudomonas Resistant EST Library. Directionally cloned cDNAs inserted into pBlueScript SK(-) at 5' end with EcoRI and 3' end with XhoI site." 139 c 133 g 137 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B70241 S93 bp DNA GSS 24-OCT-1998 CIT-HSP-2028I12.TR CIT-HSP Homo sapiens genomic clone 2028I12, genomic survey sequence.
B70241 B70241.1 GI:2709465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 593)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 11
Gaps: 0
Percent Identity: 81.818
                                                                                                                                                                                                                                                                                                                                                                                                              100 Jordan Hall, Člemson, SC 29634, USA
TE: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@cLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1 to: 578
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81.818
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  AI774609.1
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JOURNAL
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KEYWORDS
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KEYWORDS
                                                                                                                                                                    REFERENCE
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Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: eughyllophytae: Spermatophyta: Magnollophyta: eudicotyledons: core eudicots: Asteridae: euasterids I; Solanales; Solanaceae; Solanum; Potatoe: Lycopersicon.

E. (bases 1 to 613)

D. Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fulii,C.Y., Bowman,C.L., Nlerman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D., Glovannoni,J.J. and Martin,G.B.

Generation of ESTs from Pseudomonas resistant tomato Unpublished (1999)

On May 18, 1998 this sequence version replaced gi:3137089.

Contact: David Frisch

Clemson University
                                                                                         L Unpublished (1997)
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: M3 Reverse
Class: BAC ends.
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LOCUS A1775248 613 bp mRNA EST 29-JUN-1999

DEFINITION EST256348 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLER15A13, mRNA sequence.

ACCESSION A1775248

VERSION A1775248.1 G1:5273289
Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 others
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Percent Identity: 72.727
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"Grganisma" Homo sapiens"

/db_xref="GDB:7048142"

/db_xref="taxon:9606"

/clone="12028112"

/clone=lb="CIT-HSP"

/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304 AGACATCTTCTAAGAAGAGTACTCTTAAGATAT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ArgLeuLeulleArgArglleLeuLeuArgTyr 12
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4.100
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us-08-653-294-16.rst
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/ Organism="Lycopersicon esculentum"
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/clone_lib="toans"
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/clone_lib="toans"
/clone="toans"
/clone="toa
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrischeCLEMSON.EDU
5 prime sequence.
Location/Qualifiers
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ORIGIN
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alignment_scores:
Quality: 41.00
Ratio: 4.556
Percent Similarity: 81.818

Length: 11 Gaps: 0 Percent Identity: 81.818

alignment_block: US-08-653-294-16 x AI775248

Align seg 1/1 to: AI775248 from: 1 to: 613

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

February 8, 2000, 01:29:39; Search time 122.56 Seconds (without alignments) 2.319 Million cell updates/sec Run on:

US-08-653-294-17 58 1 YRLIRRIALRY 12

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

188963 segs, 23686106 residues Searched:

188963 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

A_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ro.	Description	-B2702 84-7	B2702.84-	lati	HLA-B2702 CTL modu	4-7	lating	Human DNAX toll-li	a veri	Curvularia verrucu	Chloroperoxidase.	HLA-B2702 CTL modu	Dom	œ	œ	Human neuronal nic	oţ	ō		eo.	Acetyl CoA carboxy		끍	~	creted p	nce enc	acid seque	region	ence gene	seci	4	philus	dified	subuni	Neuronal nicotinic
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	Score	53	53	53	38	39	39	36	35	35	35	34	34	34	34	34	34	34	33	33	33	32	32	32	32	32	31	31	31	30	30	30	30	30	30
	Result No.		7	m	4	Ŋ	φ	7	ھ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34

Human neuronal nicotinic Alpha4 subunit of Alpha4 subunit of Alpha4 subunit of Tetrodotoxin-sensi Tetrodotoxin-sensi HLA-B2702 CTL modu Immunomodulating d Immunomodulatory p Immunomodulatory p Feptide #4 used in
W44155 W09023 W11824 W61825 W69361 W69362 R93779 W47264 W47261
папапапапапа
529 6229 6227 1928 1988 20 20 6
51.77 51.77 51.77 51.77 51.77 51.77 51.77 51.77 51.77
20 20 20 20 20 20 20 20 20 20 20 20
000000444444 0000000000000000000000000

ALIGNMENTS

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Gaps ó; Score 53; DB 1; Length 12; Pred. No. 0.00035; 0; Mismatches 1; Indels 91.4%; 91.7%; Query Match 91.4 Best Local Similarity 91.7 Matches 11; Conservative

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1 YRLLIRRIALRY 12 ||| ||||||||| 1 YRLAIRRIALRY 12 ద ŏ

RESULT 2 W33798 W33798 standard; peptide; 12 AA. AC .W33798;

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Franting autoimmune diseases

Example 1: Page 19: 41pp: English.

Peptides W33784-98 and W33778-9 were assayed for their immunomodulating crivity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or crivity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or c-terminal amidated or esterified forms of up to 60 mino acids, where the peptide-type compound comprises the formula: A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or amil amino acid; aa82 = R or L; aa83 = G or R; and a represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amil amino acid sequences related to a Class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytocoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with amitgenic peptides or proteins of interest to activate CTLS. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, or used for detection and diagnosis. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 35; 41pp; English.
This sequence represents a specifically claimed immunomodulating
dimer peptide of the invention. A peptide-type compound or variant is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
19-JUN-1998 (first entry)

Peptide B2702.84-79/79-84 tested for immunomodulating activity.

Immunomodulating dimer: immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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Pred. No. 0.00035;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                   24-MAY-1996; US-653294.
(STRD) UNIV LELAND STANFORD JUNIOR.
BELLOW R. Clayberger C. Krensky AM;
WPI: 98-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAY-1997; UO8689.
24-MXY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.48;
91.78;
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Matches 11; Conservative
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22-MAY-1997; U08689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98-086530/08
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WO9744351-A1.
27-NOV-1997.
                                                                                                                                                                                                                            Homo sapiens
WO9744351-Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUN-1998
                                                                                                                                                          rejection.
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                                                                                                                                                                                     Synthetic.
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claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal anidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (taa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = E or hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aarepresents amino acid; aa82 = R or L; aa83 = G or R; and aarepresents amino acid; absence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytocoxic rlymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proteins of interest to activate CTLs. They can also inhibit the cluss in response to anti-CD3. The peptide can be diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis.
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R83061-R83085, R83090-R83096 and R82907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to abandant comparate to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAY-1996 (first entry)
16-MAY-1996 (first entry)
16-MAY-1996 (TL modulating peptide (B2702.84-75/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; fimunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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6
                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.4%; Score 53; DB 1; Length 12; 91.7%; Pred. No. 0.00035; 1.7%; Mismatches 1; Indels
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55.0%; Pred. No. 0.25;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Krensky AM, Parham P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R92907 standard; peptide; 20 AA.
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Best Local Similarity 55.0
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YRLLIRRIALRY 12
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WPI; 95-358582/46.
                                                                                                                                                                                                                                                                                                                                            disease...
The products can -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||| |||||||
| YRLAIRRIALRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
WO9526979-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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R92907
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Sequence
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W86351
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   While of the page 12, 29pp; English and differentiation of CTLS.

PS Example 12, 29pp; English.

PS Example 12, 29pp; English.

R95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the protein associated with T-cell lysate. P74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. P74 is found in a limited number of cell types, but is particularly captacessed on B and T cells. P74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity expressed on B and T cells. P74 can be isolated by lysis of a suitable coll with an amphoteric detergent, and then passed through an affinity collum containing a covalently bound HiA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of P74 combined with the HLA-B2702.60-84 (see R95416), induces calcum influx, and inhibits compounds can be screened for their effect on the cytolytic activity of compounds can be screened for their effect on the cytolytic activity of determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by adding to the with the extracellular portion of p74, in an amount sufficient to compete component.
                                                       12-NOV-1996 (first entry)
HLA-B2702 84-75-84 palindrome.
HLA-B2702 84-75-84 palindrome.
HLA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytofoxic T lymphocyte; CTL; differentiation;
Cytolysis; antigen presenting cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunomodulating dimer péptide #1.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beulow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
MPI: 98-086530/08.
Aphi-1 domain, used for preventing rejection of transplants or
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22-MAX-1997, U08689.
24-MAX-1996; US-653294.
24TR ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                              18-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W33778 standard; peptide; 20 AA. W33778;
                             R95428 standard; peptide; 20 AA.
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                                                                                                                                                                                                                                         Krensky AM;
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Best Local Similarity 55.05
Matches 11; Conservative
                                                                                                                                                                                                                                       Clayberger C, Kr
WPI; 95-194027/25
                                                                                                                                                                 WO9513288-A1.
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WO9744351-A1.
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RESULT
R95428
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Claim 2: Page 108-111; 171pp; English.
The present invention specifically describes human DNAX toll-like receptors 2 to 10 (DTLAZ-10). The present sequence is human DTLR3 given in the present invention. Also described are: (1) a fusion protein comprising a DTLR protein or peptide; (2) a binding compound, preferably an antibody or antibody fragment which specifically binds to a DTLR protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide; (4) an expression vector comprising the nucleic acid of (3); and (5) a host cell comprising the vector of (4). The host cell of (5) can be used to produce the DTLR proteins. The DTLR proteins can be used to alter phosphate metabolism, to modulate inflammatory function, innate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAR-1999 (first entry)
Human DNAX toll-like receptor DTLR3.

Human DNAX toll-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor; Interleukin 1 receptor; phosphate metabolism; innate immunity response; modulate inflammatory function; morphological effect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human DNAX toll-like receptors, DTLR 2-10 - used to, e.g. alter phosphate metabolism, modulate inflammatory function or innate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.2%; Score 39; DB 1; Length 20; 55.0%; Pred. No. 0.25; 1; Indels ive 0; Mismatches 1; Indels
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07-MAY-1998; UG8979.

05-MAY-1999; US-076947.

07-MAY-1997; US-044293.

22-JAN-1999; US-07212.

(SCHE ) SCHERING CORP.

Bazan JF, Hardiman GT, Kastelein RA, Rock FL;

WPI: 99-059670/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W86351 standard; Protein; 904 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l. .21
/label= signal
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/label- DTLR3
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Best Local Similarity 55.0
Matches 11; Conservative
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NOVO-NORDISK AS.
                  Berka RM, Cherry J,
WPI; 97-132641/12.
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Best Local Similarity
Matches 6; Conserv
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        (NOVO ) NC
Berka RM,
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         of g
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                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      haloperoxidase from Curvularia verruculosa - useful for oxidn. of halide, halogenation and, in presence of hydrogen peroxide and thiocyanate, as antimicrobial.

Claim 17: Page 38: 58pp: English

A haloperoxidase partial peptide (W12037) corresponds to amino acids 275-314 of the Curvularia verruculosa CBS.53 enzyme. Partial peptides (W12034-41) were obtd. from the haloperoxidase by digestion with lysyl-specific protease from Achromobacter. Primers (see also T51613-14) based on the peptides were used in the PCR emplification of genomic DNA from CBS 147.63. The PCR product was used to screen a genomic library, leading to the isolation of the haloperoxidase gene (T51612).
      immunity responses or morphological effects. The DTLR proteins can used in the treatment of conditions exhibiting abnormal expression the receptors of their ligands. These abnormalities are typically manifested by immunological disorders.

Sequence 904 AA;
                                                                                                                                                                                                                                           30-APR-1997 (first entry)
Curvularia verruculosa haloperoxidase partial peptide (aa275-314).
Haloperoxidase; halide oxidation; halogenation; antimicrobial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Curvularia verruculosa haloperoxidase.
Haloperoxidase; halide oxidation; halogenation; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                     Halkier T, Oxenboll KM;
                                                                                     DB 1; Length 904;
44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 40; 2.8;
                                                                                                               Indels
                                                                                        Score 36; DB 1
Pred. No. 44;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                          Curvularia verruculosa strain CBS 147.63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Curvularia verruculosa strain CBS 147.63.
WO9704102-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                     Cherry J, Fuglsang C,
                                                                                                                                                                                                                                                                                                                         09-JUL-1996; U11458.
14-JUL-1995; US-001194.
12-FEB-1996; US-603534.
(NOVO ) NOVO NORDISK BIOTECH INC.
(NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W12042 standard; Protein; 600 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOVO NORDISK BIOTECH INC
                                                                                                                                                                                                                       W12037 standard; Peptide; 40
                                                                                        62.1%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.3%;
50.0%;
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                                                                                        Query Match 62.1
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 60.3
Best Local Similarity 50.C
Matches 6; Conservative
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09-JUL-1996; U11458.
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484 RLMLRRVALK 493
                                                                                                                                      2 RLLIRRIALR 11
                                                                                                                                                                                                                                                                                                                                                                                     Berka RM, Cherry
WPI; 97-132641/12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disinfectant.
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21-FEB-1996;
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W12037
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                                                                           Haloperoxidase from Curvularia verruculosa - useful for oxidn. of
Haloperoxidase from Curvularia verruculosa - useful for oxidn. of
Haloperoxidase from Curvularia verruculosa peroxide and
Tathiocyanate, as antimicrobial
Claim 23; Page 36:37; Sapp; English.

The haloperoxidase of Curvularia verruculosa CBS. 63 shows optimum
activity at about 60 deg C and pH 5.5, retains at least 75%
activity after incubation for 1 hr at pH 7.0 and 60 deg C in the
presence of 0.1% H202, and prefers bromide over chloride ions as
substrate. It can be obtd. from a C. verruculosa fermentation
or by expression in host cells transformed with a vector carrying
the haloperoxidase gene (see also T51612). The isolated enzyme can
be used to oxidise halide to hypohalous acid in the presence of an
CH202 source, or to halogenate cpds. It can also, in the presence
of H202 and thlocyanate, be used as an antimicrobial.
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Use of halo:peroxidase enzymes - in antifouling paints and methods for determining the halide concn. of liquids

Example 3; Fig 6; 48pp; English.

Example 3; Fig 6; 48pp; English.

A chloroperoxidase (R82249) is obtd. by expression of a cDNA sequence (103875) isolated from Curvularia inaequalis in a procaryotic host. The apoprotein is activated by addn. of vanadate. The enzyme displays high thermostability (Tm 90 deg) and is stable in 40% methanol, ethanol or propanol. It can is used for the analysis of halide (esp: chloride) ions, e.g. in blood or withe. The enzyme may also be utilised as an environmentally-friendly antifouling agent in ship paint; it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Chloroperoxidase; haloperoxidase; antifouling paint; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 1; Length 600;
Pred. No. 44;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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WPI; 95-358602/46.
N-PSDB; T03875.
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Pred. No. 47;
3; Mismatches
Halkier T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R82249 standard; Protein; 640 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.3%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-1995.
30-MAR-1995; NL0123.
31-MAR-1994; EP-200893.
24-JUN-1994; NL-001048.
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Best Local Similarity
Conserve
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W33792;
19-JUN-1998 (first entry)
                                                                                                    Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
WO9744351-A1.
                                                                                                                                                                                                                                                                                                                                               rejection.
                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
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ID W3
AC W3
DT 19
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                                                                                                                                                                                                                                                                                           Example 15; Page 36; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to
                                                                     HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
Cytocoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84), Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (STRD ) UNIV LELAND STANFORD JUNIOR.

(Clayberger C, Krensky AM, Parham P;
WPI: 95-358982/46.

Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                    Extension of acceptance period of transplants from MHC unmatched donor hosts \, using Class I B75-84 MHC antigen of the recipient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB :
Pred. No. 2.1;
0; Mismatches
                                                                                                                                                                                                                       Krensky AM, Parham P;
                                                                                                                                                                                                         (STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 15; Page 36; 80pp; English.
                           R92909 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R92908 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YRLLIR-----RIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 58.6%;
Best Local Similarity 50.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                           US-222851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-APR-1995; U04349.
05-APR-1994; US-222851
                                                                                                                                                                          05-APR-1995; U04349.
05-APR-1994; US-2228
                                                                                                                                                                                                                     Clayberger C, Kren
WPI; 95-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             the patient
                                                                                                                                              W09526979-A1.
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                                                       16-MAY-1996
                                                                                                                                                               12-0CT-1995
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RESULT
             R92909
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administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
Sequence 20 AA;
                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                   19-JUN-1998 (first entry)
Peptide B2702.84-75%75-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autolimmune disease; Class I HLA-B alpha-1 domain;
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..
                                                                                    Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 1; Length 20;
Pred. No. 2.1;
0; Mismatches 2; Indels
                                                                                  58.6%; Score 34; DB 1;
50.0%; Pred. No. 2.1;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  27-NOV-1997.
22-MAY-1997; U08689.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used for detection and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W33792 standard; peptide; 20 AA.
                                                                                                                                                                                                                                          W33791 standard; peptide; 20 AA.
                                                                                                                                         1 YRLLIR-----RIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
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                                                                                                                                                                     1 YRLATRINERRENLRIALRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YRLLIR-----RIALRY
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Best Local Similarity 50.0
Matches 10; Conservative
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                                                                                                                 Conservative
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Pal (SIMD) UNIV DELAND STANKON JUNION.

PRINCE AND JULY BELAND STANKON JUNION.

BELLOW R. Clayberger C. Krensky AM:

New I 198-086530/08.

New I munomodulating dimer peptide(s) - based on a Class I HLA-B

appha-1 domain, used for preventing rejection of transplants or

treating autoimmune diseases

Example 1: Page 19; 41pp; English.

Example 1: Page 19; 41pp; English.

C crivity. A peptide-type compound or variant is claimed which has

c minomodulating activity, including the N-terminal arcylated and/or

C creminal amidated or esterified forms of up to 60 amino acids, where

CC the peptide-type compound comprises the formula; A-B, where A, B =

CC terminal amidated or esterified forms of up to 60 amino acids, where

CC the peptide-type compound comprises the formula; A-B, where A, B =

CC the peptide-type compound comprises the formula; A-B, where A, B =

CC tarminal amino acid; aa80 = R or G; aa80 = I or N; aad1, aa84 = a hydrophobic or

CC small amino acid; aa82 = R or L; aa83 = G or R; and as represents amino

CC acid The sequences in the brackets may optionally be absent or truncated

at any peptide type bond within the brackets. The compounds comprise

CC anino acid sequences related to a Class I HLA-B alphal domain (positions

CC anino acid sequences related to a class I HLA-B alphal domain (positions

CC undesirably attacking cells in a host or in vitro. They can also be

CC activate CTLs. They are also inhibit the proliferation of resistion

CC activate CTLs. They are also inhibit the proliferation of resistion

CC activate CTLs. They are also inhibit the proliferation of resistion

CC activate CTLs. They are also inhibit the proliferation of resistion

CC activate CTLs. They are also inhibit the proliferation of resistion

CC activate CTLs. They explide can be used for preventing rejection

CC relemmentoid arthritis and lupus erythematosis. The products can also be

CC rhemmenton arthritis and lupus erythematosis. The products can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Peptide B2702.84-75/75-84T tested for immunomodulating activity. Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-MAY-1998 (first entry)
Human neuronal nicotinic acetylcholine receptor alpha-3 subunit.
Human; neuronal nicotinic acetylcholine receptor; alpha-3 subunit; brain tissue; screening; NAChR; antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140. 265
/label= TMD1
/note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "transmembrane domain" Misc_difference 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- unspecified
/note- "encoded by AWC"
273. .296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label = unspecified
/note = "encoded by WWC"
                                                                                                                                                                        27-NOV-1997; U08689.
24-MAY-1997; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W44156 standard; Protein; 504 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used for detection and diagnosis
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/label- signal
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| YRLAIRLNERRENLRTALRY 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0
Matches 10; Conservative
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                                                                                                                  Homo sapiens.
WO9744351-Al.
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14-MAY-1998
                                                                                                                                                             27-NOV-1997
                                                                                                Synthetic.
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Gaps
                                                                                                                                                                                                                                           Human neuronal nicotinic acetylcholine receptor subunits and DNA also transformed cells useful for screening cpds. which modulate
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                                                                                                /label- unspecified
/note-"encoded by TWC"
459. .480
/label- TMD4
/note-"transmembrane domain"
327. .458
/label- cytoplasmic_loop
                           note= "transmembrane domain"
                                                                                                                                                                                    08 MARY 1993; US-028031.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
(SIBI-) SIBIA NEUROSCIENCES INC.
Elliott KJ, Ellis SB, Harpold MM;
/note= "encoded by IGY"
302. .326
/label= TMD3
                                                                       /label- unspecified /note- "encoded by AMC"
                                             /label= unspecified
/note= "encoded by WWC"
                                                                                                                                                                                                                                                                                                                                                                                             Lhat express a variety of subtypes.
Sequence 504 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YRLLIRRIALRY 12
                                                                                        Misc_difference 354
                                     Misc_difference 309
                                                              Misc_difference 347
                                                                                                                                                                               08-MAR-1994; U02447
                                                                                                                                                                                                                Elliott KJ, Ellis S
WPI; 94-303024/37.
N-PSDB; V12200.
           Domain
Domain
                                                                                                                  Domain
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| | |||::| | 232 YSLXIRRLSLFY 243

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8, 2000, 01:29:40 Search completed: February Job time: 1752 sec

Wed Feb

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 7, 2000, 11:54:27; Search time 117.7 Seconds

(without alignments)

4.809 Million cell updates/sec

11tle: US-08-653-294-17

Perfect score: 58
Sequence: 1 YRLIRRIALRY 12
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
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Minimum DB seq length: 0 Maximum DB seq length: 1000000

Total number of hits satisfying chosen parameters:

142080 seqs, 47169319 residues

Searched:

Maximum DB seq length: 1000000 Post-processing: Minimum Match 0% Listing first 45

Listing first 45 summaries

Database : PIR 62:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

probable oxidoredu chloride peroxidas ribosomal protein probable ribosomal hypothetical prote acyl-CoA oxidase (acyl-CoA oxid hypothetical prote hypothetical prote probable membrane probable acetyl-Co DNA-directed RNA p hypothetical prote TB2/DP1 protein ho conserved hypothet ribosomal protein hypothetical prote kpsD protein - Esc fimbrial assembly nicotinic acetylch acetylcholine rece Na+/H+ antiporter Description SUMMARIES JC5342 G70882 S69334 C70200 H70883 G71167 OXCKAX OXCKX4 Query Match Length DB Score . 02

nicotinic acetylch	probable DNA ligas	hypothetical prote	probable DNA-direc	nonstructural poly	hypothetical prote	ribosomal protein	LICA protein - Myc	transcription fact	probable cysw - My	conserved hypothet	ferrochelatase (EC	ferrochelatase - H	histocompatibility	lsu ribosomal prot			
A53956	672709	C70031	D72571	T08822	S15010	S74731	842124	JC1496	A70683	F72323	H64566	A71860	829990	A75148		ALIGNMENTS	
~	~	~	N	~	~	~	N	~	N	~	~	~	~	7			
503	619	636	895	1998	3165	88	238	246	272	306	334	335	348	361			
55.2	55.2	55.2	55.2	55.2	55.2	53.4	53.4	53.4	53.4	53.4	53.4	53.4	53.4	53.4			
32	32	32	32	32	32	31	31	31	31	31	31	31	31	31			
31	32	33	34	35	36	37	38	39	40	41	42	43	44	45			

Query Match 63.8%; Score 37; DB 2; Length 313; Best Local Similarity 41.7%; Pred. No. 8; Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps

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OY 1 YRLLIRRIALRY 12 | | | : : | | | : : : | | | 259 YRVVARRLSIKY 270 probable oxidoreductase - Mycobacterium tuberculosis (strain H37RV)

C;Specias: Mycobacterium tuberculosis
C;Specias: Mycobacterium tuberculosis
C;Specias: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 29-Sep-1999
C;Accession: G70882
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Deviln, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Nature 393, 537-544, 1998
A;Authors: Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Qua A;Authors: Krogh, A.; Maltebead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987

A;Accession: G/UBEZ
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A; residues: 1-309 <COL>
A; residues: 1-309 <COL>
A; crossreferences: GB:AL008967; GB:AL123456; NID:g3261491; PIDN:CAA15591.1; PID:e129
A; Experimental source: strain H37Rv
C; Genetics:

O'STRELICS:
A:Gene: Rv2776c
C;Superfamily: phthalate dioxygenase reductase; cytochrome-b5 reductase homology: fer
F;9-211/Domain: cytochrome-b5 reductase homology <CBR>
F;240-297/Domain: ferredoxin [2Fe-25] homology <FER>

Gaps

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probable ribosomal protein S15 rps0 - Mycobacterium tuberculosis (strain H37RV)
C; Species: Mycobacterium tuberculosis
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 24-Sep-1999
C; Accession: H70883
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
R; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature: 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Accession: H70883
A; Reference number: A70500; MUD:98295987
A; Accession: H70883
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-89 <COL>
A; Cross: references: GB:AL008967; GB:AL123456; NID:93261491; PIDN:CAA15580.1; PID:e117
A; Experimental source: strain H37RV
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein PH0539 - Pyrococcus horikoshii

C;Species: Pyrococcus horikoshii

C;Species: Pyrococcus horikoshii

C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 14-Aug-1998

C;Accession: G71167

R;Kawarabayasi, Y: Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu

DNA Res. 5, 55-76, 1998

A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili

A;Reference number: A71000; MUID:98344137

A;Reference number: A71007

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Residues: 1-362 < KAW>

A;Cross-references: GB:AP000002; NID:93236129; PID:d1030571; PID:93256945

A;Experimental source: strain Off3

A;Residues: List accession replaces an interim accession for a sequence replaced by GenBa

C;Genetics:

A;Gene: PH0539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: rpsO
C;Superfamily: Escherichia coli ribosomal protein S15; eubacterial ribosomal protein
F;23-89/Domain: eubacterial ribosomal protein S15 homology <ES15>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 362;
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                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                            Length
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                         ö
                     DB 2
8.9;
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Pred. No. 35;
3; Mismatches
                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; D
Pred. No. 9;
                         Score 34;
Pred. No.
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63.68;
                         58.68;
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Best Local Similarity 50.0
Matches 6; Conservative
                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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77 YRMLISKLGLR 87
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                                                                                                                                            1 YRLLIRRIALR 11
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                         Query Match
Best Local Similarity
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Best Local Similarity
Matches 7; Conserv
                                                                                    9
                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                              Chloride peroxidase (EC 1.11.1.10) - Curvularia inaequalis
N;Alternate names: vanadium-containing chloroperoxidase
C;Species: Curvularia inaequalis
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Sep-1999
C;Accession: S69334; S53117
R;Simons, B.H.; Barnett, P.; Vollenbroek, E.G.M.; Dekker, H.L.; Muljsers, A.O.; Messersc Bur. J. Blochem. 229, 566-574, 1995
A;Title: Primary structure and characterization of the vanadium chloroperoxidase from the A;Reference number: S69334; MUID:95265772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description: catalyzes the formation of two carbon-chlorine bonds and two water molecu C; Superfamily: Curvularia inaequalis chloride peroxidase C; Keywords: blocked amino end; chloride; metalloprotein; oxidoreductase; vanadium F; 404/Active site: His #status predicted F: 404/Active site: vanadate (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RiFraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
A; Authors: Smith, H.O.; Venter, J.C.
A; Arlitle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A; Reference number: A70100; MUID:98065943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: Escherichia coli ribosomal protein S15; eubacterial ribosomal protein S15
F;22-88/Domain: eubacterial ribosomal protein S15 homology <ES15>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the Brookhaven Protein Data Bank, September 1995
A;Reference number: A66871; PDB:1VNC
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, 3-543, 'E',545-578
A;Note: the authors believe that 544-61u is correct from modeling evidence
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C;Species: Borrella burgdorferi (Lyme disease spirochete)
C:Date: 13.Feb-1998 #sequence_revision 13.Feb-1998 #text_change 13.Aug-1999
C;Accession: C70200
                                                                                       Gaps
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                         Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 2; Length 609;
Pred. No. 38;
                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-609 <SIM>
A;Cross-references: EMBL:X85369; NID:g732617; PID:g732618
A;Experimental source: CBS 102.42
                         ;
                     Score 35; DB
Pred. No. 19;
                                                                                 1; Mismatches
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50.0%;
                     60.3%;
77.8%;
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Ouery Match
Best Local Similarity 77.8.
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Best Local Similarity
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65 YRIAIRRIA 73
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                                                                                                                                         1 YRLLIRRIA 9
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C; Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 30-Sep-1993
C; Accession: A2947
E; Marcasy W. W. Rachubinski, R.A.
Gene 51, 119-128, 1987
A; Title: The primary structure of a peroxisomal fatty acyl-CoA oxidase from the yeast
A; Accession: A29047; MUID:87248070
A; Accession: A29047
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: A33
A; Gene 54
A; Experimental source: strain pK233, ATCC 20336
C; Genetics: A0x
A; Gene A0x
C; Superfamily: acyl-CoA oxidase
C; Superfamily: acyl-CoA oxidase
C; Superfamily: acyl-CoA oxidase
C; Keywords: FAD; fatty acid oxidation; flavoprotein; oxidoreductase; peroxisome
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W; Contains: capsid protein C; envelope protein E; membrane-associated protein M; nons tural protein NS4a; nonstructural protein NS5

C; Species: dengue virus type 2

C; Species: dengue virus type 2

C; Species: dengue virus type 2

C; Accession: A42461; A43466; A43763

R; Blok, J; McWilliam, S.M.; Butler, H.C.; Gibbs, A.J.; Weiller, G.; Herring, B.L.; H Virology 187, 573-590, 1992

A; Title: Comparison of a dengue-2 virus and its candidate vaccine derivative: sequenc A; Reference number: A42451; MUID:92188532
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A;Residues: 1-3391 <BLO>
A;Cross-references: GB:M84727; GB:M85259; NID:g323472; PIDN:AAA73185.1; PID:g323473
A;Cross-references: GB:M84727; GB:M85259; NID:g323472; PIDN:AAA73185.1; PID:g323473
C;Superfamily: yellow fever virus genome polyprotein; DEAD/H box helicase homology
C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein
F;1-114/Product: capsid protein C *status predicted <CPC>
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C;Superfamily: acyl-CoA oxidase
C;Keywords: FAD; fatty acid oxidation; flavoprotein; oxidoreductase; peroxisome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Logarians Candida mailtosa)

(Species: Candida mailtosa)

(Species: Candida mailtosa)

(Species: Candida mailtosa)

(Space: Standar 1989 #sequence_revision 31-Mar-1989 #text_change 17-Feb-1995

(Spacession: A2944)

R;Hill, D.E.; Boullay, R; Rogers, D.

Nucleic Acids Res. 16, 355-366, 1988

A;Title: Complete nucleotide sequence of the peroxisomal acyl CoA oxidase fix

A;Reference number: A29441; MUD:88124223

A;Accession: A29441

A;Accession: 1709 <HLL>
A;Accession: A29441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acyl-CoA oxidase (EC 1.3.3.6) PXP4, peroxisomal - yeast (Candida maltosa)
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Pred. No. 68;
1; Mismatches
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Pred. No. 68;
1; Mismatches
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Best Local Similarity 64.3%;
Matches 9; Conservative
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 64.3
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321
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| 308 YRMLARVSTIALRY 321
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Best Local S
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                                                                                                                                              acyl-CoA oxidase (EC 1.3.3.6) POX4-2, peroxisomal - yeast (Candida tropicalis) (fragment N.Alternate names: acyl-CoA oxidase II.2 (Species: Candida tropicalis (Cispecies: A28584 Cispecies: A28584 N.Small, G.M.: Lazarow, P.B. Small, G.M.: Lazarow, P.B. J. Cell Biol. 105, 247-250, 1987 A.Title: Import of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of A. Reference number: A28584; MUID:87280361
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C:Comment: The peroxisomes are eukaryote subcellular organelles that generate and degrad
ic reactions as well as the enzymes involved are usually different from the mitochondria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Molecule type: DNA
A.Residues: 1-709 <OKA>
A.COSS-references: GBAN1160; NID:g170911; PIDN:AAA34362.1; PID:g170912
A.Cross-references: Strain pK233, ATCC 20336
C.Comment: This enzyme, located in peroxisomes, catalyzes the oxygen-specific oxidation this reaction is the initial step of the peroxisomal beta-oxidation system. In C. trop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: A25123
R;Okazaki, K.; Takechi, T.; Kambara, N.; Fukui, S.; Kubota, I.; Kamiryo, T.
Proc. Natl. Acad. Sci. U.S.A. 83, 1232-1236, 1986
A;Title: Two acyl-coenzyme A oxidases in peroxisomes of the yeast Candida tropicalis:
A;Reference number: A94084; MUID:86149279
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C;Superfamily: acyl-CoA oxidase
C;Keywords: FAD; fatty acid oxidation; flavoprotein; oxidoreductase; peroxisome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peroxisome
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N,Alternate names: acyl-CoA oxidase II
C.Species: Candida tropicalis
C.Species: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 11-Jun-1999
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C;Species: Candida tropicalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: POX4-2
C;Superfamily: acyl-CoA oxidase
C;Keywords: FAD; fatty acid oxidation; flavoprotein; oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A28584
A; Molecule type: mRNA
A; Residues: 1-502 <SMA>
A; Cross-references: GB:Y00623; NID:g2672; PIDN:CAA68660.1; PID:g2673
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
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Pred. No. 49;
1; Mismatches
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Pred. No. 68;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.68;
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Best Local Similarity 64.3
Matches 9; Conservative
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101 YRMLARMSTIALRY 114
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                296 YRFILKAIALGY 307
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Best Local Similarity
Matches 9; Conserv
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58.6%;
54.5%;
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60.0%;
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2728 RMLINRFTMRY 2738
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38 YVELARKIAMRY 49
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Best Local Similarity
7; Conserv?
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Best Local Similarity
Matches 6; Conserv
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A;Title: Comparison of a dengue-2 virus and its candidate vaccine derivative: sequence x Reference number: A42451; MUID:92188532
A;Accession: B42451
A;Molecule type: genomic RNA
A;Residues: 1-3391 <BLO>
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F:115-280/Product: membrane-associated protein M precursor #status predicted <MPP>F:115-205/Domain: nonterminal signal sequence #status predicted <SIG>
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                  F.115-205/Domain: nonterminal signal sequence #status predicted <2105-105/Domain: nonterminal signal sequence #status predicted <2105-105/Domain: transmembrane #status predicted <2MM.)
F.206-280/Product: membrane-associated protein M #status predicted <2MM.)
F.206-280/Domain: transmembrane #status predicted <2MM.)
F.218-773/Domain: transmembrane #status predicted <2MM.)
F.727-743/Domain: transmembrane #status predicted <2MM.)
F.727-743/Product: nonstructural protein NS2a #status predicted <2MM.)
F.726-1127/Product: nonstructural protein NS2b #status predicted <2MM.)
F.1476-2093/Product: nonstructural protein NS3 #status predicted <2MM.)
F.1755-1760/Region: nucleotide-binding motif B
F.1755-1760/Region: nucleotide-binding motif B
F.1759-1762/Region: nucleotide-binding motif B
F.1759-1762/Region: DEAH motif F
F.2044-2243/Product: nonstructural protein NS4b #status predicted <2MM.)
F.2244-2491/Product: nonstructural protein NS4b #status predicted <2MS5-F:1483.347,433/Binding site: carbohydrate (Asn) (covalent) #status predicted
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102-118/Domain: transmembrane #status predicted <TM2>
1102-118/Domain: transmembrane-associated protein M precursor #status predicted 1115-208/Product: membrane-associated protein M precursor #status predicted <2.205-200main: nonterminal signal sequence #status predicted <SIG>2.206-280/Product: membrane-associated protein M #status predicted <MPM>268-284/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 15-May-1998
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77.73/Pomain: transmembrane #status predicted <EPE>
77.73/Pomain: transmembrane #status predicted <TM4>
77.73/Pomain: transmembrane #status predicted <TM5>
77.73/Pomain: transmembrane #status predicted <TM5>
128-1345/Product: nonstructural protein NS2 #status predicted <NS2>
158-1147/Pomain: transmembrane #status predicted <TM6>
72-1288/Domain: transmembrane #status predicted <TM6>
73-1288/Domain: transmembrane #status predicted <TM7>
74-1310/Domain: transmembrane #status predicted <TM8>
74-1310/Domain: transmembrane #status predicted <TM9>
73-1389/Domain: transmembrane #status predicted <TM9>
73-1389/Domain: transmembrane #status predicted <TMA>
74-1464/Domain: transmembrane #status predicted <TMA>
74-1464/Domain: transmembrane #status predicted <TMA>
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1668-1938/Domain: DEAD/H box helicase homology <DEAD>
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2728 RMLINRFTMRY 2738
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Best Local Similarity
Matches 6; Conserv
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F;2148-2164/Domain: transmembrane #status predicted <TMC>
F;2174-2290/Pomain: transmembrane #status predicted <TMD>
F;2197-2213/Domain: transmembrane #status predicted <TME>
F;227-2243/Domain: transmembrane #status predicted <TMF>
F;227-2243/Pomain: transmembrane #status predicted <TMF>
F;224-2491/Product: nonstructural protein NS4b #status predicted <NAB>
F;241-2437/Domain: transmembrane #status predicted <TMG>
F;241-2427/Domain: transmembrane #status predicted <TMH>
F;241-2437/Domain: transmembrane #status predicted <NMS>
F;2492-3391/Product: nonstructural protein NS5 #status predicted <NS5>
F;183,347,433,905,982,1134,1174,1329,2301,2305,2346,2387,2457,2485,2644,2665,2704,271
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Cioserved hypothetical protein AF0109 - Archaeoglobus fulgidus
Cioser 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
Ciocession: B69263
R.Klenk, H.B.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
A.Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Wosee, C.R.; Venter, J.C.
A.Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch A.Reference number: A69256; MuID:98049343
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C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0962
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C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 14-Nov-1997
C;Accession: S38147
R;Pohl, T.M.; Pohl, F.M.
Submitted to the Protein Sequence Database, March 1994
A;Reference number: S37897
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 1; I
Pred. No. 3.2e+02;
; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
17;
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54;
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Pred. No. 54;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33;
Pred. No.
```

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hypothetical protein APE2493 - Aeropyrum pernix (strain Kl)
C:Species: Aeropyrum pernix
C:Species: O-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: E72481
R:Kawarabayasi, Y:; Hino, Y:; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DN Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A:Reference number: A72450; MUID:99310339
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A:Residues: E72481
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-550 < KAM>A:Residues: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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1 YRLLIRRIAL 10
:||:||: ||
223 FRLLVRRLYL 232
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Search completed: February 7, 2000, 11:54:28 Job time: 24338 sec

2 RLLIRRIALR 11 |||:||::| 405 RLLVRRVNVR 414

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us-08-653-294-17.rsp

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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(without alignments)
5.625 Million cell updates/sec Search time 63.71 Seconds February 8, 2000, 00:59:55; protein search, using sw model OM protein -Run on:

1 YRLLIRRIALRY 12 US-08-653-294-17 58 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

82229 seqs, 29864866 residues Searched:

82228 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45

summaries

SwissProt_38:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		Description	4162		051744 borrelia bu	032967 mycobacteri				candida	_	b	d genome				-		esch	bos taı		rattu	P32297 homo sapien	synec	-			тасас		gallu			P33699 rhizobium m	trepone	gal	P09483 rattus norv
SUMMARIES		a	- 1	PRXC_CURIN	RS15_BORBU	RS15_MYCLE	RS15_MYCTU	YHS5_CAEEL	CAO3_CANTR	CAO2_CANTR	CAO4_CANMA	POLG_DEN26	POLG_DEN27	YK50_YEAST	YD95_YEAST	RPOH_METJA	DP1_MOUSE	RT03_ACACA	KSS5_ECOLI	ACH3_BOVIN	ACH3_CHICK	ACH3_RAT	ACH3_HUMAN	RS15_SYNY3	LICA_MYCCA	MTT1_HUMAN	HEMZ_HELPY	HLAF_MACMU	COXX_HUMAN	ACH5_CHICK	HEMN_AQUAE	ACH6_CAEEL	EXOT_RHIME	SYP_TREPA		ACH4_RAT
		DB	Н	٦	-	-	Н	Н	Н	Н	Н	-	Н	Н		٦	Н	Н	Н	7	 1	1	Н	-	Н	Н	Н			Н	1	, - 4	Н	-	П	-
		Length	491	609	88	83	89	411	502	708	\sim	3391	m	352	869	78	185	298	389	495	496	499	503	68	238	246	334	348	443	454	456	487	494	617	622	633
đ	Query	Match	61.2	٥.	ω.	ω.	ω.	ω,	80	ω.	ω.	œ	œ	è.	9	'n.	ď.	S.	5.	'n.	S.	δ.	S.	Э.	ë.	m.	53.4	ω.	щ	m	ش	m	m	m	53.4	53.4
		Score	35.5	35	34	34	34	34	34	34	34	34	34	33	33	32	32	32	32	32	32	32	32	31	31	31	31	31	31	31	31	31	31	31	31	31
	Result	No.	н	~	m	4	S	φ	7	ω	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34

P24814 saccharomyc 041174 p genome po Q03132 saccharopol	073672 carassius a P24495 xenopus lae P40301 drosophila P35178 sarcharomyc		
GRR1_YEAST POLG_PEV9U ERY2_SACER	PRC3_CARAU PRC3_XENLA PRC3_DROME	SIP3_YEAST RS15_BACSU RS15_THETH CH10_ZYMMO	ALIGNMENTS
1151 1 2168 1 3567 1	233 1 233 1 234 1	1229 1229 188 188 195 195	
. 88 88 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	2222	52.6 51.7 51.7 51.7	
31 31	30 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	30.5	
35 36 37	8 8 8 4 8 9 0 1	4444 14646	

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                                                                                                                                                                                                                                                                                                                                                    STRAINH16;

X MEDLINE; 99060717.

X MEDLINE; 99060717.

**ILEB C., SIDDIQUI R.A., HIPPLER B., JAHN D., FRIEDRICH B.;

**ILEB C., SIDDIQUI R.A., HIPPLER B., JAHN D., FRIEDRICH B.;

**ILEB C., SIDDIQUI R.A., HIPPLER B., JAHN D., FRIEDRICH B.;

**ILEB C., SIDDIQUI R.A., HIPPLER B., JAHN D., FRIEDRICH B.;

**ILEB C., SIDDIQUI R.A., HIPPLER B., JAHN D., FRIEDRICH B.;

**ILEB C., SIDDIQUI R.A., HIPPLER B., JAHN D., FRIEDRICH B.;

**ILEB C., SIDDIQUI R.A., HIPPLER B., JAHN D., FRIEDRICH B.;

**ILEB C., SIDDIQUI R.A., HIPPLER B., JAHN D., FRIEDRICH III INTO

**ILEB C., SIDDIQUI R.A., HIPPLER B., JAHN D., FRIEDRICH III

**ILEB C., SIDDIQUI R.A., HIPPLER B., JAHN D., FRIEDRICH III

**ILEB C., SIDDIQUI R.A., HIPPLER B., JAHN D., FRIEDRICH III

**ILEB C., SIDDIQUI R.A., HIPPLER B., JAHN D., FRIEDRICH III

**ILEB C., SIDDIQUI R.A., HIPPLER B., JAHN D., FRIEDRICH III

**ILEB C., SIDDIQUI R.A., HIPPLER B., JAHN D., FRIEDRICH III

**ILEB C., SIDDIQUI R.A., HIPPLER B., JAHN D., FRIEDRICH III

**ILEB C., SIDDIQUI R.A., HIPPLER B., JAHN D., FRIEDRICH R.A., HIPPLER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                  Alcaligenes eutrophus.
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
Ralstonia.
                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DUL-1999 (Rel. 39, Last sequence update)
0xYGEN-INDEPENDENT CORROPORPHYRINGEN III OXIDASE (EC 1.-.-.)
(COPROPORPHYRINGENASE) (COPROGEN OXIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 61.2%; Score 35.5; DB 1; Length 491; Best Local Similarity 57.1%; Pred. No. 11; Matches 8; Conservative 3; Mismatches 0; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porphyrin biosynthesis; Oxidoreductase; Magnesium; NAD. SEQUENCE 491 AA; 54216 MW; 3EE82375 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            609 AA.
                                                 491 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U94742; AAB66374.1; -.
                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 RLLIRRIAL --- RY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||:||:||: ||
441 RLLVRRVAMVEDRY
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                            HEMN_ALCEU
034162;
RESULT 1
HEMN_ALCEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRXC_CURIN
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                                                      à
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PRXC_CURIN STANDARD; F P49053; 01-FEB-1996 (Rel. 33, Created)

us-08-653-294-17.rsp

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Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                            1 YRLLIRRIALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                    burgdorferi
 g
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                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bloinformatics and the EMBL outstation the between alloinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-ATCC 35210 / B31;
MEDLINE; 98065943.
RAPLER C.M., FAGJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.,
LATHGRAR R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWINN M.,
DOUGHERTY B., TOMB J.F., FLEISCHMANN R.D., RICHARDSON D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                     MESSERSCHMIDT A., WEVER R.;

MESSERSCHMIDT A., WEVER R.;

"X-ray structure of a vanadium-containing enzyme: chloroperoxidase from the fungus Curvularia inaequalis.";

Proc. Natl. Acad. Sci. U. S.A. 93:392-396(1996).

-i- CATALYTIC ACTIVITY: 2 RH + 2 CHLORIDE + H(2)O(2) = 2 RCL + 2
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
VANADIUM CHLOROPEROXIDASE (EC 1.11.1.10) (VCPO) (VANADIUM CHLORIDE
                                                             Curvularia inaequalis.
Eukaryota; Fungi; Ascomycota; Euascomycetes;
Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Curvularia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                             SIMONS B. H., BARNET P., VOLLENBROEK E.G.M., DEKKER H.L., MUIJSERS A.O., MESSERSCHMIDT A., WEVER R.; PLINETY STRUCTURE and characterization of the vanadium "Primary structure and characterization of the vanadium chloroperoxidase from the fungus Curvularia inaequalis."; Eur. J. Biochem. 229:566-574(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 609;
17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> S (IN AA SEQUENCE).
19112E80 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oxidoreductase; Peroxidase; Vanadium; 3D-structure.
ACT_SITE 404 404
METAL 496 496 VANADIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borrelia burgdorferi (Lyme disease spirochete)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
18-DEC-1998 (Rel. 37, Last annotation update)
RPSO OR BBO804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 1
Pred. No. 17;
3; Mismatches
                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                  -:- SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67530 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X85369; CAA59686.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                        COFACTOR: VANADIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304 YNQIVRRIAVTY 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YRLLIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           609 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                       95262722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                   PEROXIDASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RS15_BORBU
ID RS15_BORBU
AC O51744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S., HANSON M., VAN VUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J., UTTERBACK T., WATTHEY L., MCDONALD L., ARTIACH P., BOWMAN C., GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B., SMITH H.O., VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                           Nature 390:580-586(1997).
-i- FUNCTION: THIS PROTEIN IS ONE OF THE 16S RIBOSOMAL RNA BINDING PROTEINS (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE S15P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 88;
                                                                                                                                                                   'Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 1;
Pred. No. 3.4;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00362; RIBOSOMAL_S15; 1.
PFAM; PF00312; Ribosomal_S15; 1.
Ribosomal protein; FRNA-binding.
SEQUENCE 89 AA; 10348 MW; 0E24D709 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00362; RIBOSOMAL_S15; 1.
PFAM; PF00312; Ribosomal_S15; 1.
Ribosomal protein; RRN-10217; MW; 054549EE CRC32; SEQUENCE 88 AA; 10217 MW; 054549EE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seq
15-JUL-1998 (Rel. 36, Last anno
30S RIBOSOWAL PROTEIN 515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE001179; AAC67150.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 298741; CAB11393.1; -. HSSP; P05766; 1A32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
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77 YRMLISKLGLR 87
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ZK849.5.
Caenorhabditis elegans.
Eukaryota: Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 LLIRRTIIRY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              502 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LLIRRIALRY 12
                                                                                                                          SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Multigene family.
                                                                                                                                                                KERSHAW J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAO3_CANTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D., GORDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TEKALA F., DAVIEN S.V., EASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., DAVIES R., DEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLROYD S., HORNSBY T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPHY L., OLIVER S., OSBORNE J., QUAIL M., RAJANDREAM M.A., ROGERS J., RAYLOR K., WHITEHEAD S., BARRELL B.G., TAXLOR K., WHITEHEAD S., BARRELL B.G., COMPLES S., SQARES R., SULSTON J.E., TOALLOR K., WHITEHEAD S., BARRELL B.G., B
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: THIS PROTEIN IS ONE OF THE 16S RIBOSOMAL RNA BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -! - SIMILARITY: BELONGS TO THE S15P FAMILY OF RIBOSOMAL PROTEINS.
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                   Score 34; DB 1; Length 89;
Pred. No. 3.5;

    Length 89;

                                                              3; Indels
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HYPOTHETICAL 48.2 KD PROTEIN ZK849.5 IN CHROMOSOME I.
                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
SS RIBOSOMAL PROTEIN S15.
RPSO OR RV2785C OR MIY002.50C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 AA; 10475 MW; 374C7EB8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 58.6%; Score 34; DB 38st Local Similarity 63.6%; Pred. No. 3.5; Matches 7; Conservative 1; Mismatches
                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00362; RIBOSOMAL_S15; 1. PFAM; PF00312; Ribosomal_S15; 1. Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AL008967; CAA15580.1; -.
                     58.68;
63.68;
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Ouery Match
Best Local Similarity 63.0،
اجر 7; Conservative
                                                                                                                                                                                                                                                STANDARD;
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                                                                                                  1 YRLLIRRIALR 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 98295987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YHSS_CAEEL
ID YHSS_CAEEL
AC 018304;
                                                                                                                                                                                                                                             RS15_MYCTU 033327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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MEDLINE, 87280361.
SMALL G.M., LAZAROW P.B.;
"Import of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of Candida tropicalis.";
J. Cell Biol. 105:247-250(1987).
-!- CATALYTIC ACTIVITY: ACYL-COA + O(2) - TRANS-2,3-DEHYDROACYL-COA + H(2)0(2) (ACTS ON COA DERIVATIVES OF FATTY ACIDS WITH CHAIN LENGTH FROM 8 TO 18).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PATHWAY: INITIAL STEP OF THE PEROXISOMAL FATTY ACID BETA-OXIDATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Candida tropicalis (Yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Candidaceae; Candida.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-JUV-1997 (Rel. 35, Last annotation update)
ACYL-COENZYME A OXIDASE POX4-2 (EC 1.3.3.5) (ACYL-COA OXIDASE)
(FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 411;
18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.6%; Score 34; DB 1; Length 502; 64.3%; Pred. No. 22; 1.1ve 1; Mismatches 2; Indels
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                   411 AA; 48236 MW; B5736F70 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55528 MW; EACE80C4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     502 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: PEROXISOMAL.
PIR; A28584; OXCKAX.
                                                                                                                                                                                                                                                                                                                                         WORMPEP, ZK849.5; CE16750.
PFAM; PF01062; Worm_family_8; 1.
Hypothetical protein.
SEQUENCE 411 AA; 48236 MW; B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.6%;
                                                                                                                                                                                                                                                                                                                 EMBL; Z82095; CAB05028.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBUNIT: HOMOOCTAMER
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Conservative
                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                            307 YRMLARMSTIALRY 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||:|| | |||||
307 YRMLARVSTIALRY 320
                                                                                                                                                    1 YRLLIR--RIALRY 12
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-ATCC 20184;
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                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                          CAO4_CANMA
P05335;
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                  RESULT 9
CAO4_CANMA
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POLG_DEN26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMALL G.M., LAZAROW P.B.;
"Import of the carboxy-terminal portion of acyl-CoA oxidase into
peroxisomes of Candida tropicalis.";
J. Cell Biol. 105:247-250(1987)
-:- CAPALYTIC ACYL-COA + O(2) = TRANS-2,3-DEHYDROACYL-COA +
H(2)0(2) (ACTS ON COA DERIVATIVES OF FATTY ACIDS WITH CHAIN LENGTH
FROM R TO 18).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- COFACTOR: FAD.
-!- PATHWAY: INITIAL STEP OF THE PEROXISOMAL FATTY ACID BETA-OXIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metabolism; Peroxisome; Flavoprotein; FAD;
                                                                                                                                                                                                                                                                                                                                                        STRAIN-ATCC 20336 / PK233;
MEDLINE: 86149279.
OKAZAKI K., TAKECHI T., KAMBARA N., FUKUI S., KUBOTA I., KAMIRYO T.;
TWO acyl-coenzyme A oxidases in peroxisomes of the yeast Candida
tropicalis: primary structures deduced from genomic DNA sequence.";
Proc. Natl. Acad. Sci. U.S.A. 83:1232-1236(1986).
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-ATCZ 20336 / PK233;
MEDLINE: 92488070.
MURRAY W.W., RACHUBINSKI R.A.;
MURRAY W.W., SACHUBINSKI R.A.;
The primary structure of a peroxisomal fatty acyl-CoA oxidase from the yeast Candida tropicalis pK233.";
Gene 51:119-128(1987).
                                                                                                                         01-JAN-1988 (Rel. 06, Created)
UNOV-1988 (Rel. 09, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ACYL-COENZYME A OXIDASE II (EC 1.3.3.6) (ACYL-COA OXIDASE) (PXP-4).
                                                                                                                                                                                  Candida tropicalis (Yeast).
Eukaryota, Fungi, Ascomycota, Hemiascomycetes, Saccharomycetales,
Candidaceae, Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REF. 3).
REF. 2 AND 3).
REF. 2).
ERROR (IN REF. 2 AND 3).
                                                                                                    708 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q -> E (IN F
P -> A (IN F
N -> K (IN F
FRAMESHIFT E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: HOMOOCTAMER.
SUBCELLULAR LOCATION: PEROXISOMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M16193; AAA34322.1; -.
EMBL; M12160; AAA34362.1; -.
EMBL; Y00623; CAA68660.1; -.
EMBL; Y00623; CAA68661.1; ALT_INIT.
EMBL; Y00623; CAA68662.1; ALT_INIT.
PIR; A25123; OXCKX4.
                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 208-709 FROM N.A.
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ATCC 20336 / PK233;
MEDLINE; 86149279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oxidoreductase; Fatty acid
                                                                                                    STANDARD;
                                     101 YRMLARMSTIALRY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216
245
335
393
             1 YRLLIR--RIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-RR1;
MEDLINE; 87280361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Multigene family.
                                                                                                                                                                             OR POX-4.
                                                                                                   CAO2_CANTR
P06598;
                                                                                      CAO2_CANTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- PATHWAY: INITIAL STEP OF THE PEROXISOMAL FATTY ACID BETA-OXIDATION
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase; Fatty acid metabolism; Peroxisome; Flavoprotein; FAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1988 (Rel. 09, Created)
01-NAY-1992 (Rel. 22, Last sequence update)
01-WAY-1992 (Rel. 22, Last annotation update)
ACYL-COENZYME A OXIDASE POX4 (EC 1.3.3.6) (ACYL-COA OXIDASE) (AOX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Candida maltosa (Yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Candidaceae; Candida.
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                                                                                                                                                                                                 Query Match 58.6%; Score 34; DB 1; Length 708; Best Local Similarity 64.3%; Pred. No. 33; Matches 9; Conservative 1; Mismatches 2; Indels
H -> Y (IN REF. 2).
G -> A (IN REF. 2).
E -> S (IN REF. 2).
ELA -> DLV (IN REF. 2).
Q -> E (IN REF. 2 AND 3).
                                                                                                                          D97A4EC8 CRC32;
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D5E344D2 CRC32;
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435 H
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495 E
578 EI
697 Q
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                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
115-DEC-1998 (Rel. 37, Last annotation update)
GENOME POLYPROTEIN (COUTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E;
NONSTRUCTURAL PROTEINS NS1, NS2B, NS4B, NS4B; HELICASE (NS3);
RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (NS5)].
Dengue virus type 2 (strain 16681).
Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                              BLOK J., MCWILLIAM S.M., BUTLER H.C., GIBBS A.J., WEILLER G.,
HERRING B.L., HEMSLEY A.C., AASKOV J.G., YOKSAN S.,
BHAMARAPRAVATI N.;
"Comparison of a dengue-2 virus and its candidate vaccine derivative:
sequence relationships with the flaviviruses and other viruses.";
Virology 187:573-590(1992).

-! FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
-! SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN C AND MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00869; Flavi_glycoprot; 1.
PFAM; PF00949; Flavi_helicase: 1.
PFAM; PF00949; Flavi_helicase: 1.
PFAM; PF00972; Flavi_NS2B; 1.
PFAM; PF01002; Flavi_NS2B; 1.
PFAM; PF01004; Flavi_MS2B; 1.
PFAM; PF01004; Flavi_MS2B; 1.
PFAM; PF01005; Flavi_MS4B; 1.
PFAM; PF01005; Flavi_NS4B; 1.
PFAM; PF01350; Flavi_NS4B; 1.
PFAM; PF01570; Flavi_NS4B; 1.
PFAM; PF01570; Flavi_Dropep; 1.
Polyprotein; Glycoprotein; Transferase; RNA-directed RNA polymerase; Core protein; Coat protein; Envelope protein; Helicase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NONSTRUCTURAL PROTEIN NS1.
NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2B.
HELICASE (NS3).
NONSTRUCTURAL PROTEIN NS4B.
NONSTRUCTURAL PROTEIN NS4B.
RNA-DIRECTED RNA POLYMERASE (NS5).
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 3391 AA.
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  PRT;
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 STANDARD;
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                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 92188532.
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01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E;
PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E;
PROSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3);
RNA-DIRECTED FRAM POLYMERASE (EC 2.7.7.48) (NS5)].
Dengue virus type 2 (strain 16681-PDK53).
Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BHAMARAPRAPATI N.;

"Comparison of a dengue-2 virus and its candidate vaccine derivative:

"Comparison of a dengue-2 virus and its candidate vaccine derivative:

"Comparison of a dengue-2 virus and its candidate vaccine derivative:

"Comparison of a dengue-2 virus and its candidate vaccine derivative:

"Virology 187:573-590(1992).

"I FUNCTION: THE SMALL PROTEINS NS2A, NS2A, NS4A AND NS4B ARE

HYDROPHORIAC., SUGGESTING A POSSIELE MEMBRANE-RELAFED FUNCTION.

"SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROFIEN BYNELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:

PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA.
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Pred. No. 1.8e+02;
2; Mismatches 3; Indels
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BY SIMILARITY.
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Matches 6: Conserv
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P29991;
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                                                                                                                                                  PFAM; PF00948; Flavi_NS1; I.
PFAM; PF00949; Flavi_NB1; I.
PFAM; PF00972; Flavi_NB5; I.
PFAM; PF01002; Flavi_NS5; I.
PFAM; PF01003; Flavi_Capsid; I.
PFAM; PF01004; Flavi_NS4; I.
PFAM; PF01005; Flavi_NS4B; I.
PFAM; PF01570; Flavi_Dropep; I.
PF01YPF0161n; Goat Protein; Tanasferase; RNA-directed RNA polymerase; Core protein; Coat Protein; Envelope protein; Helicase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                          HELICASE (NS3).
NONGTRUCTURAL PROTEIN NS4A.
NONSTRUCTURAL PROTEIN NS4B.
RNA-DIRECTED RNA POLYMERASE (NS5).
ATP (POTENTIAL).
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NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2B.
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                                                                                                                                                                                                                                                                                    Nonstructural protein.
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                                                                                                          EMBL; M84727; -; NOT_ANNOTATED_CDS
BTR: 8424541; GNWY26.
HSSP: P14336; LSVB.
PFAM; PF00869; Flav1_glycoprot; 1.
                                                                                                EMBL; M84728; AAA73186.1; -.
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1-FEB-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
HYPOTHETICAL 98.7 KD PROTEIN IN SLU7-BMH2 INTERGENIC REGION.
HYPOTHETICAL 98.7 KD PROTEIN IN SLU7-BMH2 INTERGENIC REGION.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungl; Ascomycota; Hemiascomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
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1-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 34 KD PROTEIN IN METI-SIS2 INTERGENIC REGION
                                                                                              Length 3391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 352;
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                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
POHL T.M., POHL F.M.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-161 FROM N.A.
STRAIN=5288C / FY1679;
COSTER F., JONNIAUX J.-L., GOFFEAU A.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                            58.6%; Score 34; DB 1; Le 54.5%; Pred. No. 1.8e+02; Live. 2; Mismatches 3;
                               POTENTIAL.
MW; 70570314 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.9%; Score 33; DB 1; 60.0%; Pred. No. 24; 1ive 3; Mismatches
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 POTENTIAL. POTENTIAL.
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2665 2665
2704 2704
2714 2714
3391 AA; 379878 N
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Best Local Similarity 60.0
Matches 6; Conservative
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2728 RMLINRFIMRY 2738
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223 FRLLVRRLYL 232
                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
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YK50_YEAST
ID YK50_YEAST
AC P36151;
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YD95_YEAST
ID YD95_YEAST
AC P38966;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 96194804.
MEDLINE; 96194804.
MEDLINE; 96194804.
MEDLINE; 96194804.
THE ESCHLE E., PERDL G.G., HARRER N.E., BAUMRUKER T.;
The murine homolog of TB2/DP1, a gene of the familial adenomatous polyposis (FAP) locus.";
Gene 168:215-218 (1996).
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-1- SIMILARITY: TO C.ELEGANS T19C3.4.
                                                                                                                                                                                                                             PROSITE; PS01110; RNA_POL_H_23KD; 1.
PFAM; PF01191; RNA_POL_H; 1.
Transferase; Transcription; DNA-directed RNA polymerase; 3D-structure.
SEQUENCE 78 AA; 9001 MM; 9F10C0F3 CRC32;
-i- SIMILARITY: TO OTHER ARCHAEBACTERIAL RPOH AND TO THE C-TERMINAL OF EUKARYOTIC SUBUNIT ABC27 (RPB5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-Nov-1997 (Rel. 35, Created)
01-Nov-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 35, Last annotation update)
POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106).
                                                                                                                                                                                                                                                                                                                                                            ó
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                                                                                                                                                                                                                                                                                                                           Length 78;
                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3,
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                                                                                                                                                                                                                                                                                                                           55.2%; Score 32; DB 1; 75.0%; Pred. No. 7.6; 1ive 2; Mismatches 0
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POTENTIAL.
FC5BA4A2 CRC32;
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Pred. No. 19;
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106 PO
21050 MW;
                                                                                                                                                                              EMBL; U67546; AAB99042.1; -. PDB; 1HMJ; 05-APR-99.
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58.3%;
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Best Local Similarity 58.3°,
T; Conservative
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86
185 AA;
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Best Local Similarity
Matches 6; Conserv
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70 YRLVIKRI 77
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                                                                                                                                                                                                               TIGR; MJ1039;
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Q60870;
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SEQUENCE
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DP1_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fold that is present in archaea and eukaryotes.";
J. Mol. Biol. 287:753-760(1999)
-i- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D., SUTTON G.G., BLAKE J.A., FITZEERALD L.M., CLATTON R.A., GOCAYNE J.D., KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I., OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A., SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.E., FUHRMANN J.L., NGTYEN D., UTTERBACK T.R., KELLEY J.M., PETERSON J.E., FUHRMANN J.L., HANNA M.C., COTTON M.D., ROBERTS K.M., HRST M.A., KAINE B.P., BORODOVSKY M., COTTON M.D., RRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'RNA polymerase subunit H features a beta-ribbon motif within a novel
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THIRU A., HODACH M., ELORANTA J.J., KOSTOUROU V., WEINZIERL R.O., MATTHEWS S.;
                                                                                 B.G., RAJANDREAM M.A., WALSH S.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                             Length 869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methanococcus jannaschil.
Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
 SEQUENCE OF 1-260 FROM N.A. RICHARDS C., HARRIS D.E., BARRELL B.G., RAJANDREAM M.A.; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                              SECUENCE OF 248-869 FROM N.A. OLIVER K., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WAL Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UUC-1999 (Rel. 38, Last annotation update)
DNA-DIRECTED RNA POLYMERASE SUBUNIT H (EC 2.7.7.6).
                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
64;
                                                                                                                                                                                                                                                                                                                               l protein.
869 AA; 98711 MW; F8ED2ABB CRC32;
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             Score 33;
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STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE; 96337999.
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77.8%;
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EMBL; 274385; CAA98910.1;
PIR; 548778; 548778
                                                                                                                                                                                                                                                               EMBL; X82086; CAA57618.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                            Query Match 56.9
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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| 126 LIIORIALR 134
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                                                                                                                                                                                                                                                                                                                             Hypothetical
SEQUENCE 81
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Gaps

Db 133 YRRIIRPIFLRH 144

Search completed: February 8, 2000, 00:59:56 Job time: 3785 sec

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database :

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032384 synechococc 085633 sphingomona 08438 treponema p 017713 ceenorhabdi 047402 escherichia 09558 escherichia 05559 aquifex aeo 06691 aquifex aeo 06691 aquifex aeo 06691 aquifex aeo 06691 aquifex aeo 06917 mycobacteri 0598393 treponema p 06611 mycobacteri 09774 klebsiella 082580 arachia hyp 097211 leishmania p79087 embellisia 099418 aeropyrum p 06966 bacillus su 099418 aeropyrum p 06966 bacillus su 099410 aeropyrum p 06966 bacillus su 096050 rhopalosiph
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004350 cryphonectr
09z5a0 streptomyce
031072 synechococc
P71746 mycobacteri
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022063; Q93489;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TREMBLrel. 12, Last annotation update)
01-NOV-1999 (TREMBLrel. 12, Last annotation update)
1701C3.10.
1701C3.10.
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1701C3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WILD A.;
WILD A.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; 281061; CAB01939.1; J.
EMBL; 278413; CAB01667.1; J.
EMBL; 281061; CAB01667.1; J.
EMBL; P19491; IGR2.
PFAM; PF00060; 11g-chan; 1.
SEQUENCE 795 AA; 89703 MW; DD722166 CRC32;
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Last sequence update)
Last annotation update)
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 032384
085853
084583
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069517
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087211
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09X378;
01.NOV-1999 (TEMBLEE1. 12
01.NOV-1999 (TEMBLEE1. 12
PXO1-117.
Bacillus anthracis.
                                                     274
296
296
406
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417
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3164
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6 YRTSLRRLATRY 17
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 RESULT
Q22063
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Q9x378 bacillus an
P97213 clostriddium
Q9487 homo sapien
Q9xD05 myxococcus
O15455 homo sapien
O86547 mycobacteri
O07074 porphyromon
O87630 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O58274 pyrococcus
Q9yv77 melanoplus
Q19yv77 melanoplus
Q11875 dengue viru
Q09234 unidentifie
Q30127 archaeoglob
Q9yw17 melanoplus
Q9y821 aeropyrum p
Q93329 caenorhabdi
Q5389 streptomyce
Q9y483 homo sapien
Q42617 brassica na
                                                                                                                  Search time 209.03 Seconds (without alignments) 3.980 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                          225878 segs, 69334122 residues
                                                                                                                    8, 2000, 13:17:44;
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                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                summaries
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Q9X378
P97213
O94887
Q9X805
O15455
O86347
O97074
Q9YVN7
O11875
O9234
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Gapop 10.0 , Gapext 0.5
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09Y8Z1
093329
053839
09Y483
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sp_unclassified:*
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sp_invertebrate:*
sp_mammal:*
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sp_phage:*
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sp_bacteria:*
sp_fungi:*
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58
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Listing first 45
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sp_rodent: *
sp_virus: *
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Maximum DB seq length: 1000000
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Match Length
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Score

Result No.

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688 YRLLLRRLCGHY 699
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Best Local Similarity
Matches 7; Conserv
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MEDLINE; 99087487
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Q9XB05;
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                                                                                                             OKINAKA R.T., CLOUD K., HAMTON O., HOFFMASTER A., HILL K.K., KEIM P., KOEHLER T., LAMKE G., KUMANO S., MAHILLON J., MANTER D., MARTINEZ Y., RICKE D.O., SVENSSON R., JACKSON P.U.; The sequence and organization of pX01, the large Bacillus anthracis plasmid harboring the Anthrax toxin genes."; Bacteriol. 0:0-0(1999).

EMBL: AF005504; AAD32421.1;
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-1997 (TrEMBLrel. 03, Last annotation update)
cDU2, CDU1, TCDD, TCDB, TCDE, TCDC, CDD1, CDD2, CDD4
GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium difficile.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                63.8%; Score 37; DB 2; Length 132; 63.6%; Pred. No. 8.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.8%; Score 37; DB 2; Length 313; 41.7%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                         Indels
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STRAIN-VPI10463;
SURDIN-VPI10463;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; X92982; CAA635591;
EMBL; X92982; CAA635581;
EMBL; X92982; CAA635581;
EMBL; X92982; CAA635581;
EMBL; X92982; CAA635881;
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Last annotation update)
               Bacteria; Firmicutès; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus
                                                                                                                                                                                                                                                                                    SEQUENCE 132 AA; 15748 MW; 097E4E16 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1054 AA
                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
  Plasmid virulence plasmid PX01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, C: 01-MAY-1999 (TrEMBLrel. 10, Ls 01-NOV-1999 (TrEMBLrel. 12, Ls KIAA0793 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 63.8
Best Local Similarity 41.7
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                Query Match 63.8
Best Local Similarity 63.6
Matches 7; Conservative
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259 YRVVARRLSIKY 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                  2 RLLIRRIALRY 12
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87 RILLRRAALNY 97
                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 094887
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094887
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PAITAN Y., ORR E., RON E.Z., ROSENBERG E.;
"Genetic and functional analysis of genes required for the post-
modification of the polyketide antibiotic TA of Myxococcus xanthus.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ132503; CAB46503.1; -.
NAGASE T., ISHIKAWA K., SUYAWA M., KIKUNO R., MIYAJIMA N., TANAKA A., KOTANI H., NOWURA N., OHARA O.;
"Prediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; delta subdivision; Myxobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
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                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-754 FROM N.A.
SEQUENCE OF 1-754 FROM N.A.
SUN H., STONEKING T., LANGSTON Y., LAPLANT Y.;
"The sequence of Homo sapiens BAC clone RG442F18.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO18336; BAA34513.1; -.
EMBL; AC005104; AAD12224.1; -.
HSSP; PO8567; 1PLS.
SEQUENCE 1054 AA; 119888 MW; 3BA89171 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WATERSTON R.H.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MEMBRANE ASSOCIATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 62.1%; Score 36; DB 2; Best Local Similarity 58.3%; Pred. No. 31; Matches 7; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4CC64E85 CRC32;
                                                                                                                                                                                                                SEQUENCE OF 1-754 FROM N.A.
MEDLINE; 99063792.
SULSTON J.E., WATERSTON R.;
TOWARD a complete human genome sequence.";
Genome Res. 8:1097-1108(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325 AA
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58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-754 FROM N.A.
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SEQUENCE OF 1-754 FROM N.A.
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Gaps

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SEQUENCE FROM N.A.

STRAIN-CV. LANDSBERG ERECTA;

MEDLINE; 9841223358;

GAYMARD F., PILOT G., LACOMBE B., BOUCHEZ D., BRUNEAU D.,

BOUCHEREZ J., MICHAUX-FERRIERE N., THIBAUD J.B., SENTENAC H.;

"Identification and disruption of a plant shaker-like outward channel involved in R + release into the xylem sap.";

Cell 94:647-655 (1998).

EMBL, AJ223358; CAA11281.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HONGO H.;
"Nucleotide sequence upstream from the fimbrilin gene (fimA) of the oral anaelobe Porphyromonas gingivalis.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB004560; BAA330661; -3 SEDQUENCE 490 AA; 55272 MW; 385AD4FF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; eudicotyledons;
core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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                                                                                                                                                 2; Length 309
                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Cytophagales; Bacteroidaceae; Porphyromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TEMBLrel. 12, Last annotation update)
STELAR K+ OUTWARD RECTIFIING CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1997 (TrEMBLrel. 04, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
PFAM; PF00175; oxidored_fad; 1.
Hypothetical protein; Iron-sulfur.
SEQUENCE 309 AA; 33517 MW; B152B590 CRC32;
                                                                                                                                             Score 35; DB 2
Pred. No. 46;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  490 AA
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                                                                                                                                       DB
46;
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PF00023; ank; 3.
PF00914; CNG_membrane;
PF00027; CNMP_binding;
                                                                                                                                             60.3%;
77.8%;
                                                                                                                                             Query Match 60.3
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 60.3
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                 65 YRIAIRRIA 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  007074
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082630
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007074
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MEDLINE; 9829597.
COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D., GONDON S.V., EIGAMEIER K., GAS S., BARRY III C.E., TEKAIA F.,
BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R.,
DAVIES R., DEVLIN K., FELTWELL T., GENTLES S., HAMIIN N., HOLROYD S.,
HORNESP T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPY L.,
OLIVER S., OSBORNE J., QUAIL M.A., RAJANDREAM M.A., ROGERS J.,
RUTTER S., SEEGER K., SKELTON S., SQUARES S., SQARES R., SULSTON J.E.,
TAYLOR K., WHITHEHEAD S., BARRELL B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SUDMITTED (FEB. 1997) to the EMBL/GenBank/DDBJ databases.

EMBL: U88899; AAG34134.1; --

PFAM; PF00560; LRR: 15.

PFAM; PF0163; TRRCT; 1.

PFAM; PF01582; TRR.T; 1.

PROMOSED: LEWRITCHRPT.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHETICAL 33.5 KD PROTEIN.
                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           904 AA; 103828 MW; F857CE1C CRC32;
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Pred. No. 85;
                                                                                                                                                                                904 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                               Created)
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60.0%;
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12,
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                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                      01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
TOLL-LIKE RECEPTOR 3.
   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||::||:||:
484 REMERRYALK 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RLLIRRIALR 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                             015455
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086347
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Gaps

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Gaps

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Length 530;

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Dengue virus type 2.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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"Construction of infectious cDNA clones for dengue 2 virus: strain 1661 and its attenuated vaccine derivative, strain PDK-53.";
Virology 230:300-308(1997).
EMBL: U8442; AMBS8783.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 12; Length 3391;
Pred. No. 7.5e+02;
2; Mismatches 3; Indels
                                                                                                Score 34; DB 12; Length 53
Pred. No. 1.2e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379861 MW; 5F56B205 CRC32;
EMBL; AF063866; AAC97756.1; -.
SEQUENCE 530 AA; 65062 MW; D29ED6FE CRC32;
                                                                                                                                                                                                                                                                                                                                                                          PRT; 3391 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 3391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P14336; ISVB.
PF00869; Flavi_glycoprot; 1.
PF00949; Flavi_helicase; 1.
PF01004; Flavi_M; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF01570; Flavi_propep; 1 PFAM; PF01003; Flavi_capsid; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flavi_NS2A; 1
Flavi_NS2B; 1
                                                                                                   58.6%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flavi_NS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F01349; Flavi_NS4B; 1
F00972; Flavi_NS5; 1,
F01570; Flavi_propep;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flavi_NS4A;
                                                                                                Query Match 58.6
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 58.6
Best Local Similarity 54.5
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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2728 RMLINRFIMRY 2738
                                                                                                                                                                                                                                :|| :| | :||
139 HRLYLREIPIRY 150
                                                                                                                                                                                                 1 YRLLIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3391 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RLLIRRIALRY 12
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SEQUENCE FROM N.A.
STRAIN-16681;
MEDLINE; 97288308.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-PDK-53;
MEDLINE; 97288308
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unclassified
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        009234
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PFAM;
PFAM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 98344137.
KAWARABAYASI Y., SAWADA M., HORIKAWA H., HAIRAWA Y., HINO Y.,
YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAWA A., NAGAI Y.,
SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y.,
FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,
KIKUCHI H.;
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Melanoplus sanguinipes entomopoxvirus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
Entomopoxvirus B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete: Sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii OT3."; DAN Res. 5:55-76(1989).
EMBL; AB000002: BAA2528.1; -. SEQUENCE 362 AA; 41831 MW; EB8D18CF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=TUCSON; AFONSO C.L., TULMAN E.R., LU Z., OMA E., KUTISH G.F., ROCK D.L.; Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                            5;
                                                                         Length 828;
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                                                  Score 35; DB 10; Length 82/
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 99102612.
AFONSO C.L., TULMAN E.R., LU Z., OMA E., KUTISH G.F., RC
"The genome of Melanoplus sanguinipes entomopoxvirus.";
J. Virol. 73:533-552(1999).
                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
362AA LONG HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
0RF MSV205 TRYPTOPHAN REPEAT GENE FAMILY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
83;
     93898 MW; AA41E3DD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             530 AA.
                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.6%;
                                                                       60.3%;
ilarity 57.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 58.6
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                           ||:::| |||||
|143 YRMIYKRSSIALRY 156
                                                                                                                                                                             1 YRLLIRR--IALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyrococcus horikoshii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || ::: ||| |
296 YRFILKAIALGY 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YRLLIRRIALRY 12
     828 AA;
                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                     058274
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                                                                                                                                                                                                                                                                                                     RESULT 10
058274
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                                                                                                                          Matches
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38 YVELARKIAMRY 49
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                                          RESULT 15
Q9YW71
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STRAIN-VC-16 / DSM 4304 / ATCC 49558;

MEDLINE; 98049343.

KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,

KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,

KICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C.,

FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,

KIKKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,

PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,

OVERBEEK R., GOGAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,

COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M.,

SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,

MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
KINNEY R.M., BUTRAPET S., CHANG G.J., TSUCHIYA K.R., ROEHRIG J.T., BHAMMRAPRAVATI N., GUBLER D.J.;
CONSTRUCTION Of infectious cDNA clones for dengue 2 virus: strain 16681 and its attenuated vaccine derivative, strain PDK-53."; virology 230:300-308(1997).
EMBL: U87411; AAB58782.1; -.
HSSP; PI4336; 1SUS.
PFAM; PF00869; Flavi_glycoprot; 1.
PFAM; PF00949; Flavi_helicase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Mature 390:364-370(1997).
EMBL: AR001099; AAB91122.1; --
TIGR: AF0109; --
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                                                                                                                                                                                                                                                                                                 Score 34; DB 12; Length 3391;
Pred. No. 7.5e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Buryarchaeota; Archaeoglobales; Archaeoglobaceae;
Archaeoglobus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                             3391 AA; 379800 MW; A839A51C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 1;
Pred. No. 39;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     il protein.
107 AA; 13307 MW; F23652A7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 AA
                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                 PF01005; Flavi_NS2A; 1.
PF01002; Flavi_NS2B; 1.
PF01350; Flavi_NS4A; 1.
PF01349; Flavi_NS4B; 1.
PF00972; Flavi_NS5; 1.
                                                                                                                                                                                                                     PF01570; Flavi_propep; 1 PF01003; Flavi_capsid; 1
                                                                                                                                                                                                                                                                                                    58.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.9%;
58.3%;
                                                                                                                         PF01004; Flavi_M; 1.
PF00948; Flavi_NS1; 1.
                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 56.9
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                           |:|| | :||
2728 RMLINRFTMRY 2738
                                                                                                                                                                                                                                                                                                                                                          2 RLLIRRIALRY 12
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
SEQUENCE 10
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                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                         PFAM;
PFAM;
                                                                                                                                                                 PFAM;
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1 YRLLIRRIALRY 12

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Gaps
                                          01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
MSV021.
MSV021.
Melanoplus sanguinipes entomopoxvirus.
Miruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-TUCSON;
AFONSO C.L., TULMAN E.R., LU Z., OMA E., KUTISH G.F., ROCK D.L.;
SUDmitted (MAT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF063866, AAC97850.1; -
SEQUENCE 260 AA; 31180 MW; AB880E14 CRC32;
                                                                                                                                                                                                                                                                                                                                                              OMA E., KUTISH G.F., ROCK D.L.;
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MEDLINE; 99102612.
AFONSO C.L., TULAAN E.R., LU Z., OMA E., KUTISH G.F., RC
"The genome of Melanoplus sanguinipes entomopoxvirus.";
J. Virol. 73:533-552(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.9%; Score 33; DB 12;
58.3%; Pred. No. 93;
iive 1; Mismatches 4
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i AC014422 Drosophila melano
i AC018284 Drosophila melano
i 295124 Human DNA sequence
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*** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                          DMRNA3 1050 bp DNA INV 31-MAR-1992
Three Drosophila melanogaster genes for transfer RNAs (Glu specific).
V00238 JULIA GI:8458
transfer RNA; transfer RNA-Glu.
                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
Drosophilidae; Drosophila.

( (bases 1 to 1050)
Hosbach, H.A., Silberklang, M. and McCarthy, B.J.
Evolution of a D. melanogaster glutamate tRNA gene cluster
81001852
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Gaps: 0
Percent Identity: 66.667
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    /organism-"Drosophila melanogaster"
/db.xref-"taxon:7227"
    1050

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/note="transfer RNA:glu4:62Aa"
/allele=""
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/note="tRNA Glu"
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262. .333
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/gene="tRNA.E4:62Aa"
/note="tRNA Glu"
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9.5e+03
1.1e+04
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DEFINITION Drosophila melanogaster,
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AC017966.1 GI:6553224
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1050 iv00238 Three Drosophila melanogast
143914 i AC010566 Drosophila melanogast
143914 i AC010564 Drosophila melanogast
143914 i AC005847 Drosophila melanogast
100389 i AC05847 Drosophila melanogast
100389 i AC005802 Leishmania major chr
10142 i AL008256 S. Solfataricus iloo kt
10000 i AC009602 Leishmania major chr
19142 i AL13800 Homo sapiens chromo
29688 i 281502 Caenorhabditis elegans
207672 i AC005834 Homo sapiens chromo
29689 i 285311 Caenorhabditis elegan
229644 i AL121872 Homo sapiens chromo
29689 i 285311 Caenorhabditis elegan
624 i AL035310 Mycobacterium leprae
67935 i AC005834 Homo sapiens chromo
18750 i AC009341 Drosophila melanogas
102044 i AL121872 Homo sapiens chromo
18750 i AC009613 Homo sapiens chromo
188574 i AL121956 Homo sapiens chromo
188574 i AL121956 Homo sapiens chromo
188574 i AL12959 Uncultured archaeon
1047 i AF01592 Uncultured archaeon
1047 i AF01593 Horoltured archaeon
1066 i AF055731 HIV-1 strain CMR709-3
24942 i 282276 Caenorhabditis elegans
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-MODEL-frame-promodel -DEV-x1p
-MODEL-frame-promodel -DEV-x1p
-MODEL-frame-promodel -DEV-x1p
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9b_htg2:HSD5689N3
9b_htg2:HSD5555
9b_ba1:BD11275
9b_ba1:AF142982
9b_ba1:AF142982
9b_ba1:AF015978
9b_ba1:AF015978
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                                                 Date: Feb 8, 2000
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9D_in2.AC005834
9D_htg1:HSB348B13
9D_htg1:CEY47H10
9D_pat:A46810
9D_ph:B72002303
9D_bal:MCB2533
9D_bal:UC00017
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gb_pi2:SPAC2F3
gb_htg1:CEX113B8_3
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9b_htg7:AC017966
9b_htg4:AC010564
9b_ba1:AC005847
9b_ba1:MTCY427
9b_ba1:S100KBFR
9b_htg3:AC009602
9b_htg1:CNS01DTM
9b_sts:G18985
9b_ba2:AF096137
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gb_htg7.AC017368
gb_htg3.AC009341
gb_pl2:F10A2
gb_htg2:AC005805
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gb_vi:AF055732
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      Sukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                               Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Adams,M. and Venter,J.C.
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Submitted (16-5EP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Sep 22, 1999 this sequence version replaced gi:5916428.

* NOTE: This is a "working draft, sequence. It currently * consists of 89 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Blazej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B., Lomotan, M.A., Maxda, P., Moshrefi, A.R., Moshrefi, M., Mixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Zhang, R., Zieran, L.L. and Rubin, G.M. Sequencing of Drosophila chromosome 3L, region 61F3-62A2
Unpublished (1997)
E. (Dases i to 268369)
E. Celniker, S.E., George, R.A., Galle, R.F., Hoskins, R.A., Baxter, E., Svirskass, R.R., Harris, N.L., Agbayani, A., Arcain, D.E., Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Punch, E., Snir, E., Twomey, B., Pacleb, J.M., Park, S., Pfeiffer, B., Punch, E., Snir, E., Twomey, B., Pacleb, J.M., Park, S., Pfeiffer, B., Punch, E., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lubratted (22-001-1998) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US Sequence submitted by:

Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
For further Information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to baggefruitfly.berkeley.edu.

Library locations: 11-34, 21-67, 44-36, 73-50, 92-76.
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/map="61F3-622"
/clone="Pls D803179 (D226), D806357 (D230), D803404
/clone="Pls D803179 (D226), D806357 (D230), D803404
(D231), D806962 (D232), and D807291 (D240)"
//note="These five Pls were completed as a project. The coordinates are the Pl ends for each Pl. D803404
(D231)extends from bp 1 to bp 80,732. D803179 (D226)
extends from bp 32,734 to bp 117,954. D806357 (D230)
extends from bp 127,117 to bp 209,427. D806962 (D232)
extends from bp 127,117 to bp 209,427. D807291 (D240)
extends from bp 194,759 to bp 268,369."
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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/organism="Drosophila melanogaster"
/db.xref="taxon,7227"
/chromosome="31."
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US-08-653-294-17 x AC005847/rev
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DNA sequence (P1s DS03179 (D226), DS06357
DS06962 (D232), and DS07291 (D240)),
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

(Dases 1 to 268369)
Celniker, S.E., George, R.A., Galle, R.F., Hoskins, R.A.,
Svirskas, R.R., Harris, N.L., Agbayani, A., Arcaina, T.T., Baxter, E.,

      seq_documentation_block:
      22-c

      LOCUS
      AC005847
      268369 bp
      DNA

      LOCUS
      AC005847
      268369 bp
      DNA

      DEFINITION
      Drosophila melanogaster
      DNA
      sequence (PIS DS03179 (DZ32)

      (D230), DS03404 (D231), DS06962 (D232), and DS07291 (Complete sequence.
      AC006847 AC004431

      ACCESSION
      AC005847 AC004431
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/db_xref="taxon:7227"
/chcnosome="3L/62A1"
/clone="RPCT98-2701"
/ 33523 c 32072 g 39042 t 557
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of 2425
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      68874
70020
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MEDLINE REMARK

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COMMENT

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EVGSGGQAEI NYQFNSLLHAADDMQLYKYII KNTAWONGKTVTFMPKPLFGDNGSGMH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO ISA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk on Jun 27, 1998 this sequence version replaced gi:1261921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Rv2220, (MTCY190.31-MTCY427.01), len: 478.glnAl, Probable glutamine synthetase, glnA, similar to many eg SW:GLMA_STRCO P15106 (71.4% identity in 475 aa overlap); contains PS00180 Glutamine synthetase signature 1, PS00181 Glutamine synthetase putative ATP-binding region signature, PS00182 Glutamine synthetase class-I
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PYSRDPRNIARKAENYLISTGIADTAYFGAEAEFYIFDSVSFDSRANGSFYEVDAISG
WWNTGAATEADGSPNRGYKVRHKGGYFPVAPNDQYVDLRDKMLTNLINSGFILERGHH
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/translation="MTEKTPDDVFKLAKDEKVEYVDVRFCDLPGIMQHFTIPASAFDK
                          1 (bases 1 to 38110)
Cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C.,
Haris, D., Gordon, S.V., Eiglmeler, K., Gas, S., Barry III, C.E.,
Haris, D., Gordon, S.V., Eiglmeler, K., Gas, S., Barry III, C.E.,
Tekaia, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T.,
Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J.,
Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A.,
Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S.,
Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S.,
Barrell, B.G.
Berrell, B.G.
Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C.
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/organism="Mycobacterium tuberculosis"
/strain="H37Rv"
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/db_xref="GI:3261568"
                                                                                                                                                                                                                                                                                                                                                                                                                                             complete genome sequence
Nature 393 (6685), 537-544 (1998)
98295987
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163. .1599
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Parkhill,J.
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Direct Submission
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FEATURES

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ginE_Probable ginE, similar to SW:GLNE_ECOLI P30870
glutamate-ammonia-ligase adenylyltransferase (24.4%
identity in 721 aaoverlap) and SW:GLNE_HABIN P44419 (28.1%
identity in 199 aa overlap); initiation codon uncertain
unless at 39346 or 39247
CHOSLWKDGAPLMYDETGYAGLSDTARHYIGGLLHHAPSLLAFTNPTVNSYKRLVPGY
EAPINLYYSQRNRSACVRIPITGSNPKAKRLEFRSPDSSGNPYLAFSAMLMAGLDGIK
NKIEPQAPVDKDLYELPEEAASIPQTPTQLSDVIDRLEADHEYLTEGGVFTNDLIET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AALDIJAATVEDEPVIPFTVVAARILADAADAALAAALRVAEASVCGEHPPPRLAVIAMG
KCGARELNIVYSDYDVIFVAERSDPRRARVASERMRVASAAFFEVDAALRPEGRNGELV
RILESHIAYYORWAKTREJALLARRVVVGDAELGERVITALMPWVWRACEREDFVVE
VQAMRRRVEQLVPADVRGRELKIGSGGLRDVEFAVQLLQLVHARSDESLRVASTVDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AALGEGGY I GREDAANNTAS Y EFLIR LIEHRLOLOR LIKRTHLLPPDEDEEAVRWLARAA
H I RPDGRNDAAGVLREELKKONVRVSKLHTKL FYQPLLES I GPTGLEI AHGWTLEAAG
RRLAALGY EGPQTALKHMSALVNQSGRRGRVOSVLLPRLLDHMSYAPDPDGGLLAYRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref-"swiss-prot:010378"
/translation="MDRQKEFVLRTLEERDIREVRLWFTDVLGFLKSVAIAPAELEGA
FEEGIGFDGSSIEGFARVESDTVAHDPSTFQVLPWATSSGHHHSARMFCDITMPDG
SPSWADPRHULRRQLTKAGELGFSCYVHPEIEFFLLKPGPEDGSVPPVDNAGTFDQA
VHDSALMFRRHAIDALEFMGISVEFSHHEGAPGQEIDLRFADALSMADNVWIFRYVI
KEVALEEGARASFMPRPFGQHPGSAMHTHMSLFEEDNAFHSADDPLQLSEVGRSFIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="Myytklatorrkipsygrigivdppagerlaqigmdrheddahy
DLLWSLSRAPDADAALRALIRLSENPDTGWDELNAALLRERSLRGRLFSVLGSSLALG
DHLVAHPQSWKLLRGKVTLPSHDQLQRSFVECVEESEGMPGSLVHRLRTQYRDYVLML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSEALATESWYLATLRDKPAVARRLMHVLGTSAYVPDLLMRAPRVIQOYEDGPAGPRL
LEPEPAVARALIASASRYPDPERALAGARTLERRELARIGSADLLGLEVTEVCRAL
TSWWYALQAALDVHRASLEDDRAPAA.IAVIGMGRLGGAELGYGSDADVMFVCEPA
TGVDDARAVKWSTSIAERVRALLGTPSVDPPLELDANLRPEGRNGPLVRTLGSYAAYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQWAQPWEIQALLRAHAVAGDAELGGRFLRWVDKTRYPPDGVSADSVREIRRIKARIE
SERLPRGADPNTHTKLGRGGLADIEWTVQLLQLQHAHQVPALHNTSTLQSLDVIAAAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVPAADVELLRQAWLTATRARNALVLVRGKPTDQLPGPGRQLNAVAVAAGWRNDDGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Rv2222c, (MTCY427.03c), len: 446. glnA2, probable allo, (overlaps MTCY190.33c partial sequence) probable classII glutamine synthetase, similar to MTCY190.31 (and partiallorf MTCY427.01) (34.3% identity in 300 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GILEHACEISAVTNOWVNSYKRLVQGGEAPTAASWGAANRSALVRVPMYTPHKTSSRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEVRSPDSACNPYLTFAVLLAAGLRGVEKGYVLGPQAEDNVWDLTPEERRAMGYRELP
                                                                                                                                                                                                                                                                                                                                                                                                                         Glutamine synthetase putative ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note-"PS00182 Glutamine synthetase class-I adenylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MTCY190.32c-MTCY427.02c), len: 994
                                                                                                                                                       382. .>38110
/organism="Mycobacterium tuberculosis"
                                                                                                                    WISFKRENEIEPVNIRPHPYEFALYYDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAA94664.1"
/db_xref="GI:1261923"
/db_xref="SWISS-PROT:Q10379"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAA94645.1"
/db_xref="G1:1261924"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(1917. .4901)
/gene="glnE"
                                                                                                                                                                                                                                                             /db_xref="taxon:1773"
/clone="Y427"
955. .1002
/gene="glnA1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1917. .4901)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(4950. .6290)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(4950. .6290)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        region signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product-"glnA2"
                                                                                                                                                                                                                                  /strain="H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Rv2221c,
                                                                                                                                                                                                                                                                                                                                                                                                                     'note-"PS00181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"glnE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="glnA1"
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Crenarchaeota;
           Sulfolobus solfataricus
                                                                                                                                                                                                                                                                                                                                                                                                                             Sensen, C.W.
Direct Submission
                                                                                                                                                                                                                                                                                                                  Mol. Micr
97055432
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           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                           JOURNAL
MEDLINE
REFERENCE
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                                                                                      REFERENCE
                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                            complement(2385. .7947)

complement(2385. .7947)

gene="Rv2223c,"

/note="Rv223c,"

/note="Note="Rv22"

/note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="Note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RFGALLVNPGGPGASAVDMVAAMAPATADTDIIRHFDIVGFDPRGVGHSTPALRCRTD
ABFDAYRRDPMADYSPAGVTHVEQVYRQLAQDCVDRMGFSFLANIGTASVARDMDMVR
QALGDDQINYLGYSYGTELGTAYLERFGTHVRAMVLDGAIDPAYSPIEBSISQMAGFQ
TAFNDYAADCAFACTELGTBSAQWYRYHALVDPLVQKPGKTSDPRGLSYADATTGT
INALYSPORWXYLTSGLLGLQRGSDAGDILVLADDYDGRBDADGHYSNDQDAFNAVRC
DAPTPADPAANVAADQRIRQVAPFLSYGQFTGSAPRDLCALMPVPATSTPHPAAPAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MAAMMRRRPLSSALLSFGLLLGGLPLAAPPLAGATEEPGAGGTP
GAPVVAPQQSWNSCREFIADTSEIRTARCATVSVPVDYDQPGGTQAKLAVIRVPATGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKVVVVSTTHDPATPYQSGVDLARQLGAPLITFDGTQHTAVFDGNQCVDSAVMHYFLD
                                   6349. 6366
/note="lnverted repeat between 3' end of MTCY427.04c and
5' end of MTCY427.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acylamino-acid-releasing enzyme; alpha-amylase; amidase; aminopeptidase; daunorubicin resistance protein; glycorol kinase; glycogen operon protein GlgX; HIT protein; IS element; L-lactate permease; oxidoreductase; pyruvate ferredoxin oxidorecuctase;
SSLDSALRAMEASELVAEALGEHVFDFFLRNKRTEWANYRSHVTPYELRTYLSL"
6349. .6366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="GGTGA, possible ribosome binding site upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="PS00120 Lipases, serine active site" complement(7952. 7956)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                riboflavin biosynthesis protein; sugar transporter Sulfolobus solfataricus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
/product="hypothetical protein Rv2223c"
/protein_id="CaA94646.1"
/db_xref="G1:1.261925"
/db_xref="SWISS-PROT:Q10508"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 38110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS SSIOOKBER 100389 bp DNA
DEFINITION S.SOLfataricus 100 kbp DNA fragment.
ACCESSION Y08256
VERSION Y08256.1 GI:1707679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to reverse of: MTCY427 from: 1
                                                                                                                                                         complement(6385. .7947)
/gene="Rv2223c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="Rv2224c"
complement(8009. .9571)
/gene="Rv2224c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(7243. .7272)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Rv2223c"
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US-08-653-294-17 x MTCY427/rev
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4.200
83.333
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores
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                                                                                                                                                                 gene
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SOURCE

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Sensen, C.W., Klenk, H.P., Singh, R.K., Allard, G., Chan, C.C.,
Liu, O.Y., Penny, S.L., Young, F., Schenk, M.E., Gaasterland, T.,
Doolittle, W.F., Ragan, M.A. and Charlebois, K.L.
Organizational characteristics and information content of an
archaeal genome: 156 kb of sequence from Sulfolobus solfataricus P2
Mol. Microbiol. 22 (1), 175-191 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QKYYEVYKSLEDKGLVRVIEGRPKKVKLIDPSISLKYYRDKIVSELDYAIGNVISYWS
EKGKGEADRSLHIKGKTIVWRMIRELVDKSNKIKVVWDILPEWLIKIIKKYKGNLTVI
TSSNNLSLNAEVKYVKNIKSKFIIFDDSVLYTFNDQDEIVVDSCRGCVLQAEEHFDLL
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                                                                                                                                                                                                                                                                                                                                                  Submitted (19-5EP-1996) C.W. Sensen, Institute for Marine Biosciences, National Research Council of Canada, 1411 Oxford Street, Halifax, N.S., Canada, B3H 3Z1, CANADA Related sequence: Y08257.

Related sequence: Y08257.

Location/Qualifiers

1. 100389

/organism="Sulfolobus solfataricus"
/strain="P2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transl_table=11
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clone L2259 strain Friedlin, ***
unordered pieces.
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ACO09602.2 GI:6006095
HTG: HTG.PHASEL.
Leishmania major.
Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 100389
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Gaps: 0
Percent Identity: 81.818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (7829, .8332)
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complement (7829, .8332)
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complement(7257, .7793)
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LOCUS AC005602 40000 bp DNA
DEFINITION Leishmania major chromosome 35
SEQUENCING IN PROGRESS ***, 6 u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to reverse of: SS100KBFR
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US-08-653-294-17 x SS100KBFR/rev
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1 (bases 1 to 40000)
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores
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KEYWORDS
                                                 CDS
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COMPIEMENT (5112. 5990)
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REFERENCE

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to: CNS01DTM
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3.727
91.667
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US-08-653-294-17 x CNS01DTM
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Ratio:
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                   phage,
Contig
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ORIGIN
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IMPORTANT: This sequence is unfinished and does not necessarly
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continue. The sequence may be
Myler,P.J., Sisk,E., Hixson,G., Kiser,P., Rickel,E., Hassebrock,M.,
Cawthra,J., Marsolini,F., Sunkin,S. and Stuart,K.D.
                              Direct Submission
Submitted (28-MG-1999) Seattle Biomedical Research Institution, 4
Nickerson Street, Seattle, MA 98109-1651, USA
ON Oct 1, 1999 this sequence version replaced q1:801666.
* NOTE: This is a "working draft" sequence. It currently consists of 6 contigs. The true order of the pieces
* is not.known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Submitted (04-NOV-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 191442)
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                                                                                                                                                                                                                                        of 2595 bp in length tunknown length of 1486 bp in length unknown length
                                                                                                                                                                                                                                                                                                                                                                                                               in length
                                                                                                                                                                                                                                                                                                                                        of 5678 bp in length
unknown length
of 7691 bp in length
                                                                                                                                                                                                                                                                                                         of 3892 bp in length
unknown length
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contig of 17259 bp
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/organism="Leishmania major"
/strain="Friedlin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:5664"
/chromosome="35"
                                                                                                                                                                                                                                          contig c
gap of c
contig c
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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10082 c 10936 g
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gap of
                                                                                                                                                                                                                                                                                                                                                                               contig
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AL132800.1 GI:6272127
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US-08-653-294-17 x AC009602/rev
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91.667
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14772
22463
22742
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Percent Similarity:
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/standard_name="AA194835"
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software (G. Schuler)"
133712. .133887
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ooftware (G. Schuler)"
132481. .132607
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/note="matching EMBL:T15974; Identified using the e-PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e-PCR
                                          : 13 10 12 11 14 15 9, 1000 N's separate segments
contaminated with foreign sequence from E.coli, yeast, vector,
                                                        Contig 13: length 19976 bp
Contig 10: length 5980 bp
Contig 10: length 9112 bp
Contig 11: length 8124 bp
Contig 14: length 8117 bp
Contig 15: length 81177 bp
Contig 9: length 4117 bp.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /standard_name="R37382"
/note="matching EMBL:R37382; Identified using the software (G. Schuler)"
146875. 146986
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hote="matching EMBL:R52665; Identified using the
software (G. Schuler)"
154885. .154748
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software (G. Schuler)"
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/note="matching EMBL:T31019; Identified
software (G. Schuler)"
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Gaps: 0
Percent Identity: 58.333
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/standard_name="M69137"
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/clone="R-80A15"
67422. 6750A
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/protein_id="AAC97585.1"
/db_xref="G1:2072511"
/translation="MKHQLFCNIFEPRYXQWRLQEAQKEYESGFERLSQMNSYSVRTA
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/note="for orfA and orfAB"

join(466. 816,816. 1421)

/note="orfAB; -1 frame shift in the frame-shift window

during translation produces the full length fusion protein

orfAB, presumably the active protein"
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IRHSARSKKGKRAYGCRPOKRHONVSIIGAIALKGVISOYSILGTSDGLFFEAYISOK
LVPKLWEAACVIMDNCSIHKGGDIEKLIESAGAKLIYLPPYSPDFSPIENCWSKIKNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mkaySLDFRQKIFDTYKTGGISQRQLANKFCVSLGFIEKLLKQY
RETASIAPKVRTKQTPPKLNEEQMKILEEIVEAKNDLTLSEIRFILKEKTGITIGIST
Cai,Y.A., "Lantoine,F.L. and Glazer,A.N.
Characterization of Anabaena sp. PCC 7120 mutants defective in the
large core-membrane linker protein of the light-harvesting
                                                                                                                            Direct Submission
Submitted (02-APR-1997) Department of Molecular and Cell Biology,
University of California, Berkeley, CA 94720-3206, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294. .314
/note="direct repeat A, copy 2"
/rpt_type=direct
319. /note="inverted repeat B, copy 1"
/rpt_type=inverted
/s83. .393
/note="inverted repeat B, copy 2; transposable element
ISAn1"
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/note-"ISAn1 terminal inverted repeat, copy 1 (IRL)"
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466. .861
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                                                                                                                                                                                                                        /organism="Anabaena PCC7120"
/strain="PCC7120"
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'note="inverted repeat C,
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/protein_id="AAC97588.1"
/db_xref="G1:2072514"
                                                                                                                                                                                                                                                                 /isolate="mutant SB12"
                                                                                                                                                                                                                                                                              /db_xref="taxon:1174"
complement(<1. .268)
                                                                                                                                                                                                                                                                                              /note="hypothetical"
/codon_start=1
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/transposon="ISAn1"
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                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
                                                                        Unpublished
4 (bases 1 to 7948)
                                                     phycobilisomes
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م
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:

Apryle137 7948 bp DNA BCT 22-DEC-1998
DEFINITION Anabaena PCC7120 apcEABC gene cluster, phycobilisome core-membrane
linker protein (apcE), allophycocyanin alpha subunit (apcB) and phycobilisome core linker
protein Lc7.8 (apcC) genes, complete cds.

ACCESSION U96137.1 GI:2072510
                   13-MAR-1996
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Anabaena PCC7120
Bacteria: Cyanobacteria; Nostocales; Nostocaceae; Anabaena
1 (bases 5592 to 7391)
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Transposon insertion in genes coding for the blosynthesis structural components of the Anabaena sp. phycobilisome Photosyn. Res. (1997) in press
(bases 1 to 1560)
                                                                                                                                                                                                                                                                            U.S. Meat Animal Research Center
U.S. Dept. of Agriculture - Agricultural Research Service
Tel: (402) 762-4165
Fax: (402) 762-4173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 others
                     SIS
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Ratio: 3.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 50.000
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    .333
    /organism="Bos taurus"

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Primer B: GCCTGGCAAAGAGAAATTC
STS size: 223.
Location/Qualifiers
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104. .123
complement(307.
a 64 c 88
                                                                       G18985.1 GI:1223442
STS sequence; primer;
                   333 pb
                                                                                                                                                                                                                                                                 Contact: Roger Stone
                                                                                                                                                                     (bases 1 to 333)
                                                                                                                                                                                                         Cow Markers
Unpublished (1996)
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US-08-653-294-17 x G18985/rev
                            cow STS BMS2840.
G18985
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taurus.
                                                                                                                                  Bos taurus
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                                                                                                                                                                                                                                                                                                                                        /transl_table=11
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KLVPRLWEAACVIMDNCSIHKGGDIEKLIESAGAKLIYLPPYSPDFSPIENCWSKIKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141. .855
// Anote inverted repeat D, copy 2; stem-loop formation from
inverted repeat D facilitates the -1 frame shift during
                                                                                                                                 /translation="mkaysldfrokifdtyktggisorolankfoyslgfieklikoy
RETASIAPKVRTKQTPPKLNEEQMKILEEIVBAKNDLTLSEIRFILKEKTGITIGIST
VDRMLQRIEISLKKKHCTPQKKRLKEFNY"
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DDARPLRYATAIVAGDENIIVUNTROLERIERMASGSBATTRALGETRAASLSYFRK
DPDABATIVALOETRAASLSYFRK
DPDABATIVALGETRAASLSYFRK
TGLSATEKNEVITERKAPTPSKKLRQRESGDQGGLQLPQIYFSBABRREKFWK
TGLSATEKNEVIKAAYRQIFERDITRAYSLSISDLESKVKNGDISMKEFVRRLAKSPL
YOKOPYOPFT INSRVIELAFRHILGREPSSREEVQKYFSIISNGGLPALVDALVDSBEY
SDYRGFETVPYLRGLGGGAQGCRNMOPQOLENYSAFRKVOPFITTRAAYDELPDA
HPYGSGNDPLEIQFGAIFPKETRNFSTSPAPFGKDTRRILIHQGFGINNQVSNPSAG
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LKVQEIKLENGEISVRDFVRALAKSDLFRKLYWTPFYVCKAIEYIHRRLLGRPTYGRQ
ENNKYFDIASKKGLXAVVDAILDSLEYTETFGEDTVPYERYLTPAGVALRQLRVGTIR
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LVINAIYRQVLDVFSGQVPDYYRRTELDSKLRNGEISVREFVREIASSEIYRKRFYTP
YPNTKVIEFLFRHLLGRAPATQGEIRQYNKLLADNGLRAAVEAIVDSPEYSRYFGEDV
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IKTLISAAYRQIFERDIAPYIAQNEFSGWESKLGNGEITVKEFIEGLGYSNLYLKEFY
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SYFASGAKRLEIAQLLTENSEIIVSRAANRIFVGGSPMAFLEKPREPELAMAAVGGGG
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'protein_id="AAC97589.1"
'db_xref="GI:2072515"
                                                                                                                                                                                                                                <810. .1421
/note="orfB of ISAn1; follows translation frame-shift</pre>
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1417. 1432
/note="ISAn1 terminal inverted repeat, copy 2 (IRR)"
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1606. 1619
/note="direct repeat B, copy 1"
/rpt_type=direct
1609. 1620
/note="inverted repeat E, copy 2"
/rpt_type=inverted
1624. 1637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         818. .831
/note="inverted repeat D, copy 1"
/rpt_type=inverted
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hote="direct repeat B, copy 2"
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note="inverted repeat E,
                                                                      /protein_id="AAC97586.1"
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                                                    /transl_table=11
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908. .1911
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transl_table=11
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1908. .5323
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/gene="apcE"
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gene="apcE"
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
I (basea 1 to 29283)
I (basea 2 to 29283)
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LOCUS CEF14B6 29283 bp DNA INV 02-SE
DEFINITION Caenorhabditis elegans cosmid F14B6, complete sequence.
ACCESSION 281502.1 GI:2814053
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Gaps: 0
Percent Identity: 58.333
                                                                                                                         /rpt_type=direct
5345. 5351
/note="direct repeat C, copy 3"
/rpt_type=direct
5352. 5358
/note="direct repeat C, copy 4"
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/note="direct repeat D, copy 1"
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5388. 5401
/note-"direct repeat E, copy 1"
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note="direct repeat D, copy 2"
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   repeat C, copy
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note="direct repeat
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/note="direct rep:
/rpt_type=direct
5425. 5450
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                                                                  338. .5344
/note="direct
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Caenorhabditis elegans
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US-08-653-294-17 x APU96137/rev
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Current sequence finishing criteria for the C. elegans genome sequence finishing criteria for the C. elegans genome sequenced constrium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones.

Exceptions are indicated by an explicit note.

In PORTANT: This sequence is Nor necessarily the entire insert of the specified clone. It may be shorter because we arrange for a small overlapping sections once, or longer because we arrange for a small once, or longer because we only sequence overlapping sections once, or longer because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone F41D3 is at 29177 in this sequence. The true right end of clone C15C6 is at 19321 in this sequence. The start of this sequence (1. .109) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-"MFSVFEWILIFFGILNWFKFTQDSTPEPASRFFTRVCQOLRETV
LIEIDSSGWYOFVGIVESGSKPYFSPHVGCAECMOWMDVYGEQPHRYEFTBODDTDE
GVEEESEIEDSDFDDGITFVRPTPAPLSPETENFIEDKMKFHFQATDIINSYLGKGT
DMGIVSNLIRISQTYGVOLKQVSSSKKSSMKEIEGILKSLQKEFFQEIEGLNGEISEAE
ENNESDIDESFEFVENLELDSDFE"
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                                                                                                                                      Submitted (06-NOV-1996) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu on Jan 28, 1998 this sequence version replaced gi:1665918. Coding sequences below are predicted from computer analysis, usin predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                 For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(2938. .3065,3115. .3212,3260. .3345))
/gene="F1486.7"
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/gene="F1486.1"
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6093. .6375,6563. .6657))
/gene="F14B6.2"
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/db_xref="taxon:6239"
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/gene="F14B6.7"
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complement(947. .2169)
/gene="F1486.1"
  Nature 368 (6466), 32-38 (1994)
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                                                  (bases 1 to 29283)
                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                     COMMENT
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join(17155. 17218,17267. 17455,17898. 18232,18389. 18591,
19031. 19178,19319. 19537)
/gene="F14B6.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comes from this gene; JOHA EST EMBL: 008202 comes from this gene; CDNA EST EMBL: 00873 comes from this gene; CDNA EST FOOR this gene; CDNA EST Y198f11.3 comes from this gene; CDNA EST y198f11.5 comes from this gene; CDNA EST y19329612.3 comes from this gene; CDNA EST y193887.3 comes from this gene; CDNA EST y193887.3 comes from this gene; CDNA EST y1940463.5 comes from this gene; CDNA EST y194050.3 comes from this gene; CDNA EST y195050.3 comes from this gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSNNIITSPEYFDESSEEPEFANGESECHENNINGESETATELINGESETATE
SETSDSELGQDSPNNILSEALNUCIENFOQLVDEVVRHKDFHERSQLLRVLEECLGNM
NSFLQNENLTVDDI STGACALLNETAEKLKQMFSSSGISGRKESSEGTNKDLIKFGEL
REGGREEDDDDESYVEGEEDSSDEDLDDEOGESSIEPRLSETFKKSEARRSLSS
KEAPVKDLYTYGKFRDEHEDLEESENBPRMSDEAEKLVEDKIIEESDESPIIGRDE
17155. 19537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAB04109.2"
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VLVLIVLIKCLCISFWIIREHETFDFRCAAWNGGOPTDYMYRAKRSIAFEKSDPRKFS
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                                                                                                                                                                                                                                                                                                                                     HLVGKSSSLGFTTPREKSSWANGYLDPODPNESNOGDIRGYPAGREEDER HLVGKSSSLGFTTPREKSSWANGYLDPODPNESNOGDIRGYPAGREEDER HLVGKSSLGFTTPREKSSWANGYLDPODPNESNOGDIRGYPAGREEDER FEATTASPE EKDEDEEKLKLSESTRAMMDMDELKYTTFLAPKTTEGTKQVEGEGVKEVIQEAHERSQK PMLKETFEERTTSTEKPLPGGMSKNOMEKKREAFEAYTPPISLSDLQPSHSSHSGPAG MGHLESTTSTEKTPPAFHFIPPSSEAPYYVEINDADTETVYVSSVTPMYRPVFEN MGHLESTTKSYDPLHLEVSFESFFCCVGQLLCHFVFDP complement (986.12)
                                                                                                                                                                                                                              RKIDSNHIPAVPPYEPDDDLPMTMVTLTNTQIVQLSGEETGVVKMKTIRNRVEKVGS
DEBQPIEIDIANAPRIYVSKIKSRHGGEBEBHFDLLKELKKDEBEKEKKKEKKKKGKG
LKKAKKLTEAEKLLNNSTSTSVIPDTAVSRKPKGKGLKKSKKLNQKPKSDEEVTKQPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="GI:3875878"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANMOGKIKEVVMAEAKLFGDIVVTSMEDRYSKLSFKTLTLLLFGVSKVPSAQLIGKID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDVLFFPULFLSTIKNENSMINVTSASVYGKIAEAGVPIVSNCCKRFLKYNFRRNSLI
SFGCTRYAFYLAGPFYLYTRSAALRLLEASKHRNFHKIEDTLITGVLADDTDVSRVQL
HRINLGGEKGTDLVFAWHSPLNDPEYKDLXYKTMSSQQFKEKLRLQEINVT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDVOSTFKWIHIPKISGSPEILLIVLSRPDDFSRRNVIRHTWMSQENEIKYLFLIGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="CAT Met M-tRNA; predicted using tRNAscan-SE-1.11;
prellininary prediction; similar to tRNA-Met"
complement(9869. .9940)
/gene="F1486.t2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        predicted using tRNAscan-SE-1.11; similar to tRNA-Met"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note "predicted using Genefinder; cDNA EST yk329e12.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .16695)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(15024. .15079,15134. .15329,15847.
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13752. .13823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="CAT Met M-tRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .t1"
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gene="F14B6.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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Svirskas, R.R., Harris, N.L., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, K.G., Chav, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Madda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Zhang, R., Zieran, L.L. and Rubin, G.M. Direct Submission

L. Submitted (20-COT-1998) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley C. Ag 94720, US
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://fruitfly.berkeley.edu/sequence/) or send email to Daggefruitfly.berkeley.edu.
Library locations: 53-17, 90-16, 5-27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (03-NoV-1999) Wellcome Trust Genome Campus, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquires:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 4, 1999 this sequence version replaced 9i:605938.
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"These three pls were completed as a project. The coordinates are Pl end to Pl end. DS02501 (D281) extends from bp 1 to bp 85,627. DS01529 (D280) extends from bp 74,631 to bp 155,821. DS01589 (D279) extends from bp 126,132 to bp 207,672. " 42102 c 41711 g 62161 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="Pls DS01589 (D279), DS01529 (D280), and DS02501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome X clone RP13-348B13, *** SEQUENCING IN PROGRESS ***, in unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 229644)

    .207672
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"

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Gaps: 0
Percent Identity: 41.667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="2L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /map-"28B1-28B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL121872
AL121872.2 GI:6249374
HTG; HTGS_PHASE1.
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LOCUS HSB348B13 229644 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio: 3.333
Percent Similarity: 100.000
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ORIGIN
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                                                                                                                                                                                                                                                               TITLE
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VERSION
KEYWORDS
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
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SM Drosophila melanogaster (Eukaryota) Arthropoda; Tracheata; Hexapoda; Insecta; Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilade; Drosophila.

E (Celniker, S.E., George, R.A., Galle, R.F., Hoskins, R.A., Svirskas, R.R., Harris, N.L., Agbayani, A., Arcaina, T.F., Baxter, E., Blazej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, R.A., Hummasti, S.R., Karra, K., Karra, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join[23603...23727,23784. .24048,24104. .24209,24287. .24373,
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25566. .25580,25729. .25933,25988. .26251)
join(20434. .20524,21137. .21250,21298. .21659,21969. .22168,
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LISSSMLILSKNILTYYIGDISSLYLIHWPIYAYWKLAFDGDVNLILLSLLSSIILAI
IVFEFFEKWYLKLSYSIGLLIVFLFFLNVILINKDELIPDREENNHNSSMNTDDAI
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(D279), DS01529
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Celniker,S.E., George,R.A., Galle,R.F., Hoskins,R.A.,
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Drosophila melanogaster DNA sequence (P1s DS01589
(D280), and DS02501 (D281)), complete sequence.
AC005834 AC004577 AC005733 AC004717 AC004718
AC005834.1 GI:377655
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Submitted (07-52P-1999) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1R0, UK and Department of Genetics, Washington University, St. Louis, Mo 63110, USA. E-mail: hes@sanger.ac.uk or rw@nematode.wustl.edu on Aug 10, 1999 this sequence version replaced gi:4938508. Order of segments is not known; 800 n's separate segments. IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CEY47HI0 296589 bp DNA HTG 07-SEP-1999
Caenorhabditis elegans chromosome I clone Y47H10, *** SEQUENCING IN PROGRESS ***, in unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. [ (bases 1 to 296589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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                                                                                                                                                     /chromosome="x"
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1 31906 c 32427 g 57543 t 47255 others
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1. .296589
/organism="Caenorhabditis elegans"
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    .229644
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/chromosome="1"
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Caenorhabditis elegans.
Caenorhabditis elegans
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US-08-653-294-17 x_HSB348B13
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TGRCGPTEYSRFFKCPDAFSYLDKPTTVTCPGSSNYRVIFCPTA"

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida;
Zingiberales; Marantaceae; Thaumatococcus.
1 (bases 1 to 624)
Uriach-Marsal,J., Rubio-Susan,V., Patino-Martin,C., Iossif,K.E.,
Del-Moral-Juarez,C., Faus-Santasusana,I., Del-Rio-Pericacho,J. and
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Preparation process of a natural protein sweetener
Patent: EP 0684312-A 7 29-NOV-1995;
UDOUMA S A (ES)
Other publication ES 2080689 960201
Other publication FI 991868 951022
Other publication CA 2147541 951022
Other publication CA 2147541 951022

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Sequence 7 from Patent EP0684312.
A46810 GI:2300906
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Polynucleotide sequence fro
TIM gene. Nuclear transloca
Timeless gene. New protein
Enterococcus faecalis genom
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Claim 1: Page 1853-1855; 2084pp; English.

A computer readable medium has been developed which has recorded on it.

A computer readable medium has been developed which has recorded on it.

X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importence. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcus infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the collypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-FEB-1999 (first entry)
EST clone DT478.
EST clone DT478.
EST clone ctay; secreted protein; haematopoiesis regulator;
EST clone provent, activin; inhibit tumour invasion suppressor; EST; human;
chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
Homo sapiens.
W09845437-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 99-045171/04.
New isolated Enterococcus faecalis polynucleotides and polypeptides
- used to develop products for the detection of Enterococcus and for
use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                  Enterococcus faecalis genome contig SEQ ID NO:603.
Enterococcus faecalis, contig, detection, Enterococcal infection,
vaccine; attenuation; computer readable medium; ds.
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Gaps: 0
Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     471 C;
                                                                                                                                                                                                                                                                                                                   Entercoccus faecalis.
(A09850555-A2.
12-NOV-1998.
04-MAY-1998; U08985.
14-NOV-1997; US-066009.
06-MAY-1997; US-04655.
16-MAY-1997; US-04655.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Dillon PJ, Kunsch CA;
90.99
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                                                                                                                                                                                 X13540 standard; DNA; 2469 BP. X13540;
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ID V88170 standard; cDNA; 321
                                                                                                                                                                                                                                 19-MAR-1999 (first entry)
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US-08-653-294-17 x X13540/rev
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Ratio:
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N_Geneseq_36:X20635
N_Geneseq_36:T60333
N_Geneseq_36:X27127
N_Geneseq_36:X13141
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                                                                                                                                                                            About: Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
    out_format : pfs
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Database sequences: 311585
Database length: 125096042
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                                                                                                                                                            Command line parameters:
                                             Date: Feb 8, 2000 1:28
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Query length: 12
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N_Geneseq_36:V74441 --
N_Geneseq_36:T58840_5
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N_Geneseq_36:v80665
N_Geneseq_36:Q79140
N_Geneseq_36:Q81920
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N_Geneseq_36:r09355
N_Geneseq_36:r093564
N_Geneseq_36:x105648
N_Geneseq_36:x07548
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N_Geneseq_36:T26331
N_Geneseq_36:X21079
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N_Geneseq_36:V12200
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_Geneseq_36:X20573
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N_Geneseq_36:X13210
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N_Geneseq_36:X27129
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phosphate metabolism, modulate inflammatory function or innate
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  A THE FERRE OF THE FORM OF THE
                                                                                                                                                                                      ovary, pituitary, retina and colon cDNA libraries

"Towary pituitary, retina and colon cDNA libraries

"Solaim"; page 306; 641pp; Emplish.

"The present sequence represents an expressed sequence tag (EST), and is

"The present sequence represents an expressed sequence tag (EST), and is

"The present sequence represents an expressed sequence tag (EST), and is

"The present sequences isolated from a variety of human tissue

"Sources. The EST sequences isolated from a variety of human tissue

"Sources. The EST sequences and proteins encoded by them are predicted to

have useful biological activities which would make them suitable for

treating, preventing or ameliorating medical conditions in humans and

animals, although no supporting data is given. Suggested activities

animals, although activity, immune stimulating or suppressing activity,

haematopoiesis regulating activity, tissue growth activity, haemostatic

activity, cadherin/tumour invasion suppressor activity, tumour inhibition

contitity. The EST sequences are also stated to be useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human DNAX toll-like receptor DTLR3 encoding cDNA.

DNAX toll-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor; interleukin 1 receptor; phosphate metabolism; innate immunity response; modulate inflammatory function; morphological effect; immunity response; immunological disorder; ss.
                                                                                           Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D, Racie LA, Spaulding V, Treacy M;
WPI; 99-070078/OG.
New polynucleotides encoding human secreted proteins - derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e.g. alter
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Ratio: 3.273 Gaps: 0
Percent Similarity: 91.667 Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 G;
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WPI; 99-059670/05.
P-PSDB; W86351.
Human DNAX toll-like receptors, DTLR 2-10 - u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
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1. .2715
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ID V80665 standard; cDNA; 2715 BP.
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/*tag= b
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/*tag= c
                                                                      (GEMY ) GENETICS INST INC.
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                       10-APR-1998; U06956.
10-APR-1997; US-837312.
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07-MAY-1997; US-044293.
22-JAN-1998; US-072212.
(SCHE ) SCHERING CORP.
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US-08-653-294-17 x V88170
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07-MAY-1998; U08979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9850547-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy
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Figurative movements of the problem 
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ID 079140 standard; cDNA; 9487 BP.

AC 079140:

DT 07-SEP-1995 (first entry)

DE Hepatitis C virus; HCV; non-B; HC-G9; treatment; ss. Hepatitis C virus; HCV; non-A non-B; HC-G9; treatment; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aa:Cys
aa:Ser
aa:Leu
aa:Thr
aa:Pro
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aa:Arg
aa:Ser
aa:Lys
aa:Tyr
aa:Asp
aa:Val
aa:Val
aa:Val
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio: 3.600 Gaps: 0 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 60.000
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pos: 7956.
pos: 7962.
pos: 7965.
pos: 7965.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: V80665 from: 1 to: 2715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1450 CGACTGATGCTCCGAAGGTGGCCCTTAAA 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ArgleuLeuIleArgArgIleAlaLeuArg 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 342. .9377
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/transl_except= i
/transl_except= i
/transl_except= i
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US-08-653-294-17 x V80665
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Align seg 1/1
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                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interferon-gamma to the activity or function or claim 4; Page 23; 43pp; English.

Claim 4; Page 23; 43pp; English.

Oligonuclectides which bind to interferon-gamma are useful for modulating, inhibiting or enhancing the activity or function of the TFN. Particularly, they are useful for treatment of septic shock, rheumatoid arthritis and HIV infection. Preferred oligonucleotides are given in Q81894-Q81909 and Q81913-Q81932; esp. the oligonucleotides omprise at least one of the sequences AAGUUG, UGANGCUC, Q81903 or Q81904.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-1995 (first entry)
Interferon-gamma binding oligonucleotide 8.
Interferon gamma; IFN-gamma; inhibition; binding; immunomodulation;
septic shock; rheumatoid arthritis; HIV infection; ss.
                                                                                                                                                                       A hepatitis C virus gene and oligo-nucleotide(s) - used for the treatment of hepatitis C claim 1: Pages 10-15; 41pp; Japanese. 079140 is the hepatitis C virus (HCV) gene HC-G9 cDNA, it encodes the protein described in R67588. Both the cDNA and protein can be used in the treatment of HCV infection Sequence 9487 BP; 1905 A; 2798 C; 2687 G; 2097 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligo-nucleotide(s) which bind to interferon-gamma - used for modulating, inhibiting or enhancing the activity or function of
/transl_except= pos:8028. .8030, aa:Gly /transl_except= pos:8031. .8033, aa:Thr /transl_except= pos:8034. .8036, aa:Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: Q79140 from: 1 to: 9487
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Gaps: 0
Percent Identity: 63.636
                                                                                                                                                                                                                                                                                                                                                                             Gaps: 0
Percent Identity: 58.333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beutel BA, Coppola GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 C;
                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-17 x Q79140/rev · ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID Q81920 standard; RNA; 98 BP.
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                                                                                                                                                                                                                                                                                                                                                        36.00
3.600
83.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JAN-1995.
17-JUN-1994; U06897.
18-JUN-1993; US-079677.
17-MAR-1994; US-210222.
(PHAR-) PHARMAGENICS INC.
                                                                                   13-MAY-1993; 147133.
13-MAY-1993; DP-147133.
(IMMO ) IMMUNO JAPAN KK.
WPI: 95-040318/06.
P-PSDB: R67588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: N_Geneseq_36:Q81920
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Percent Similarity: 100.000
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US-08-653-294-17 x Q81920
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Ratio:
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Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
WO9500529-A.
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                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                      22-NOV-1994
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Particularly for inducing or regulating protective immune response
1 particularly for inducing or regulating protective immune response
1 particularly for inducing or regulating protective immune response
2 pisclosure; Page 16; 49pp; English.

A DNA encoding a polypeptide (PP) and/or antigen (Ag), where each
coding sequence is under the control of a promoter for expression
in a non-invasive or non-pathogenic bacterium (e.g. the present
lactococcus lactis Pl promoter), can be used to transform such a
bacterium. The bacterium, which expresses the PP and/or Ag, can be
beending on the nature of the PP and/or Ag, the delivery method
can be used to regulate growth, survival, differentiation, effector
function and susceptibility to infection of cells and tissues,
Depending on the nature of the PP and/or Ag, the delivery method
can be used to regulate growth, survival, differentiation to response
tunction and susceptibility to infection of cells and tissues,
boost the immune response to tumour cells or infections that
colonise mucosal, or other tissues, modulate the immune response
gainst a pathogen, regulate infiltration of normal tissues by
inflammatory or tumour cells, ondered apoptosis in tumour cells or
down regulate the immune response in treatment of allergy,
autoimmune and other immunity related diseases. The method is
useful in human or especially veterinary medicine, with an adjuvant,
bacterium formulated as a vaccine. The bacterium can express an Ag,
particularly one of low immunogenicity, together with an adjuvant,
particularly one of low immunogenicity, together with an adjuvant,
particularly one of viokine is limited to the site of application there
production of cytokine is limited to the site of application there
should be no systemic side effects.
                                                                                                                                                                                                                                                                                                                                                                                                               09-FEE-1998 (first entry)
Lactococcus lactis P1 promoter.
Non-invasive; non-pathogenic; bacterium; bacteria; P1 promoter;
transformation; expression; delivery; antigen; vaccine; ss.
Lactococcus lactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
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Gaps: 0
Percent Identity: 50.000
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21-00T-1996; G02580.
20-00T-1995; GB-021568.
(UVCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
Le Page RWF, Remaut E, Steidler L, Wells JM; WPI; 97-245121/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 G;
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                                                                            12
                                                                                                                     30 AGGCUCGUAUUUCGCCGGAUCGUCUUAGAGUAU 62
                                                                        2 ArgleuleulleArgArglleAlaLeuArgTyr
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2
to: Q81920 from: 1
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ID T00803 standard; DNA; 1830 BP.
                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID T38465 standard; DNA; 142
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3.500
83.333
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US-08-653-294-17 x T38465/rev
                                                                                                                                                                                                                              seq_name: N_Geneseq_36:T38465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                        Use of halo peroxidase enzymes - in antifouling paints and methods for determining the halide concn. of liquids
Example 3; Fig 6; 48pp; English.
A CDNA sequence (T03875) codes for a chloroperoxidase (R82249) of Curvularia inaequalis. The CDNA was obtd. by PCR using primers based on known sequences of the gene and by 5 FRACE. The approtetin encoded by the CDNA can be reactivated by addn. of vanadate. The CDNA can be inserted into a vector for expression in procaryotic host cells.
                                                                                                                                                                       halo:peroxidase, esp. from Curvularia inaequalis, halide and halo:peroxidase, esp. from Curvularia inaequalis, halide and halo:peroxidase, esp. from Curvularia inaequalis, halide and hydrogen peroxide source (Taim II); Fig 2, 48pp; English.

A gene (ToB0803) encoding the vanadium chloroperoxidase of Curvularia inaequalis CBS102.42 was isolated from a genomic library using a probe obtd. by amplification of cDNA using primers based on isolated fragments of the gene. The gene can be inserted into a vector and used to produce recombinant chloroperoxidase in host cells, e.g. Saccharomyces cerevisiae. The enzyme is used together with a halide source and H202 in antimicrobial compositions active against e.g. Streptococcus faecalis and food spoilage microorganisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chloroperoxidase CDNA.
Chloroperoxidase; haloperoxidase; antifouling paint; preservative; halide; chloride; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wever R;
 Chloroperoxidase; vanadium haloperoxidase; disinfectant;
                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 35.00 Length: 12
Ratio: 3.500 Gaps: 0
Percent Similarity: 83.333 Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dekker HL, van Schijndel JWPM, Vollenbroek EGM,
WPI; 95-358602/46.
P-PSDB; R82249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-1994; EP-200893.
24-JUN-1994; NL-001048.
(SCHE-) STICHTING SCHEIKUNDIG ONDERZOEK IN NEDER.
(TEWE-) STICHTING TECH.
                                                                                                                                  Ter Steeg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                910 TACAACCAGAICGIACGIACGICGCAICGCAGITACGIAC 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: T00803 from: 1 to: 1830
            antimicrobial, antiseptic, ss.
Curvularia inaequalis strain CBS102.42.
                                                                                                                                 Simons LH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T03875 standard; cDNA; 2088 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                  (UNIL ) UNILEVER NV.
(UNIL ) UNILEVER PLC.
Barnett P, Hondmann DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: N_Geneseq_36:T03875
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                                                        12-OCT-1995.
31-MAR-1995; E01229.
31-MAR-1994; EP-200893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-17 x T00803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Curvularia inaequalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-1995.
30-MAR-1995; NL0123.
31-MAR-1994; EP-2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seg_documentation_block:
                                                                                                                                                              WPI; 95-358625/46.
                                           W09527046-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09527009-A1.
                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
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                                                                                                                                              Wever R;
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infection.

Claim 1: Page 1261-1263; 2084pp; English.

Claim 1: Page 1261-1263; 2084pp; English.

A computer readable medium has been developed which has recorded on it and other confide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcus faecalis in faction in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the collypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 99-045171704.

New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ly-MAR-1999 (first entry)
Enterococcus faecalis genome contig SEQ ID NO:268.
Enterococcus faecalis genome contig SEQ ID NO:268.
Enterococcus faecalis, contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
MO9850555-A2.
12-NOV-10.00
The recombinant chloroperoxidase is utilised in halide (esp. chloride) analysis, or as an environmentally-friendly antifouling agent in ship paint.

Sequence 2088 BP; 465 A; 622 C; 531 G: 470 T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 897
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Gaps: 0
Percent Identity: 50.000
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Gaps: 0
Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 985 TACAACCAGATGGTACGTCGCATCGCAGTTACGTAC 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 2088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Dillon PJ, Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: T03875 from: 1
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3.500
83.333
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14-NOV-1997, US-066009.
06-MAY-1997; US-044031.
16-MAY-1997; US-046655.
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3.182
91.667
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US-08-653-294-17 x T03875
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US-08-653-294-17 x X13205
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                                                                                                                                                                                                               Quality:
Ratio:
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Ratio:
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Disclosure; Page 70-72; 110pp; English.
Saccharomyces cerevisiae DKD5D, which is sensitive to aureobasidin, was mutagenized with EMS and genomic libraries of 2 resistant strains were prepared. Resistant gene scaurlk (Q75954) was isolated from 1 library, and resistant gene scaur2k (Q75956) from the other. A DNA fragment of scaurl was used as a probe to isolate a sensitive gene, scaurls (Q75955), from the sensitive strain. A T852A mutation leading to a F158Y conversion gave rise to the sesistance of scaurlk.
Sequence 2340 BP; 583 A; 462 C; 430 G; 865 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fungal chromosome integration vector contg. aureobasidin resistance gene - which acts as selection marker, useful in genetic engineering of fung 10 fung.

Bobisclosure; Page 26-28; 66pp; English.

The wild-type aureobasidin sensitivity gene scaurISR (T09350) was obtd. from a genomic library of Saccharomyces cerevisiae using a mutant aureobasidin resistance gene (T09355) as probe. The gene encodes a protein (R88127) sensitive to aureobasidin.

Mutagenesis of the gene at codon 240 resulting in a substitution, deletion or insertion at Ala-240 is used to impart aureobasidin resistance, and the mutated DNA may be used as a selectable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAR-1996 (first entry)
Aureobasidin sensitivity gene scauris.
Aureobasidin resistance; selectable marker; fungus transformation; chromosome integration vector; scauris; ds.
Saccharomyces cerevisiae.
                                                                                                          New genes regulating aureobasidin sensitivity - used to develop prods. for the diagnosis and treatment of diseases such as \ensuremath{\mathsf{e}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN 1996.

15-JAN 1995; 304165.

29-JUN 1995; JP-108501.

30-MAR-1995; JP-095955.

30-MAR-1995; JP-095831.

17-MAY 1995; JP-1041391.

17-MX J PRARAR SHUZO CO LID.

Kato I, Ogawa J, Okado T, Oshima A, Takesako K;

Yoshioka H;

WPI: 96-010176/08.

P-PSDB; R88127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouality: 35.00 Length: 10 Ratio: 3.500 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1 to: 2340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
28-DEC-1993; JP-348893.
(TAKI ) TAKARA SHUZO CO LTD.
KRALO I, Okada T, Takesako K;
WPI; 95-022386/04.
P-PSDB: R67690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T09350 standard; DNA; 2340 BP.
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US-08-653-294-17 x Q75955
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Sequence 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                              mycoses
    Disclosure; Page 67-68; 110pp; English.
Saccharomyces cerevisiae DKD5D, which is sensitive to aureobasidin, was mutagenized with EMS and genomic libraries of 2 resistant was mutagenized with EMS and genomic libraries of 2 resistant factual strains were prepared. Resistant gene scauriR (075954) was isolated from 1 library, and resistant gene scauriR (075956) from the other. A DNA fragment of scauri was used as a probe to isolate a sensitive gene, scauris (075955), from the sensitive strain. A T852A mutation leading to a F158Y conversion gave rise to the
                                                                                                                                                       04-AUG-1995 (first entry)
S. cerevisiae scaurlR gene.
Aureobasidin-resistance; aureobasidin-sensitivity; scaurlR gene; mycoosis; antimycotic; fungicide, diagnosis; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S. cerevisiae scaurIS gene.
Aureobasidin.resistance; aureobasidin-sensitivity; scaurIS gene;
mycosis; antimycotic; fungicide; diagnosis; therapy; ds.
Saccharomyces cerevisiae DKDSD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New genes regulating aureobasidin sensitivity - used to develop prods. for the diagnosis and treatment of diseases such as
                                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                      /*tag= a
/note= "bases at positions 765-66 are unclear
in the specification"
misc_difference 1544
                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= b
/note= "base at position 1544 is unclear in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 10
Gaps: 0
Percent Identity: 50.000
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  1514 TITAGGATAATCITCAGGAAGATAGCCCTTTITAT 1549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: Q75954 from: 1 to: 2340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2291 ATCTTAGTGAAAAGGGTGGTTTTGCGTTAT 2320
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                                                                                                                                                                                                                                                   Saccharomyces cerevisiae DKD5D.
Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-1993; JP-142523.
28-DEC-1993; JP-348893.
(TAKI ) TAKARA SHUZO CO LTD.
KATO I, OKAGA I, TAKESAKO K;
WPI; 95-023286/04.
P-PSDB; R67689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification"
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ID Q75955 standard; DNA; 2340 BP.
AC Q75955;
                                                                                                              ВР
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                                                                                    seq_documentation_block:
ID Q75954 standard; DNA; 2340
AC Q75954;
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                                            seq_name: N_Geneseq_36:Q75954
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Ratio: 3.500
Percent Similarity: 100.000
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16-MAY-1994; 063129.
24-MAY-1993; JP-142523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        resistance of scaurlR.
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alignment_block:

Seguence

mycoses

Ë 865 us-08-653-294-17.rng

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Furgal chromosome integration vector contg. aureobasidin resistance gene - which acts as selection marker, useful in genetic engineering of fung.

Disclosure: Page 23-24; 66pp; English.

The aureobasidin resistance gene scaurlR (T09355) was obtd. from a genomic library of Saccharomyces cerevisiae following EMS mutagenesis. Comparison with the wild-type aureobasidin sensitive gene (T09350) showed a T to A mutation at position 852, resulting in a F158Y mutation in the encoded protein (R88132). The gene may be used as a selectable marker component of chromosome integration vectors used for fungus transformation.

S84 A; 505 C; 387 G; 864 T;
                                                                                                                                                                                                                                                                                                                    Aureobasidin resistance gene scaurlR.
Aureobasidin resistance; selectable marker; fungus transformation;
chromosome integration vector; Saccharomyces cerevisiae; scaurlR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takesako K;
                            Length: 10
Gaps: 0
Percent Identity: 50.000
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Ratio: 3.500 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 50.000
                                                                                                                                  to: 2340
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                                                                                                                                                                3 LeuLeuIleArgArgIleAlaLeuArgTyr 12
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380. 1585
/*tag= a
                                                                                                                                  Align seg 1/1 to: T09350 from: 1
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ID T09355 standard; DNA; 2340 BP.
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30-MAR-1995; JP-095955.
30-MAR-1995; JP-095831.
17-MAX-1995; JP-141393.
(TAKI ) TAKARA SHUZO CO LIDD.
Kato I, Ogawa J, Okado I, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAR-1996 (first entry)
                            Quality: 35.00
Ratio: 3.500
Percent Similarity: 100.000
                                                                                                                                                                                                                            seq_name: N_Geneseq_36:T09355
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                                                                                      alignment_block:
US-08-653-294-17 x T09350
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US-08-653-294-17 x T09355
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15-JUN-1995; 304165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yoshioka H;
WPI; 96-070176/08.
P-PSDB; R88132.
                                                                                                                                                                                                                                                                                                                                                                                                                                          EP-692534-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
               alignment_scores
                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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detecting
                                                                                                                                                                                                                            Products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis (laim 1; Page 825-826; 1150pp; English. X20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detection diseases related to Borrelia infections in animals, and for the production of blosynthetic products such as enzymes. Sequence 2529 BP: 589 A; 670 C; 699 G; 567 T;
05-MAY-1999 (first entry)
Polynucleotide sequence from the genome of Treponema pallidum.
Treponema pallidum infection; syphilis; Borrelia infection; animal; enzyme production; ds.
Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T51612;
30-APR-1997 (first entry)
Curvularia verruculosa haloperoxidase gene.
Haloperoxidase; halide oxidation; halogenation; antimicrobial;
disinfectant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Faloperoxidate from Curvularia verruculosa - useful for oxidn. halide, halogenation and, in presence of hydrogen peroxide and thiocymante, as antimicrobial artineration and salops. English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oxenboll KM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 2529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= b
/note= "primer aHaPl binding site"
2293. .2311
/*tag= c
/note= "primer aHaPlA binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 11
Gaps: 0
Percent Identity: 72.727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-FEB-1997.
09-JUL-1996; U11458.
14-JUL-1996; US-001194.
(NOVO ) NOVO NORDISK BIOTECH INC.
(NOVO ) NOVO-NORDISK AS.
WPI; 97-132641/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2398 TACAGATTATACGCCCGATCCATTGCGTTACGC 2366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: X20664 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TyrArgLeuLeulleArgArglleAlaLeuArg 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Curvularia verruculosa strain CBS 147.63
Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (477. .496)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВР.
                                                                                                                       30-DEC-1998.
23-JUN-1998, U13041.
24-JUN-1997; US-050667.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        477. .2279
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
ID T51612 standard; DNA; 2822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-653-294-17 x X20664/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.00
4.375
72.727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: N_Geneseq_36:T51612
                                                                                                                                                                                                               WPI; 99-081273/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; W12042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9704102-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer_bind
                                                                                                                                                                                                Fraser CM
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CC The haloperoxidase gene (T51612) of Curvularia verruculosa CBS.63 codes for an enzyme (W12042) that shows optimum activity at about CC odes for an enzyme (W12042) that shows optimum activity at about CC 60 deg C and pH 5.5, which retains at least 75% activity after CC incubation for 1 hr at pH 7.0 and 60 deg C in the presence of 0.1% CC +1202, and which prefers bromide over chloride as substrate. It was CC isolated from a genomic library using a PCR amplified partial clone (see also T51613-14) as probe. The 2822 bp fragment in a positive CC plaque has been deposited (in pHPA+1, in E. coli DH10B) as NRRL CC =15159. The gene can be used to express the haloperoxidase in cransformed host cells for use in halide oxidation, cpd. can arranformed host cells for use in halide oxidation, cpd. CC halogenation and (with H202 and thiocyanate) as an antimicrobial. SQ Sequence 2822 BP; 651 A; 808 C; 674 G; 689 T;
```

alignment_scores:
200 Length: 12
Ratio: 3.500 Gaps: 0
Percent Similarity: 83.333 Percent Identity: 50.000

alignment_block: US-08-653-294-17 x T51612 Align seg 1/1 to: T51612 from: 1 to: 2822

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3.6e+03
3.6e+03
3.6e+03
3.6e+03
                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Bliot, Kathryn J.
APPLICANT: Elis, Steven B.
APPLICANT: Harpold, Michael M.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
   82.51
82.51
82.51
82.51
33.00
33.00
33.00
                                                                                                                                                            seq_name: /cgn1_6/ptodata/2/ina/5C_COMB.seq:US-08-466-589-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn1_6/ptodata/2/ina/5D_COMB.seq:US-08-700-636-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 58.333
   /cgnl_6/ptodata/2/1na/5C_COMB.seq:US-08-530-198-5 + 

cgnl_6/ptodata/2/1na/5C_COMB.seq:US-08-469-880-5 + 

/cgnl_6/ptodata/2/1na/5D_COMB.seq:US-08-728-470-5 + 

/cgnl_6/ptodata/2/1na/5D_COMB.seq:US-08-617-697-5 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Brown, Martin, Haller & McClaim
1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-08-466-589-3 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        732 TACTCGCTGATCATCCGGCGGCTGTCGTTGTTCTAC 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCHWARE: FRASEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,589
FILING DATE: June 5, 1995
CLASSIFFICATION: 536
PRIOR APPLICATION NUMBER: US 08/028,031
FILING DATE: MATCH 8, 1993.
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                       seq_documentation_block:
    Sequence 3, Application US/08466589
    Patent No. 5837489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-17 x US-08-466-589-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Seidman, Stephanie L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1756 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39..1553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 92101-2926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
US-08-466-589-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence (1951)
Sequence (1964)
Sequence (1964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .9e+03
                                                                                                                                                                                                                                          -MODEL-frame-plumodel -DEV-xlp
-MODEL-frame-plumodel -DEV-xlp
-Q-(cgnl_1/USPTO-spool/US08653294/runat_04022000_160701_15794/app_query.fasta.1
-DB-ISSued_Patents_NA -OFMT-fastap -SUFFIX=rni -GAPOP-12.000
-GAPDXT-4.000 -MINMATCH=0.100 -LOOPEXT=0.000
-GAPDXT-4.000 -MINMATCH=0.100 -LOOPEXT=0.000
-GAPDXT-4.000 -MINMATCH=0.050 -XGAPOP-10.000 -YGAPDEXT=0.500
-GAPDEXT-7.000 -YGAPOP-10.000 -YGAPDEXT=0.500
-DELOP=6.000 -DELEXT-7.000 -YAAPOP-10.000 -YGAPDEXT=0.500
-DELOP=6.000 -DELEXT-7.000 -YAAPOP-10.000 -THR_SCORE-pct
-TRANS=human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-MAXLEN-1100000 -USER-USO8653294 -NCFW-ext -MINLEN-0
-MAXLEN-11000000 -USER-USO8653294 -NCFU-6 -ICPU-3 -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.51
82.51
                                                                                                                           software, version 4.5,
      out_format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.00
OM of: US-08-653-294-17 to: Issued_Patents_NA:*
                                                                                                                           About: Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database sequences: 207703
Database length: 57918730
Search time (sec): 310.290000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database: Issued_Patents_NA:*
                                                             Ы
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search information block:
Query: US-08-653-294-17
Query length: 12
                                                             Date: Feb 7, 2000 6:04
                                                                                                                                                                                                                   Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          score_list:
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NUMBER OF SEQUENCES:
                                                                        GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.
APPLICANT: Elliot, Steven B.
APPLICANT: Harbold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Coppola, George R.
APPLICANT: Beutel, Bruce A.
APPLICANT: Bettelsen, Arthur H.
TITLE OF INVENTION: Inhibition of Interferon- with Oligonucleotides
                                                                                                                                                                                  seq_name: /cgn1_6/ptodata/2/ina/5A_COMB.seq:US-08-210-222-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIOM TIPE: FIDEPY GISK

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,636

FILING DATE: 16-JUL-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031

FILING DATE: 08-MRR-1993
ATTORNEY/AGENT INFORMATION:
NAME: RELEAT STEPHONE:
NAME: REPERENCE/DOCKET NUMBER: 21,192

REGISTRATION NUMBER: 31,192

REGISTRATION NUMBER: 31,192

REGISTRATION NUMBER: 241 9368

TELEPHONE: 619-546-4737

TELECOMMUNICATION INFORMATION:
TELEFAK: 619-546-4737

TELEFAK: 619-546-4737

TELEFAK: 619-546-332

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1756 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-700-636-3 from: 1 to: 1756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          732 TACTCGCTGATCATCCGGCGCGCTGTCGTTGTTCTAC 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TyrArgLeuLeulleArgArglleAlaLeuArgTyr 12
seq_documentation_block:
    sequence 3, Application US/08700636
    patent No. 5910582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
; Sequence 8, Application US/08210222
; Patent No. 5599917
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-17 x US-08-700-636-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 37.00
Ratio: 3.700
Percent Similarity: 83.333
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) NAME/KEY: CDS
; LOCATION: 39..1553
US-08-700-636-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: both
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
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ADDRESSEE: No. 58663930 No. 5866393disk of No. 5866393th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Fuglsang, Claus
APPLICANT: Halker, Torben
APPLICANT: Oxenboll, Karen M.
APPLICANT: Oxenboll, Karen M.
APPLICANT: Berka, Randy M.
APPLICANT: Cherry, Joel
TITLE OF INVENTION: Verruculosa and Nucleic Acids Encoding Same
TITLE OF INVENTION: Verruculosa and Nucleic Acids Encoding Same
TITLE OF SQUENCES: 21
CORRESPONDENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 586639301SK Of NO. 5866393th American
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn1_6/ptodata/2/ina/5C_COMB.seq:US-08-679-405-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 63.636
CORRESPONDENCE ADDRESS:
ADDRESSE: Carella, Byrne, Bain, Gilfillan, ADDRESSE: Cecchi, Stewart & Oistein STREET: 6 Becker Farm Road CITY: Roseland STATE: New Jersey COUNTRY: USA ZIP: 07068
COMPUTER: STABABLE FORM:
MEDIUM TYPE: 3.5 inch diskette COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ArgleuleulleArgArglleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 AGGCUCGUAUUVCGCCGGAUCGUCUUAGAGUAU 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-210-222-8 from: 1
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; Sequence 1, Application US/08679405
; Patent No. 5866393
                                                                                                                                                                                                                                                                OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/210
FILING DATE: Unassigned
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HERTON, Charles J.
REGISTRATION NUMBER: 28/019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-17 x US-08-210-222-8
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 2:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 98 BASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 201-994-1744 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10174
COMPUTER READABLE FORM:
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: New York
RY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
COMPUTER: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: L
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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UMBER: US/08/842,799
16-APR-1997
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APPLICATION NUMBER: 60/001,194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-17 x US-08-842-799-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.00
3.500
83.333
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                 APPLICATION NUMBER:
                                                     FILING DATE: 16-APR-CLASSIFICATION: 435
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: U.S.A.
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY;
; LOCATION;
US-08-842-799-1
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ADDRESSEE: No. 59654180 No. 5965418disk of No. 5965418th America, Inc. STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haloperoxidases from Curvularia
Verruculosa and Nucleic Acids Encoding Same
: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 12
Gaps: 0
Percent Identity: 50.000
       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/679,405
FILING DATE: July 9, 1996
CLASSIFICATION: 435
FILING DATE: July 14, 1995
FILING DATE: OJLY 14, 1995
FILING DATE: OJLY 14, 1995
FILING DATE: PEDILOATY 21, 1996
FILING DATE: PEDILOATY 21, 1996
ATORNEY AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTATION NUMBER: 4441.210.
FREIERRENCE/DOCKET NUMBER: 4441.210.
TELEPHOME: (212) 867-0123
TELEPHOME: (212) 878-955
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2825 DASE PAIRS
TELEPHOME: CLARACTERISTICS:
LENGTH: 2825 DASE PAIRS
TELEPHOME: ATORNEY CS:
LENGTH: ATORNEY
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    Sequence 1, Application US/08842799;
    Patent No. 595418
    GENERAL INFORMATION:
    APPLICANT: Fuglsang, claus
    APPLICANT: Halkier, Torben
    APPLICANT: Oxenboll, Karen M.
    APPLICANT: Oxenboll, Karen M.
    APPLICANT: Cherry, Joel
    TITLE OF INVENTION: Halperoxidase
    TITLE OF INVENTION: Harloperoxidase
    TITLE OF INVENTION: Verruculosa an NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PLOPPY disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
us-08-653-294-17 x us-08-679-405-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.00
3.500
83.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: 477...2276
US-08-679-405-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
   Quality:
   Ratio:
   Percent Similarity:
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TITLE OF INVENTION: Haloperoxidases from Curvularia TITLE OF INVENTION: Verruculosa and Nucleic Acids Encoding Same NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn1_6/ptodata/2/ina/PCTUS9_COMB.seq:PCT-US96-11458-1
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ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11458
FILING DATE: 9-JUL-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 0
Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-08-842-799-1 from: 1 to: 2822
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STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1377 TACAATCAGATTGTGCGTCGCATCGCAGTGACTTAC 1412
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CLASSIFICATION DATA:
PURDA PPELICATION DATA:
APPLICATION NUMBER: 08/679,405
FILING DATE: JULY 9, 1996
APPLICATION NUMBER: 60/001,194
FILING DATE: JULY 14, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/603,534
FILING DATE: February 21, 1996
ATTONNEY/AGENT INFORMATION:
NAME: Lambiris, Elas J.
REGISTRATION NUMBER: 33,728
REGISTRATION NUMBER: 33,728
TELEPHONE: (212) 867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
; Sequence 1, Application PC/TUS9611458
; GENERAL INFORMATION:
; APPLICANT:
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to: 3096
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APPLICANT: Sehgal, Amita
APPLICANT: Sehgal, Amita
APPLICANT: Vosshall, Leslie B.
APPLICANT: Price, Michael
TITLE OF INVENTION: WICHEAR LOCALIZATION FACTOR ASSOCIATED
TITLE OF INVENTION: WITH CIRCADIAN RHYTHMS
NUMBER OF SEQUENCES: 8
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn1_6/ptodata/2/ina/5C_COMB.seq:US-08-619-198-2
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Gaps: 0
Percent Identity: 63.636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2526 TICAGAITIAAAAICAAACGIATAGCCIIGCGG 2494
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US-08-653-294-17 x PCT-US96-05320A-897/rev
                     APPLICATION NUMBER: 08/476,102 FILING DATE: June 7, 1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/487,429 FILING DATE: June 7, 1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                               TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 897:
SEQUENCE CHARACTERISTICS:
LENGTH: 3096 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Klauber & Jackson
411 Hackensack Avenue
                                                                                                                                   NAME: ELIC K. Steffe
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 146
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                            vudilty: 34.00
Ratio: 3.400
Percent Similarity: 90.909
       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: 1
PCT-US96-05320A-897
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                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hamilton O. Smith
APPLICANT: J. Craig Venter
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome,
NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn1_6/ptodata/2/ina/PCTUS9_COMB.seq:PCT-US96-05320A-897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CILL. ....
COUNTRY: USA
ZIF: 20003-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
COMPUTER: MSDOS Version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 0
Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                   FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4441.204-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 867-0123
TELEFAX: (212) 878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2822 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Genome Sciences 9410 Key West Avenue Rockville, MD 20850 United States of America Johns Hopkins University 720 Rutland Avenue Baltimore, MD 21205 United States of America Mark D. Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT/US96/05320A
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FILING DATE: 14-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/603,534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C.
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US-08-653-294-17 x PCT-US96-11458-1
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                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.00
3.500
83.333
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                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
COCATION: 477..2276
PCT-US96-11458-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                              linear
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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TOPOLOGY: linear
MOLECULE TYPE: CDNA
DESCRIPTION: tim CDNA sequence wherein R at position 1335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713D
FILING DATE: 13-SEP-1993
CLASSIFICATION: 514
ATTONREY/AGENT INFORMATION:
NAME: COSMAN RACHARD #5,627
REGISTRATION NUMBER: 36,627
RESPENCE/DOCKET NUMBER: 36,627
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1873-4341
TELEFRAX: (415) 343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to reverse of: US-08-619-198-2 from: 1
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Gaps: 0
Percent Identity: 70.000
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APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-653-294-17 x US-08-619-198-2/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
    Sequence 59, Application US/08121713D
    Patent No. 5639856
    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 3560 base pairs
TELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3369 base pairs
TYPE: nucleac acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                     34.00
3.778
90.000
                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: 1..3369
US-08-619-198-2
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USA
                                                                                                                                                                                            HYPOTHETICAL: NC
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Dros
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94104
                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                   FEATURE:
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seq_name: /cgn1_6/ptodata/2/1na/5B_COMB.seq:US-08-835-268-59
                                                                                                                                                                                                                               Length: 12
Gaps: 0
Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,268
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
ITILE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            3151 TACACACACTCATATCTAACGTGGCGCTGCGATAT 3186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 Bush Street, Suite 3200 CITY: San Francisco STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                       1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-08-121-713D-59 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713
FILING DATE: 13.5EP-193
ATONIEV/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELECHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-17 x US-08-121-713D-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                               34.00
3.778
75.000
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STRANDEDNESS: double
                                                                                                                         1..1953
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APPLICANT: GOODMAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                               Quality:
Ratio:
Percent Similarity:
                                                                                                 NAME/KEY: CDS
LOCATION: 1...
US-08-121-713D-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 111
MOLECULE TYPE:
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NAME/KEY:

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Percent Similarity:
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                                                                                                                                                                                                                                                              to: 3560
                                                                                                                                   Gaps: 0
Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,692
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Goodman, Corey S.
APPLICANT: Goodman, Alex L.
APPLICANT: Matthes, David
APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: O'CONNOR, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 Bush Street, Suite 3200 CITY: San Francisco
                                                                                                                                                                                                                                                                                                        1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                              Align seg 1/1 to: US-08-835-268-59 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713
FILING DATE: 13-5EP-1993
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: B94-002-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                            eq_documentation_block:
Sequence 59, Application US/09060692
Patent No. 5935865
                                                                                                                                                                                               alignment_block:
US-08-653-294-17 x US-08-835-268-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION TELEPHONE: (415)343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 3560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 343-4342
                                                                                                        34.00
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75.000
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; LOCATION: 1.1953
US-08-835-268-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1..1953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: GOODMAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: 1..1
US-09-060-692-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
Quality:
                                                                                                           Quality:
Ratio:
Percent Similarity:
                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: C.
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seq_name: /cgn1_6/ptodata/2/ina/PCTUS9_COMB.seq:PCT-US94-10151A-59
                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
Sequence 59, Application PC/TUS9410151A
Sequence 59, Application PC/TUS9410151A
Sequence 50, Application PC/TUS9410151A
TITLE OF INVENTION: The Regents of the University of California TITLE OF INVENTION: The Semaphorin Gene Family
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR HOHBACH TEST ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STRATE: CA
SCOUNTRY: USA
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC COMPA:
COMPUTER: DatentIN Release #1.0, Version #1.25
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10151A
FLING DATE: 13-SEP-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COMBAN ALChard A:
REGISTRATION NUMBER: 36,627
REGISTRATION NUMBER: 36,627
REJERNOC-POCKET UNMBER: 36,627
FELECOMMUNICATION INFORMATION:
TELEFNX: (415) 781-1989
TELEFX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 3350 base pairs
"Ver."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn1_6/ptodata/2/ina/5C_COMB.seq:US-08-619-198-4
Gaps: 0
Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 58.333
                                                                                                                                                                                                                                       3151 TACACACACATCATATCTAACGTGGCGCTGCGATAT 3186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3151 TACACAACTCATATCTAACGTGGCGCTGCGATAT 3186
                                                                                                                                                                                                            1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TyrArgLeuLeulleArgArglleAlaLeuArgTyr 12
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                                                                                                                                                        Align seg 1/1 to: US-09-060-692-59 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-653-294-17 x PCT-US94-10151A-59
                                                                            alignment_block:
US-08-653-294-17 x US-09-060-692-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 34.00
Ratio: 3.778
Percent Similarity: 75.000
3.778
75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..1953
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Quality:
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MOLECULE TYPE: CDNA DESCRIPTION: tim CDNA sequence wherein R at position 1335
                                                                                         APPLICANT: Young, Michael W.
APPLICANT: Sehgal, Amita
APPLICANT: Sehgal, Amita
APPLICANT: Vosshall, Leslie B.
APPLICANT: Price, Jeffrey L.
APPLICANT: Myers, Michael
TITLE OF INVENTION: NUCLEAR LOCALIZATION FACTOR ASSOCIATED
TITLE OF INVENTION: WITH CIRCADIAN RHYTHMS
CORRESPONDENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn1_6/ptodata/2/ina/5C_COMB.seq:US-08-619-198-8
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,198
FILING DATE: 20-MAR-1996
CLASSIFICATION: 514
ATTONEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
RECERENCE/POCKET NUMBER: 26,742
RECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAKX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: US-08-619-198-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1563 AGCTTCTGGTGCTGCGGCTTGCCTGCGGG 1534
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                                                                                                                                                                                                                                                                               ALAUBER & Jackson
CITY: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-17 x US-08-619-198-4/rev
seq_documentation_block:
; Sequence 4, Application US/08619198
: Patent No. 588581
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 133521
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 4170 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.00
3.778
90.000
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STRANDEDNESS: double
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; LOCATION: 1..4
US-08-619-198-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
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Sequence 8, Application US/08619198 Patent No. 5885831

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APPLICANT: "SINGLY AND A STAIL AND A STAILCANT: "SUSSMAIL" LESSIE B.
APPLICANT: Price, Jeffrey L.
APPLICANT: Price, Jeffrey L.
APPLICANT: Michael B.
TITLE OF INVENTION: WITH CIRCADIAN RHYTHMS
TITLE OF INVENTION: WITH CIRCADIAN RHYTHMS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson STREET: 411 Hackensack Avenue
CITY: Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTR: USA
ZIP: 07601
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPATIBLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn1_6/ptodata/2/ina/5C_COMB.seq:US-08-619-198-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,198
FILING DATE: US-0.MAR-1996
CLASSIFICATION: 514
ATTONREY/AGENT INFORMATION:
NAME: Jackson Esq., Javid A.
REGISTRATION NUMBER: 26,742
-REFERENCE/DOCKET NUMBER: 600-1-128A CP1
TELECOMMUNICATION INFORMATION:
TELEPRAS: 201 487-5800
TELEFRAS: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from: 1
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Percent Identity: 70.000
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US-08-653-294-17 x US-08-619-198-8/rev
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APPLICANT: Vosshall, Leslie B.
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APPLICANT: Price, Jeffrey L.
APPLICANT: Myers, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 5192 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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ADDRESSEE: Klauber & Jackson

STRET: 411 Hackensack Avenue
CITY: Hackensack Avenue
STATE: New Jersey
COUNTRY: We Jersey
COUNTRY: We Jersey
COUNTRY: Boy disk
COUNTRY: Boy disk
COUNTRY: Boy disk
CONFUTER READBLE FORM:
MUDIUM TIPE: Floppy disk
CONFUTER PROBLE FORM:
CONFUTER PROBLE FORM:
MUDIUM TIPE: Floppy disk
CONFUTER: Properties
SOFTENTIAN NUMBER: US/08(619,198
FLIANG DATE: 20-NAR-1966
CLASTICATION NUMBER: 26,742
REDETENBENGE/DOCKTY INFORMATION:
NAME: Jackson Esq., David A.
REDISTRATION NUMBER: 26,742
REDETENBENGE/DOCKTY NUMBER: 26,742
REDISTRATION NUMBER: 26,742
REDISTRATION NUMBER: 26,742
REDISTRATION NUMBER: 26,743
REDISTRATION NUMBER: 27,778
REDISTRATION NUMBER:
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AQ815539 HS_5348_A2_A09_SP6E
AA78141 zu42e09.rl Soares o
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Fax: 415 206 3353
Email: malaria@itsa.ucsf.edu
Seq Annotation Data see http://medsfgh.ucsf.edu/id/CpTags/home.html
Seq primer: T3
Class: shotgun.
                                                                                                                                                                                             SKB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xxef__txxon:5807"
/dlob_lost_="CplOWAgDNA1"
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/note="Vector: pBlueScript II (SK-); Site_1: EcoRV; C.
parvum (IOWA isolate) genomic DNA was hydrodynamically sheared to produce fragments having a tight size distribution between 2-4 kb by Dr. Yvonne Thorstenson of the Stanford DNA Sequencing and Technology Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://sequence-
www.stanford.edu/group/techdev/shear.htm). The randomly
sheared gDNA was chromatographed on Sephacryl S-400 to
remove any small fragments and DNA eluting in the void
volume was subcloned into an EcoR V-digested, alkaline
phosphatase-treated pBlueScript II (SR-) vector and
transformed into E. coli strain XL2 Blue MRF'.
Recombinant clones from the first plating of the library
were selected for sequence analysis using T3 and T7
                                                                                                                                                                                                                                                                                                                                   Cryptosporidium parvum.

Cryptosporidium parvum.

Eukaryota: Alveolata: Apicomplexa; Coccidia: Eimeriida:

Cryptosporididae; Cryptosporidium.

E 1 (bases 1 to 724)

S Strong, M. B. and Nelson, R.G.

Cryptosporidium parvum GSS Project

Unpublished (1997)

On Sep 10, 1998 this sequence version replaced gi:3553959.

Contact: Nelson, R. G.

Depts. of Medicine & Pharmaceutical Chemistry

San Francisco General Hospital-University of California, San
                                                                                                                                                                 A0851612 724 bp DNA GSS 18-OCT-1999 CpG1352B CpIOWAgDNA1 Cryptosporidium parvum genomic similar to Shomologue (negative regulator of mitosis) (regulator of Shk1, a p21(CdC42/Rac)-activated kinase (PAK)), genomic survey sequence. A0851612 G1:6063307
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Gaps: 0
Percent Identity: 90.909
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/organism="Cryptosporidium parvum"
/strain="LOWA"
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                                                                                               seq_name: gb_gss6:AQ851612
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gb_gss3:B74688
gb_gss5:AQ815539
gb_est15:AA478141
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AA572328 v188a05.rl Stratagene
AI050480 uc86g01.yl Sugano mous
AW091827 EST285007 tomato mixed
AU031224 AU031224 Rice cDNA fra
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AQ075747 CIT-HSP-2354G2 TR CIT-
8085646 HS 5555 A2 E12 SP6E RF
B31543 HS-1011-A2-A06-MF.ab1 CI
                                                                                                                                                                                        MODEL-frame-promodel - DEV-x1p

- MODEL-frame-promodel - DEV-x1p

- G-Cgnl_J/USPTO-spool/US08653294/runat_04022000_160700_15770/app_query.fasta.1

- DB-EST - OFMT-fastap - SUFFIX-rst - GAPOP-12.000 - GAPEXT-4.000

- MINMATCH-0.100 - LOOPCL-0.000 - LOOPEXT-0.000 - QGAPOP-4.500

- FGAPOP-6.000 - START-0.000 - CARAPEXT-0.500 - FGAPOP-6.000

- FGAPEXT-7.000 - YGAPOP-10.000 - YGAPEXT-0.500 - DELOP-6.000

- DELEXT-7.000 - START-1 - MATRIX-blosum62 - TRANS-human40.cd1

- LOST-45 - DOCALIGN-200 - THR_SCORE-PCT - ALIGN-15 - MODE-LOCAL

- OUTFMT-PFs - DOCALIGN-200 - MAXENE-1000000 - USER-US08653294

- NCPU-6 - ICPU-3 - NO_XLPXY - WAIT - THREADS-1
                                                                                               About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         out_format : pfs
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1340.920
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138.53
134.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search information block:
Query: US-08-653-294-17
Query length: 12
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 8553.360000
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gb_est36:AV182651
gb_est36:AV015503
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gb_est15:AA523786
gb_est19:AA748739
gb_est49:AW197413
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gb_est22:AI050480
gb_est23:AW091827
gb_est24:AU031224
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gb_est24:AI202172
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                                               Date: Feb 8, 2000
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gb_gss8:AQ075747
gb_gss6:AQ826246
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gb_gss13:AQ429279
gb_est26:AU005267
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gb_gss1:CNS00T90
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Eukaryota; Metazoa;
Eutheria; Primates;
1 (bases 1 to 513)
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4.100
90.909
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US-08-653-294-17 x AQ429279
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162
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Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Prade, R. and Roe, B.

An Aspergillus nidulans EST Database

Unpublished (1989)

On Jan 19, 1998 this sequence version replaced gi:2285706.

Other. ESTS: 19612all fl

Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the CDNA clones to the Fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="FGSC A26"
/db_xref="taxon:5072"
/clone="j9c12al"
/clone=lib="Aspergillus nidulans 24hr asexual
developmental and vegetative cDNA lambda zap library"
/tissue_type="vegetative mycella, asexual structures"
/note="vector: pBlueScript SK-; Site_1: EcoRI; Site_2:
Ahol; 5' end of cDNA cloned into EcoRI site of pBluescript
3' end of cDNA cloned into Xhol site of pBluescript
                                                   seq_documentation_block:
LOCUS A1210579 377 bp mRNA EST 19-OCT-1998
DEFINITION j9c12a1.TA Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emericella nidulans cDNA clone j9c12a1 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQ42979 513 bp DNA GSS 24-MAR-1999
CITBL-E1-2565K5.TR CITBL-E1 Homo sapiens genomic clone 2565K5,
AQ429279
                                                                                                                                                                                                                            Emericella nidulans
Eukaryota; Fungi; Ascomycota; Eurotiales; Trichocomaceae;
Emericella.
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Gaps: 0
Percent Identity: 72.727
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US-08-653-294-17 x AI210579/rev
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Percent Similarity: 100.000
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                 seq_name: gb_est24:AI210579
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Shao,S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and Venter, J.C.
Venter, J.C.
Venter, J.C.
Venter, J.C.
Venter, J.C.
Venter, J.C.
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Venter, J.C.
Venter, J.C.
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Venter, J.C.
Venter, J.C.
Venter, J.C.
Venter, J.C.
Venter, J.C.
Venter, Search
Map Building
Unpublished (1997)
Other_GSSs: CITHE.El-2565KS.TF
Contect: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
Calrech Human BAC Library D"
1 128 c 101 g 122 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AU005267 810 bp mRNA EST 19-JAN-1999
AU005267 Bombyx mori p50(Dalzo) Bombyx mori cDNA clone ws30474,
MRNA sequence.
AU005267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysla; Bombycoidea; Bombycoidea; Bombycoidea; Bombycoidea; Bombycoidea; Bombycoidea; Bombycoidea; Bombycoidea; Morimyo,M., Shimada,T., Okano,K. and Maeda,S. Establishment of cDNA database of Bombyx mori Unpublished (1999)
On Jan 19, 1998 this sequence version replaced gi:2150717.
Chordata; Craniata; Vertebrata; Mammalia;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 11
Gaps: 0
Percent Identity: 81.818
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National Institute of Radiological Sciences
Anagawa 4.9-1, Inage, Chiba 263-8555, Japan
Email: kmita@uexs64.nirs.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. 513
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="256565"
/clone_lib="CITBI-E1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TyrArgLeuLeulleArgArglleAlaLeuArg 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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%#1005267 810 bp
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Water Land

1

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to: AV182651
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Ratio:
Percent Similarity:
                                                                                                                                                                                                 Ratio:
                                                                                                                                                                        Quality:
                                                               37
                                                                                                                                                      alignment_scores:
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 21)

S Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R., The WashU'NCI Mouse EST Project 1999

C Onpublished (1999)

On May 7, 1998 this sequence version replaced gi:3119865.

Contact: Marra M/WashU'NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS
LOCUS
A1426843 271 bp mRNA EST 09-MAR-1999
DEFINITION mm95b08.x1 Stratagene mouse heart (#937316) Mus musculus cDNA clone
IMAGE:536151 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
High quality sequence stop: 232.

Location/Qualifiers

1. 271

/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="heart"
/dev_stage="13 day embryos"
/lab_nost="SOLR (kanamycin resistant)"
/note="Organ: heart; Vector: pBluescript SK-; Site_1:
/note="Organ: heart; Cloned unidirectionally. Primer:
Oligo dT. 93 pooled NIH/Swiss 13 day embryo hearts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="IMAGE:536151"
/clone_lib="Stratagene mouse heart (#937316)"
                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 810
                                                                             /strain="p50(Daizo)"
/db_xref="taxon:7091"
/clone="ws30474"
/clone=lib="Bombyx mori p50(Daizo)"
118 c 215 g 203 t
                                                                                                                                                                                                                                                                                Length: 12
Gaps: 0
Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         455 TATTCATTGCTCGTCCATCAAGTGGCACTCCGTTAT 420
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/organism="Bombyx mori"
'CREST project by JST'
Location/Qualifiers
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AI426843.1 GI:4272769
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                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-17 x AU005267/rev
                                                                                                                                                                                                                                                                              41.00
3.727
91.667
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PROJECT
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Caenorhabditis elegans.

Caenorhabditis elegans

Caenorhabditis elegans

Bukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;

Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 300)

Kohara,Y., Shin-1,T., Thierry-Mieq,J., Thierry-Mieg,D., Mitsuki,H., Nishlgaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Nishlgaki,A., Mitani,Y., Iida,K., Uesugi,H., Sugimoto,A., Nomotoco,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS AV182651 300 bp mRNA EST 21-JUL-1999
DEFINITION AV182651 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans cDNA clone yk640g7 3', mRNA sequence.
ACCESSION AV182651 GI:5562552
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTTGGCACGAG 3' -3' adaptor sequence: 5 CTCGAGTTTTTTTTTTTTT 3'"
109 c 66 g 59 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="yk640g7"
/clone_lib="xuji Kohara unpublished cDNA:Strain N2
/crmaphrodite embryo"
/sex="hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
On Jun 5, 1998 this sequence version replaced g1:3189500.
Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     others
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Gaps: 0
Percent Identity: 72.727
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Gaps: 0
Percent Identity: 58.333
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                                                                                                                                                                                                                                                                                                                                                                                                              1 TyrargLeuLeulleArgArglleAlaLeuArg 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 TATCGTCTTCTTGCCCGCCGTGTTGCTGCTCGT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="N2"
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1. .300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expressed genes in C.elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="embryo"
68 c 54 g
                                                                                                                                                                                                                                                                                                                                                                 from: 1
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4.000
83.333
                                                                                                                                                                                                                      4.444
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                                                                                                                                                                                               40.00
                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-17 x AI426843
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US-08-653-294-17 x AV182651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_est36:AV182651
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DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

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Redocova,M., Pierson,B.L., Samac,D.A., Gantt,J.S., Vance,C.P., Gonzalas,M.B. and Ellis,L.

Edorova,M., Pierson,B.L., Samac,D.A., Gantt,J.S., Vance,C.P.,

Gonzalas,M.B. and Ellis,L.

ESTS from the infected leaf cDNA library of Medicago truncatula

Unpublished (1999)

On Jul 7, 1999 this sequence version replaced gi:5406207.

Contact: Carroll P. Vance

Department of Agronomy and Plant Genetics

University of Minnesota

411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA

Tel: 612-625-7219

Fax: 651-644-55058

Email: vance0046maroon.tc.umn.edu

Developmental stage: leaf infected with Colletotrichum; Date:

9/15/99; Submitted to the Database of Expressed Sequence Tags

(dbEST) on 10/22/99; More information is available at

'http://chrysie.tamu.edu/medicago'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 534)
Mahalras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, euphyllophytes, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS AQ883371 534 bp DNA GSS 09-NOV-1999
DEFINITION HS_5471_B2_CO5_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=9239 Col=10 Row=F, genomic survey sequence.
ACCESSION AQ883371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 310
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Gaps: 0
Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone-"IL19"
/clone_11b-"DSIL"
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US-08-653-294-17 x AW127330/rev
barrel medic.
Medicago truncatula
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Ratio: 3.900
Percent Similarity: 100.000
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SOURCE
ORGANISM
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ORIGIN
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                                                                                                                                                                                                            TITLE
JOURNAL
COMMENT
                                                                                                                                            REFERENCE
AUTHORS
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AUTHORS
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MEDLINE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                             Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia; Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia; Eutheria: Primates: Catarrhini; Hominidae; Homo.

1. (bases 1 to 447)

2. Adams.M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

L. Unpublished (1998)

Other_GSSs: CIT-HSP-2309J17.TF

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: Mil Reverse
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 447
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Gaps: 0
Percent Identity: 72.727
                        1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to reverse of: AQ015503 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132
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/db_xref="taxon:9606"
/clone="2309117"
/clone_lib="CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .ocation/Qualifiers
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AQ015503.1 GI:3194239
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US-08-653-294-17 x AQ015503/rev
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Ratio: 3.636
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_est39:AW127330
                                                                                        seq_name: gb_gss8:AQ015503
                                                                                                                                       seq_documentation_block:
LOCUS AQ015503
                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                             human.
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source

FEATURES

BASE COUNT ORIGIN

and

KEYWORDS

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AG000734.1 GI:2579542
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3.545
91.667
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Locus AG000734
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Percent Similarity:
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KEYWORDS
SOURCE
ORGANISM
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TITLE
JOURNAL
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TITLE
JOURNAL
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 559)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                         401 Queen Annabling Conf. (206) 616-3618
Tel: (206) 616-3618
Tex: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBACe3.6; Genomic sequence of BAC ends"
98 c 112 g 171 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
LOCUS A0433893 559 bp DNA GSS 31-MAR-1999
DEFINITION HS_5056_A1_D05_T7 RPCI-11 Human Male BAC Library Homo sapiens
genomic_clone Plate=632 Col=9 Row=G, genomic_survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                   1. .534 // Organism="Homo sapiens" // Organism="Homo sapiens" // Ob_xxef="taxon:9606" // Clone="Plate=9239 Col=10 Row=F" // Clone_lib="RPCI-11 Human Male BAC Library" // Sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 12
Gaps: 0
Percent Identity: 66.667
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 469 TACCGATTGTTATTATGACGTATTGGGCTTCAATAT 504
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                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 534.
Location/Qualifiers
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3.545
91.667
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US-08-653-294-17 x AQ883371
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                                                                                                                                                                                                                                                                                               Seq primer: T7
Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores
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COMMENT
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                    FEATURES
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  COMMENT
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(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACBAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 632 row: G column: 9
Seq primer: T7
Class: BAC ends
High quality sequence stop: 559.
Location/Qualifiers
I. .559
//db_xref="haxon:6606"
//db_xref="haxon:6606"
//clone_lplate=632 Col=9 Row=G"
//sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
E. (Dases 1 to 666)

B. Direct Submission
L. Submitted (31-OCT-1997) to the DDBJ/EMBL/GenBank databases.
Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1, Saqamihara 228, Japan (E-mail:hattorichgc.ims.u-tokyo.ac.jp, Tel:0427-78-9561)
E. (Dases 1 to 666)
S. Hattori,M., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q
L. Published only in Database (1997) In press
                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBACe3.6; Genomic sequence of BAC ends"
166 c 91 g 158 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGO00734 666 bp DNA GSS 06-FEB-1999
Homo sapiens genomic DNA, 21q region, clone: 1171Bm40, genomic
Survey sequence.
AGO00734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              others
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Gaps: 0
Percent Identity: 66.667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   445 TACCGTCTTCTAAGAAAGAGATAGCGTTACAATAC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens DNA, clone:T171Bm40. Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115
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1 (bases 1 to 359)
Salanoubat,M., Choisne,N., Artiguenave,F., Brottier,P., Wincker,P.,
Samson,D., Saurin,W., Weissenbach,J. and Quetier,F.
Unpublished
2 (bases 1 to 359)
                                          seq_documentation_block:
LOCUS CNS00T90 359 bp DNA GSS 28-JUN-1999
DEFINITION Arabidopsis thallana genome survey sequence T7 end of BAC T3N2 of
TAMU library from strain Columbia of Arabidopsis thallana, genomic
survey, sequence.
                                                                                                                                                                                                                                                         Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Euchyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission

Submitted (25-707-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mahairas, G.G., Waliace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ166595 386 bp DNA GSS 16-OCT-1998 HS_3146_Al_B09_MR CIT Approved Human Genomic Sperm Library D sapiens genomic clone Plate=3146 Col=17 Row-C, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Prinates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 386)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 11
Gaps: 0
Percent Identity: 63.636
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1. 359
/organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 AGAGCCTTGGTGGTGAAGTTTGCTCTCCGATAC 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="Columbia"
/db_xref="taxon:3702"
/clone_lib="TAMU"
/clone="T3N2"
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AQ166595.1 GI:3564790
                                                                                                                                                                                               AL089394.1 GI:5290534
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3.800
90.909
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US-08-653-294-17 x CNS00T90
seq_name: gb_gss1:CNS00T90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_gss9:AQ166595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS AQ166595
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                                                                                                                                                                                                                                                  thale cress.
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Ratio:
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                                                                                                                                                                      AL089394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
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AUTHORS
TITLE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eubheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 201)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Barry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            library availability, please contact Pieter de Jong MCC BAC (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html

      seq_documentation_block:
      201 bp
      DNA
      GSS
      21-APR-1999

      LOCUS
      AQ238101
      201 bp
      DNA
      GSS
      21-APR-1999

      DEFINITION
      RPCIII-73J18.TK RPCI-11 Homo sapiens genomic clone RPCI-11-73J18, genomic survey sequence.
      ACCESSION AQ238101
      GI:3670392

      ACCESSION
      AQ238101
      GI:3670392
      GI:3670392

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                           999
     Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps: 0
Percent Identity: 80.000
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/sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="GDB:7527881"
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1. .201
                                                                                                                         Align seg 1/1 to reverse of: AG000734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 9
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                                                  alignment_block:
US-08-653-294-17 x AG000734/rev
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Percent Similarity: 100.000
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  91.667
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                                                                                                                                                                                                                                                                      seq_name: gb_gss10:AQ238101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human.
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ORGANISM

REFERENCE AUTHORS

VERSION KEYWORDS SOURCE

TITLE JOURNAL COMMENT

source

FEATURES

BASE COUNT ORIGIN

and

Homo

F M KNOWN

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source
                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 461)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone=lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
LOCUS AQ137850 461 bp DNA GSS 24-SEP-1998
DEFINITION HS_3058_B2_C09_MF CIT Approved Human Genomic Sperm Library D F sapiens genomic clone Plate=3058 Col=18 Row=F, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3146 row: C column: 17
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
Voll Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
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Plate: 3058 row: F column: 18
Class: BAC ends
High quality sequence stop: 461.
Location/Qualifiers
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US-08-653-294-17 x AQ166595
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AUTHORS
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COMMENT
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Human neuronal nic RINGII antigenic p HLA-B2702 CTL modu Immunomodulating d Immunomodulatory p Immunomodulatory p Peptide #3 used in Peptide #2 used in

Human adrenaline b Human beta-3 adren Murine somatostati

Perfect score: Sequence: Scoring table:

Run on:

Searched:

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WILL'S 9-1940/12/25.

WHILL'S 9-1940/12/25.

WHILL'S 9-1940/12/25.

Inhibit cytolytic activity and differentiation of CTLS.

Example: Page 12: 29pp: English.

Example: Page 13: 20pp: English.

Example: Page 14: 20pp: English.

Example: Page 13: 20pp: English.

Example: Page 13: 20pp: English.

Example: Page 14: 20pp: English.

Example: Page 15: 20pp: English.

Example: Page 25:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-NOV-1996 (first entry)
HLA-B2702 84-79-84 palindrome.
HLA-B2702 84-79-84 palindrome.
HLA-B2702 84-79-84 palindrome.
HLA-D74: alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CLL; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.4%; Score 53; DB 1; Length 12; 91.7%; Pred. No. 0.00042; 1ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytolysis; antigen presenting cell.
Synthetic.
W09513288-Al.
W53847
R54991
R39264
W44152
R25591
W33779
W47263
W33782
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W33798;
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Best Local Similarity 91.7
Matches 11; Conservative
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HLA-B2702 CTL modu
HLA-B2702 CTL modu
Peptide B2702.84-7
HLA-B2702 84-75T/7
Human alpha 2 beta
Human alpha-2b adr
Human neuronal nic
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H. Pylori OR 09ap
Lung cancer associ
Lung cancer associ
Protein with Oxeta
Mus musculus SOCS7
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Homo sapiens don-1
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Human MHC 1 alpha
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Canine beta-3 adre
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HLA-B2702 84-75-84
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                                                                                                                                                                                                                      (without alignments)
2.319 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                          Search time 122.56 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188963 seqs, 23686106 residues
                                                                                                                                                                                             February 8, 2000, 01:29:40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
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                                                                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Listing first 45
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Maximum DB seq length: 1000000
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Score

Result Š.

Database :

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Gaps ; 0

Wed Feb

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Example 1: Page 19: 41pp: English.

Peptides W33784-98 and W33778-9 were assayed for their immunomodulating activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B (R aa76-77L) (aa79-84) or (aa88-79) (laa77-76R); aa76 = E or V; aa77 = D. S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            941. They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be activate of in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rhemmatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Claim 17: Page 35: 41pp; Enlantsh.
This sequence represents a specifically claimed immunomodulating dimer peptide of the invention. A peptide-type compound or variant
19-JUN-1998 (first entry)
Peptide B2702.84-79/79-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunomodulating dimer peptide #3.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                       New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 53; DB 1; Length 12;
Pred. No. 0.00042;
0; Mismatches 1; Indels
                                                                                                                                                                                                        24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                Beulow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
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91.7%;
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Best Local Similarity 91.7
Matches 11; Conservative
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22-MAY-1997; U08689.
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WO9744351-Al.
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WO9744351-A1.
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                                                                                       rejection.
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claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R anf6-77L) (aa79-84) or (aa64-79) (laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HLA-B compounds comprise amino acid sequences related to a Class I HLA-B compounds comprise amino acid sequences related to a class I HLA-B compaid domain (positions 784). They can be used to inhibit cytocxic. T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLS. They can also inhibit the proteins of interest to activate CTLS. They can also inhibit the proteins of interest to activate CTLS. They can also inhibit the confidence of the preventing rejection of transplants or for treating autoimmune used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 15; Page 36; 80pp; English.
R83061-R83085, R83090-R83096 and R92207-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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                                                                                                                                                                                                                                                                                                                                                        diseases, e.g. diabetes, rheumatoid arthritis and lupus en
The products can also be used for detection and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.4%; Score 53; DB 1; Length 12; 91.7%; Pred. No. 0.00042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parham P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R92907 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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55.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YRLAIR-----RILLRY
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WPI; 95-358582/46.
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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R92907
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autoimmune diseases
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WO9526979-A1.
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                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                        This is a superior of the proteins of the may compared to the protein of the protein plaintenant. These sequence represents the human-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the protein py 4 from a T-cell lysate. Py 4 is a T-cell surface membrane protein py 4 from a T-cell lysate. Py 4 is a T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. Py 4 is found in a limited number of cell types, but is particularly py is so found in a limited number of cell types, but is particularly py is so immunologically cross reactive with the neat shock protein assistable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B702 palindromic peptide. Compositions comprising the extracellular fragment of py4 combined with HLA-B2702.60-84 (see R95416), indices calcum influx, and inhibits compositions comprising the mount of binding between the candidate compound and py4. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by adding to the containing T-cells and antigen presenting cells (APCS), by adding to the containing the binding of the p74 ligand.
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                                                   12-NOV-1996 (first entry)
HLA-B2702 84-75-84 palindrome.
HLA-B2702 84-75-84 palindrome.
HLA-D74: alphal-helix: human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunomodulating dimer péptide #1.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.2%; Score 39; DB 1; Length 20; 55.0%; Pred. No. 0.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                      10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI; 95-194027/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beulow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
                            R95428 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W33778 standard; peptide; 20 AA.
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22-MAY-1997; U08689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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WO9744351-Al.
                                                                                                                                                           WÔ9513288-A1.
18-MAY-1995.
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S
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RESULT
R95428
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Triangly autonominute diseases.

It is sequence represents a specifically claimed immunomodulating dimer to peptide of the invention. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acids, where the peptide-type compound comprises the formula acquired and/or C-terminal amidated or estarified forms of up to 60 amid acids, where the peptide-type compound comprises the formula A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and a represents amino acid; The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HA-B alphal domain (positions 79-84). They can be used to inhibit cyctoxic ripmonocytes (CTL) from undesirably attacking cells in a host or in proteins of interest to activate CTLs. They can also inhibit the proteins of interest to activate CTLs. They can also inhibit the profice of or proteins of interest to activate CTLs. They can also inhibit the close of or seventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis.
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R83061-R83085, R83090-R83096 and R82207-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
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WPI; 95-358882/46.
Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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55.0%; Pred. No. 0.28;
iive 0; Mismatches 1
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50.0%; Pred. No. 2.4;
tive 0; Mismatches ;
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05-ABR-1994, US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R92909 standard; peptide; 20 AA.
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Best Local Similarity 50.0
Matches 10; Conservative
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Best Local Similarity 55.0
Matches 11; Conservative
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Synthetic
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 888888888888888888888
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                                                                                                                    HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                      Example 15; Page 36; 80pp; English.
R83061-R83085, R83096 and R92907-F92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (comparate to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Peptide B2702.84-75Ty75-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                 Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I 975-84\ \mathrm{MHC} antigen of the recipient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.6%; Score 34; DB 1
50.0%; Pred. No. 2.4;
Live 0; Mismatches
                                                                                                                                                                                                                            05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-NOV-1997, 22-NAY-1997, 22-NAY-1997, 24-NAY-1996, US-653294, 24-NAY-1996, US-653294, (STRD ) UNIV LELAND STANFORD JUNIOR. Beulow R, Clayberger C, Krensky AM;
                                                                               R92908 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W33791 standard; peptide; 20 AA.
1 YRLAIRLNERRENLRTALRY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YRLAIR-----RILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||| |
| YRLATRINERRENLRIALRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0
Matches 10; Conservative
                                                                                                                                                                                                          12-UCT-1995.
05-APR-1995; U04349.
                                                                                                                                                                                                                                                          Clayberger C, Krer
WPI; 95-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 98-086530/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the patient.
Sequence 20 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
WO9744351-A1.
27-NOV-1997.
                                                                                                                                                                                        W09526979-A1.
                                                                                                        16-MAY-1996
                                                                                                                                                                                                      12-0CT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W33791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                σ
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W33791
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C. C. territal andiated on esverintied forms of up to for anno acids, where continuous andiated conserviced formulas A-19, where A, B = 10, S of N, S and S = 10 to N, and N = 10, S of N, and S = 10 to N, and N = 10, S of N, and S = 10 to N, and N = 10, S of N, and S = 10 to N, and N = 10, S of N, and S = 10 to N, and N = 10, S of N, and S = 10 to N, and N = 10, S of N, and N = 10, S of N, and S = 10 to N, and N ```

DB 1;

Score 34;

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Gaps

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Assay for alpha-2b adrenergic receptor ligands - using membranes of cells expressing recombinant receptor
Disclosure: Fig 2A-E; 16pp; English.
Human alpha-2B adrenergic receptor (Wil804) is a member of the rhodopsin-like signal transducer family. Its amino acid sequence was deduced from a genomic DNA clone (T59499) obtd. from a human spleen DNA library. Vectors have been adapted to allow prodn. of alpha-2B adrenoceptor in bacterial, yeast or mammalian cells; transfected Ltk- cells, designated L-NGC-alpha-2B, are deposited as AVCC CRL 10275. Membranes of transfected mammalian cells an novel methods to identify drugs which specifically interact Sequence 487 AA;
 Discioure, Fig 2; 15pp; English.
Clone NGC-alpha2beta was isolated from a human spleen genomic
Library by screening with a fragment of the human 5-Hirb receptor
gene. The gene was used to express recombinant receptor protein
which can be used to produce antibodies for inhibition of receptor
 Isolated DNA encoding human adrenergic receptor - for detecting nucleic acids encoding alpha, 2-beta adrenergic receptor, for screening drugs.
 06-MAY-1997 (first entry)
Muman alpha-2b adrenergic receptor.
Alpha-2b adrenergic receptor; adrenoceptor; adrenaline; epinephrine; signal transduction; neurotransmitter; ligand.
 Score 32; DB 1; Length 487;
Pred. No. 1.4e+02;
1; Mismatches 3; Indels
 3; Indels
 Score 32; DB 1;
Pred. No. 1.4e+02;
 1; Mismatches
 1; Mismatches
 W11804 standard; Protein; 487 AA.
 W44156 standard; Protein; 504 AA.
 (SYNA-) SYNAPTIC PHARM CORP. Hartig PR, Weinshank RL; WPI: 97-107576/10. N-PSDB; T59499.
 55.2%;
63.6%;
 55.2%;
 W44156;
14-MAY-1998 (first entry)
 Ouery Match
Best Local Similarity 63.0.
 Ouery Match
Best Local Similarity 63.0
Post Local 7; Conservative
 21-JAN-1997.
30-OCT-1889; 428856.
30-OCT-1989; US-428856.
30-WAY-1991; US-707604.
22-OCT-1992; US-965040.
 (NEUR-) NEUROGENETIC COR.
Weinshank RL, Hartig PR,
WPI; 91-310087/42.
 470 FRRAFRRILCR 480
 470 FRRAFRRILCR 480
 1 YRLAIRRILLR 11
 1 YRLAIRRILLR 11
 487 AA;
 N-PSDB; 014151
 Homo sapiens.
US5595880-A.
 unction.
 Sequence
 W11804;
 RESULT 14
W44156
 RESULT
W11804
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 Will 31-1940.7(2).

Tomposns. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example 12: 29pp: English.

R95413, and R95415-R9543 represent palindromes and fragments of human-leucocyte-associated antigens. This sequences can be used too the activity of a protein p74 from a T-cell lysate. P74 is a T-cell surface membrane protein p74 from a T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein CT as as a laso immunologically cross reactive with the heat shock protein R970. P74 is found in a limited number of cell types, but is particularly expressed on B and T cells. P74 can be isolated by lysis of a suitable cell with an amphototric detergent, and then passed through an affinity column containing a covalently bound HA-B2702 palindromic affinity column containing a covalently bound HA-B2702 palindromic combined with HA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis.

Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound can determining the amount of binding between the candidate compound companient of TL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount candidate composition companies with p74 for the binding of the p74 ligand.
 1;
 ä
 12-NOV-1996 (first entry)
HLA-B2702 84-75T/75-84T palindrome.
HLA-B2702 84-75T/75-84T palindrome.
HLA-D2702 84-75T/75-84T palindrome.
T-Call 1ysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotcxic T lymphocyte; CTL; differentiation;
CYtolysis; antigen presenting cell.
 Gaps
 Gaps
 .;
8
 8;
 Human alpha 2 beta adrenergic receptor.
Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta.
 ;
 Pred. No. 2.4;); Mismatches
 18-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD) UNIV LELAND STANFORD JUNIOR.
 R14149 standard; Protein; 487 AA.
 standard; peptide; 20 AA.
 ö
 1 YRLAIR-----RILLRY 12
 1 YRLAIRLNERRENLRIALRY 20
 Query Match 55.2%;
Best Local Similarity 52.6%;
Matches 10; Conservative (
 50.0%;
 1 YRLAIR-----RILLR 11
 1 YRLAIRLNETRENLRIALR 19
 Krensky AM;
 06-JAN-1992 (first entry)
 Conservative
 30-OCT-1989; 428856.
30-OCT-1989; US-428856.
Best Local Similarity
Matches 10; Conserv
 Clayberger C, Kr
WPI; 95-194027/25
 WO9513288-A1.
 Homo sapiens.
US5053337-A.
 01-OCT-1991
 R95430 :
R95430;
 RESULT 11
R95430
 RESULT 12
```

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Gaps

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R14149

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Length 487;

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Example 2: Page 72-73: 99pp: English.

Example 2: Page 72-73: 99pp: English.

The present sequence represents a human neuronal nicotinic acetylcholine receptor (NAChR) subunit. The cells expressing the alpha and/or beta receptor (NAChR) subunit. The cells expressing the alpha and/or beta nethod of screening compounds to identify any which modulate the activity of human neuronal NAChR.

Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits or specific receptor subunit combinations with a variety of potential agonists or antagonists provides information with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with one or more receptor subtypes. The resulting drugs should exhibit fewer that express a variety of subtypes.
Human neuronal nicotinic acetylcholine receptor alpha-3 subunit.
Human; neuronal nicotinic acetylcholine receptor; alpha-3 subunit;
brain tissue; screening; NAChR; antibody.
 Human neuronal nicotinic acetylcholine receptor subunits and DNA also transformed cells useful for screening cpds. which modulate
 /note= "encoded by TWC"
459..480
/label= TMD4
/note= "transmembrane domain"
327..458
 /label= unspecified
/note= "encoded by AWC"
273. 296
/label= TMD2
/note= "transmembrane domain"
 /note= "transmembrane domain"
 /note= "transmembrane domain"
 (SALK) SALK INST BIOTECHNOLOGY IND ASSOC
 /label= cytoplasmic_loop
 /label= unspecified
/note= "encoded by WWC"
240. 265
/label= TMD1
 /label= unspecified
/note= "encoded by WWC"
 /label= unspecified
/note= "encoded by AMC"
 /note= "encoded by IGY"
302. .326
/label= TMD3
 Location/Qualifiers
 (SIBI-) SIBIA NEUROSCIENCES INC.
Ellott KJ, Ellis SB, Harpold MM;
WPI: 94-303024/37.
N-PSDB; V12200.
 .. .30
/label= signal
 08-MAR-1993; US-028031
 Misc_difference 354
 Misc_difference 235
 Misc_difference 246
 Misc_difference 309
 Misc_difference 347
 Misc_difference
 Homo sapiens
 Peptide
 Domain
 Domain
 Domain
 Domain
 Region
 Key
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```
Pricobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection and to diagnosis of H. pylori infection and the sequence of a H. pylori cell envelope flagellar protein. This is the sequence of a H. pylori cell envelope flagellar protein. The protein may be used in a vaccine to prevent or treat H. pylori life cycle activators or inhibitors. The protein as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of the pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies and against the protein can be used in immunoassays to evaluate the abundance and distribution of H. pylori actions. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for significant homology to other known or exported coding regions are analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR by analification for recombinant polypeptide production, e.g. in E. coli
 protein.
 Gaps
 24-JUN-1998 (first entry)

H. pylori ORF hp4e13394_3368767_c1_80 cell envelope flagellar prote Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis. Helicobacter pylori.
W99737044.A1.
 3,
 Score 31.5; DB 1; Length 803;
Pred. No. 3e+02;
2; Mismatches 2; Indels
 Ouery Match
Best Local Similarity 53.3
Matches 8; Conservative
 06-DEC-1996; US-761318.
29-MAR-1996; US-76811.
25-OCT-1996; US-788731.
25-OCT-1996; US-738659.
28-OCT-1996; US-738659.
AMR RA. SMITH D;
WPI: 97-503122/46.
 287 YKQAVRYYKRILLEY 301
 1 YRLAIR---RILLRY 12
232 YSLXIRRLSLFY 243
 03-001-139/.
27-MAR-1997; U05223.
06-DEC-1996; US-7613
 09-0CT-1997
 Sequence
 RESULT
W55668
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Search completed: February 8, 2000, 01:29:40 Job time: 1752 sec

ò

Query Match 55.2 Best Local Similarity 58.3 Matches 7; Conservative

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Gaps

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55.2%; Score 32; DB 1; Length 504; 58.3%; Pred. No. 1.5e+02; tive 1; Mismatches 4; Indels

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

sw model using protein search, OM protein 7, 2000, 11:54:28; Search time 117.7 Seconds (without alignments) 4.809 Million cell updates/sec February Run on:

US-08-653-294-18 58 Title: Perfect score: Sequence:

1 YRLAIRRILLRY 12

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

142080 segs, 47169319 residues Searched:

142080 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

PIR\_62:\* Database :

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| pti                 | histocompatibility | P-glycoprotein - Č | P-glycoprotein - C | p-qlycoprotein iso | ribosomal protein | probable oxidoredu | L17 ribosomal prot | hypothetical prote |        | iron-sulfur cluste | conserved hypothet | probable bioB prot | _      |        | -4     |        | DNA-directed RNA p | DNA-directed RNA p | RNaseP C5 chain - | hypothetical prote | F420-nonreducing h | hypothetical prote | Na+/H+ antiporter | type II restrictio | glyceraldehyde-3-p | MHC class I histoc |        | hemo | COA    | probable DNA misma |
|---------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------|--------|--------|--------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------|------|--------|--------------------|
| ID                  | \$29990            | 148120             | 148119             | 148123             | $\leftarrow$      | $^{\circ}$         | C72053             | S15593             | A47377 | E72382             | G69807             | G70542             | S54211 | T13646 | T00953 | C71618 | RNBY2L             | F64429             | S73487            | D72110             | A69422             | T16556             | JC5342            | B71808 .           | S34254             | S07114             | A60384 | -    | G70986 | _                  |
| DB                  | ~                  | 7                  | 7                  | 7                  | ~                 | ~                  | 7                  | 7                  | ď      | ~                  | ~                  | ~                  |        |        |        |        |                    | ď                  |                   |                    |                    |                    |                   |                    |                    | 7                  | 7      | 7    | 7      | N                  |
| Length              | 348                | 252                | 259                | 1281               | 141               | 309                | 142                | 388                | 1283   | 152                | 280                | 349                | 069    | 735    | 814    | 1712   | 1733               | 78                 | 118               | 133                | 168                | 194                | 313               | 326                | 334                | 345                | 362    | 453  | 532    | 576                |
| %<br>Query<br>Match | 7.07               |                    | 63.8               | 63.8               | 62.1              | 62.1               | 60.3               | 60.3               | o.     | œ,                 | œ.                 | œ,                 | œ.     | 8      | œ      | ъ.     | ω.                 | 9                  | e.                | 9                  | ٠                  | ė.                 | è.                | ٠.                 | ٠.                 | ė.                 | ė.     | ė.   | 56.9   | ė.                 |
| Score               | 41                 | 37                 | 37                 | 37                 | 36                | 36                 | 35                 | 35                 | 35     | 34                 | 34                 | 34                 | 34     | 34     | 34     | 34     | 34                 | 33                 | 33                | 33                 | 33                 | 33                 | 33                | 33                 | 33                 | 33                 | 33     | 33   | 33     | 33                 |
| Result<br>No.       |                    | 7                  | ю                  | 4                  | 2                 | 9                  | 7                  | 80                 | σ      | 10                 | 11                 | 12                 | 13     | 14     | 15     | 16     | 17                 | 18                 | 19                | 20                 | 21                 | 22                 | 23                | 24                 | 25                 | 56                 | 27     | 28   | 53     | 30                 |

| ABC-type transport<br>probable ABC-type<br>hypothelical prote | gene 18.7 protein<br>hypothetical prote<br>ribosomal protein | regulatory protein regulatory protein probable ABC trans | hypothetical prote hypothetical prote iron-sulfur bindin | fimbrial assembly hypothetical prote alpha-2B-adrenerg1 |
|---------------------------------------------------------------|--------------------------------------------------------------|----------------------------------------------------------|----------------------------------------------------------|---------------------------------------------------------|
| F64186<br>H64045<br>D65032                                    | W8BPT3<br>S69745<br>F72250                                   | S07359<br>S30287<br>G72598                               | A75167<br>S74282<br>E69499                               | D70365<br>D6441<br>I51883                               |
| 000                                                           | H 70 70                                                      | ~~~                                                      | 000                                                      | 000                                                     |
| 586<br>587<br>1124                                            | 128                                                          | 218                                                      | 356                                                      | 408<br>421<br>448                                       |
| 0,0,0                                                         | 444                                                          | üüü                                                      | 444                                                      | 222                                                     |
| 5<br>5<br>5<br>6<br>6                                         | 50 50 50<br>50 50 50                                         | 555                                                      | , 25<br>55<br>55                                         | 555                                                     |
|                                                               | 333                                                          | 3 3 3 3                                                  | 333                                                      | 322                                                     |
| 33<br>33<br>33<br>33<br>33                                    | 8 8 8<br>4 73 78                                             | 3 3 3<br>7 8 8 0                                         | 0 4 4<br>0 1 2 4                                         | 444<br>844                                              |

## ALIGNMENTS

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Associated to the substance of the subst
 Length 348;
RESULT
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ö Gaps ö Indels ; 0 Query Match 70.7%; Score 41; DB 2; Best Local Similarity 63.6%; Pred. No. 1.8; Matches 7; Conservative 4; Mismatches (

## |:|:|::|||| RVALRKLLLRY 108 2 RLAIRRILLRY 12 8 ò 셤

RESULT

P48120 P-91ycoprotein - Chinese hamster (fragment) C;Species: Cricetulus griseus (Chinese hamster) C;Species: Cricetulus griseus (Chinese hamster) C;Species: O4-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 20-Aug-1999 C;Accession: 148120 R;Ng, W.F.; Sarangi, F.; Zastawny, R.L.; Veinot-Drebot, L.; Ling, V. Mol. Cell. Biol. 9, 1224-1232, 1989 A;Title: Identification of members of the P-9lycoprotein multigene family. A;Reference number: 148119; MuID:89261726 A;Scatus: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-252 <RES> A;Cross-references: GB:M25792; NID:9576810; PIDN:AAA53440.1; PID:9576813 C;Genetics:

A; Introns. 56/3; 135/3; 184/3 C;Superfamily: multidrug resistance protein; ATP-binding cassette homology C;Reywords: ATP: P-loop C;Reywords: ATP-binding cassette homology <ABG2> F;25-221/Domain: ATP-binding motif A (P-loop)

Query Match

Length 252; 63.8%; Score 37; DB 2;

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A; Accession: H71504
A; Molecule type: DNA
A; Residues: 1-141 < ARN>
A; Reference number: 1-17, 2594-2601, 1995
A; Fitle: Chlamydia trachomatis RNA polymerase alpha subunit: sequence and structural A; Reference number: 140743; MUID:95247702
 C;Accession: G70882
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Cole, S.T.; Brosch, R.; Devlin, R.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Nature 393, 537-544, 1998
A;Authors: Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Qua, Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A; Accession: G70882
 Aravind, L.; Mitche
 A;Residues: 1-309 <COL>
A;Cross-references: GB:AL008967; GB:AL123456; NID:g3261491; PIDN:CAA15591.1; PID:e129
A;Experimental source: strain H37Rv
 Gene: Rv2776c
Superfamily: phthalate dioxygenase reductase; cytochrome-b5 reductase homology; fer
9-211/Domain: cytochrome-b5 reductase homology <CBR>
2240-297/Domain: ferredoxin [2Fe-25] homology <FER>
 humans: Chlamydia
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
 C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 13-Aug-1999
C;Accession: H71504; 140747
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, I
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: C}
A;Reference number: A71570; MUID:99000809
 C, Species: Mycobacterium tuberculosis
C, Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 29-Sep-1999
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A;Residues: 20-115, 78', 117-141 <GUL>
A;Cross-references: GB:L33834; NID:g620026; PIDN:AAA74990.1; PID:g620030
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 probable oxidoreductase - Mycobacterium tuberculosis (strain H37RV)
 Length 141;
 Length 309;
 Indels
 Indels
 C;Superfamily: Escherichia coli ribosomal protein L17
C;Keywords: protein biosynthesis; ribosome
 Score 36; DB 2;
Pred. No. 15;
1; Mismatches
 DB 2;
 Score 36; DB 2
Pred. No. 6.9;
4; Mismatches
 ribosomal protein L17 - Chlamydia trachomatis
 62.18;
87.58;
 62.1%;
54.5%;
 Query Match
Best Local Similarity 87.5.
The Conservative
 6; Conservative
 2 RLAIRRILLRY 12
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64 RLAVGRLMVRY 74
 Query Match
Best Local Similarity
Matches 6; Conserv
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65 YRIAIRRI 72
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 1 YRLAIRRI
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 C; Species: Cricetulus griseus (Chinese hamster)
C; Date: Oz-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C; Accession: 148123
R; Endicott, J.A.; Sarangi, F.; Ling, V.
NA Seq. 2, 89-101, 1991
A; Title: Complete Cyna sequences encoding the Chinese hamster P-glycoprotein gene family A; Reference number: 148121; MUID:92135896
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 P-glycoprotein - Chinese hamster (fragment)
C:Species: Cricetulus griseus (Chinese hamster)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 20-Aug-1999
 A; Introns: 566/3; 142/3; 191/3
C:Superfamily: multidrug resistance protein; ATP-binding cassette homology
C:Keywords: ATP: P-loop
F;25-228/Domain: ATP-binding cassette homology <ABC2>
F;42-49/Region: nucleotide-binding motif A (P-loop)
 A.Cross-references: GB:M60042; NID:g191168; PIDN:AAA68885.1; PID:g191169
C.Superfamily: multidrug resistance protein; ATP-binding cassette homology
C.Superfamily: multidrug resistance protein; ATP-binding cassette homology
F:412-606/Domain: ATP-binding cassette homology <ABC1>
F:423-436/Region: nucleotide-binding motif A (P-loop)
F:1034-1250/Domain: ATP-binding cassette homology <ABC2>
F:1071-1078/Region: nucleotide-binding motif A (P-loop)
 C; Accession: 148119
R; Ng, W.F.; Sarangi, F.; Zastawny, R.L.; Veinot-Drebot, L.; Ling, V.
Mol. Cell. Biol. 9, 1224-1232, 1989
A; Title: Identification of members of the P-glycoprotein multigene family.
A; Reference number: 148119; MUID:89261726
A; Accession: 148119
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 Gaps
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A;Residues: 1-259 <RES>
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 DB 2; Length 1281;
 Length 259;
 Indels
 Indels
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 1;
 A:Status: preliminary; translated from GB/EMBL/DDBJ A:Molecule type: mRNA A:Residues: 1-1281 <RES>
 DB 2;
 A;Status: preliminary; translated from GB/EMBL/DDBJ
Pred. No. 7.8;
1; Mismatches
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 Pred. No. 37;
1; Mismatches
 Score 37; Di
Pred. No. 8;
 glycoprotein isoform III - Chinese hamster
 Score 37;
 63.8%;
80.0%;
 63.8%;
80.0%;
80.08;
Similarity 80.0
8; Conservative
 Conservative
 Query Match 63.8
Best Local Similarity 80.0
Matches 8; Conservative
 |||||| |:|
1184 RLAIRRALIR 1193
 |||||| |:|
|155 RLAIRRALIR 164
 ||||||| |:|
162 RLAIRRALIR 171
 Query Match
Best Local Similarity
Matches 8; Conserv
 RLAIRRILLR 11
 2 RLAIRRILLR 11
 2 RLAIRRILLR 11
 A; Accession: 148123
Best Local
Matches
 7
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Gaps

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conserved hypothetical protein yfkC - Bacillus subtilis
conserved hypothetical protein yfkC - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Accession: G69807
R;Kunst, F:; Ogasawara, N:; Moszer, I:; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C; Bronn, S; Bruulliet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
A;Authors: Foulger, D.; Fritz, C.; Hilbert, H.; Holsappel, S.; Hullo, M
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Mssuda, S.; Mau
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Pornete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
 Across references: GB:L07065
C;Genetics:
A;Cross references: GB:L07065
A;Cross references: FlyBase: FBgn0010241
A;Cross references: FlyBase: FBgn0010241
A;Introns: 87/3: 182/2: 832/3: 934/3: 981/2: 1168/3: 1217/3
A;Introns: 87/3: 182/2: 832/3: 934/3: 981/2: 1168/3: 1217/3
A;Introns: 87/3: 182/2: 832/2: 832/3: 934/3: 981/2: 1168/3: 1217/3
C;Superfamily: unasigned ATP-binding cassette proteins; ATP-binding cassette homology cABCl>
F;418-613/Domain: ATP-binding cassette homology cABCl>
F;1058-1254/Domain: ATP-binding cassette homology cABC2>
F;1075-1082/Region: nucleotide-binding motif A (P-loop)
 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
 GB:AE000512; NID:g4980893; PID:g4980900; TIGR:TM0396
 Nature 399, 323-329, 1999
A;Tille: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A;Reference number: A72200; MUID:99287316
A;Accession: E72382
 iron-sulfur cluster-binding protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun_1999 #sequence_revision 11-Jun-1999 #text_change 20-Sep-1999
 60.3%; Score 35; DB 2; Length 1283; 70.0%; Pred. No. 91; 1.1ve 2; Mismatches 1; Indels
 A;Gene: TM0396
C;Superfamily: nrfC protein; ferredoxin 2[4Fe-45] homology
 58.6%; Score 34; DB 66.7%; Pred. No. 18; iive 3; Mismatches
 A;Molecule type: DNA
A;Residues: 1.152 CARN>
A;Cross references: GB.AE001719; GE
A;Experimental source: strain MSB8
 Query Match 60.3
Best Local Similarity 70.0
Matches 7; Conservative
 Conservative
Molecule type: DNA
Residues: 1-1283 <GER>
 |:|||| |:|
547 RIAIRRALIR 556
 Local Similarity
nes 6; Conserv
 2 RLAIRRILLR 11
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3 IAVRRILIR 11
 3 LAIRRILLR 11
 A; Status: preliminary
 C; Accession: E72382
 Query Match
Best Local Si
Matches 6;
 A; Residues:
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 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-142 <ARN>
A;Residues: 1-142 <ARN>
A;Cross-references: GB:AE001647; GB:AE001363; NID:g4376920; PIDN:AAD18764.1; PID:g437692
 Genomics 17, 83-88, 1993
A;Title: Analysis of Mdr50: a Drosophila P-glycoprotein/multidrug resistance gene homolo A;Teterence number: A47377; MUID:94010914
A;Steference number: A47377
A;Stetus: preliminary
 5
 L.; Grimwood,
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 multidrug resistance protein Mdr50 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 10-Jul-1998
C;Accession: A47377
R;Gerrard, B.; Stewart, C.; Dean, M.
 C;Species: Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 13-Aug-1999
 Gaps
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 R;Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A;Reference number: A72000; MUID:99206606
A;Accession: C72053
 ö
 ö
 Score 35; DB 2; Length 142;
Pred. No. 11;
4; Mismatches 1; Indels
 Length 388

 Chlamydia, pneumoniae (strain CWL029)

 A;Gene: rll7
C;Superfamily: Escherichia coli ribosomal protein Ll7
 DB 2;
29;
 2; Mismatches
 C:Genetics:
A:Mobile element: insertion sequence ISH27-3
A:Start codon: GTG
 Score 35;
Pred. No.
 A, Experimental source: strain CWL029
C, Genetics:
 60.3%;
54.5%;
 60.3%;
 Conservative
 Conservative
 2 RLAIRRILLRY 12
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64 RIAIGRLMVRY 74
 Query Match
Best Local Similarity
 Best_Local Similarity
Matches 6; Conserv
 154 YRLAVRRL 161
 1 YRLAIRRI 8
 C; Accession: C72053
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 Query Match
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2; Length 152; Indels

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A;Accession: S53971
A;Mocession: S53971
A;Molecule type: DNA
A;Residues: 1-690 <CON>
A;CONS-1-690 <CON
A;CONS-1-690 <CON>
A;CONS-1-690 <CON
A;
 hypothetical protein F20b22.3 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (5pecies: Arabidopsis thaliana (mouse-ear cress) (5pacies: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Sep-1999 (5.7 c.) Accession: T00953 (7.7 c.) Agenome: nuclear

C; Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog
C; Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog
C; Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog
C; Squard ATP-binding cassette homology cassette homology
F; 11-127-Domain: transmembrane #status predicted cTM2>
F; 233-249/Domain: transmembrane #status predicted cTM3>
F; 258-274/Domain: transmembrane #status predicted cTM4>
F; 452-648/Domain: ATP-binding cassette homology cABC>
F; 469-476/Region: nucleotide-binding motif A (P-loop)
 A;Cross-references: EMBL:AL021728; NID:e1355643; PID:e1301392; PIDN:CAA16821.1
C;Genetics:
 C; Species: Drosophila melanogaster
C; Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
C; Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
C; Accession: 713646
B; Ferraz, C; Yidal, S; Brun, C; Bucheton, A; Demaille, J.G.
Submitted to the EMBL Data Library, April 1999
A; Description: Sequenching the distal X chromosome of Drosophila melanogaster.
A; Reference number: 217694
A; Accession: T13646
A; Accession: T13646
A; Molecule type: DNA
A; Residues: 1-735 <FER>
 A;Molecule type: DNA
A;Residues: 1-27,'RNHS',28-690 <LEI>
A;Cross-references: EMBL:X82612; NID:9575392; PIDN:CAA57938.1; PID:9575393
C;Genetics:
 hypothetical protein EG:95B7.9 - fruit fly (Drosophila melanogaster)
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 Length 690;
 Length 735;
 Indels
 58.6%; Score 34; DB 2; 75.0%; Pred. No. 82; iive 2; Mismatches
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 Score 34; DB 2
Pred. No. 77;
2; Mismatches
 A;Gene: SGD:ATM1; MDY
A;Cross-references: SGD:S0004916; MIPS:YMR301c
A;Map position: 13R
 A; Introns: 39/3; 93/2; 294/2; 387/2
A; Note: EG:95B7.9
 Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
 Query Match 58.6
Best Local Similarity 75.0
Matches 6; Conservative
 |||| |:||:
580 RLAIARVLLK 589
 2 RLAIRRILLR 11
 111:1:11
473 IRRLLIRY 480
 5 IRRILLRY 12
 A; Accession: S51801
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akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Alathors: Yoshikawa, H.; Zanamatein, E.; Yoshikawa, H.; Danchin, A. A.Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Reference number: A69580; MUID:98044033
 R.Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

Nature 393, 537-544, 1998

A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A.Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A.Reference number: A70500; MuID:98295987
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-349 <COL>
A;Cross-references: GB:295586; GB:AL123456; NID:g3261785; PIDN:CAB09080.1; PID:e317168;
A;Experimental source: strain H37Rv
C;Genetics:
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Rosacidues: 1-280 ***CKND> A;CTOSS-Teferences: GB:259108; GB:AL009126; NID:g2633055; PID:e1182784; PID:g2633118 A;Experimental source: strain 168
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 ATM1 protein precursor - yeast (Saccharomyces cerevisiae)
N;Alternate names: MDY protein; protein YM952.03c; protein YM8301c
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999
C;Accession: 554211; S53971; S51801
R;Kispal, G; Lill, R.; Neupert, N.
submitted to the EMBL Data Library, November 1994
A;Reference number: S54211
A;Reference number: S54211
 C.Species: Mycobacterium tuberculosis
C.Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 16-Jul-1999
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A:Residues: 1-690 <KIS>
A:Cross-treferences: EMBL:X81715; NID:g793876; PIDN:CAA57359.1; PID:g793877
A:Connor, R.; Churcher, C.M.
submitted to the EMBL Data Library, April 1995
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 probable bioB protein - Mycobacterium tuberculosis (strain H37RV)
 Length 280;
 Length 349;
 core 34; DB 2;
red. No. 40;
Mismatches 2
 Score 34; DB 2;
Pred. No. 32;
 3; Mismatches
 Score 34;
Pred. No.
 58.6%;
 58.6%;
 C:Superfamily: biotin synthetase
 Ouery Match
Best Local Similarity 50.0%
Local 6; Conservative
 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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280 FRLALPRIMLRF 291
 1 YRLAIRRILLRY 12
 252 LAVRRVLVR 260
 3 LAIRRILLR 11
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K.; Feng, J.; Kim, C.; Kurtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.;
submitted to the EMBL Data Library, May 1998
A.Pescription: Arabidopsis thaliana chromosome 1 BAC F20D22 complete sequence.
A.Reference number: 214214
A.Accession: T00953
A.Status: preliminary: translated from GB/EMBL/DDBJ
A.Molecule type: DNA
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A.Cross-references: EMBL.AC002411; NID:g2570223; PID:g3142290; GSPDB:GN0059; ATSP:F20D22
A.Gene: Inc.
A.Gene: A.S. A.Molecule type: DNA
A.Residues: 1-814 <VYS>
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A.Molecule type: DNA
A.Residues: 64/1; 144/1; 239/3; 304/1; 386/1; 415/2; 473/3; 516/3; 554/3; 594/2; 624/3; 614/3;
 Ouery Match 58.6%; Score 34; DB 2; Length 814; Best Local Similarity 60.0%; Pred. No. 91; Matches 6; Conservative 2; Mismatches 2; Indels
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Search completed: February 7, 2000, 11:54:29 Job time: 24339 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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protein search, using sw model OM protein Search time 63.71 Seconds (without alignments) 5.625 Million cell updates/sec ٠. 8, 2000, 00:59:56 February Run on:

1 YRLAIRRILLRY 12 US-08-653-294-18 58 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

82229 seqs, 29864866 residues Searched:

82229 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

SwissProt\_38:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|           | Description    | P33617 macaca mila | cricet     | _          |            | _          |            |            | Q58443 methanococc |            | Q59309 clostridium | P16215 pan troglod | P30511 homo sapien | P45082 haemophilus | P44407 haemophilus |            |           |            | _          |            | O18304 caenorhabdi | _          |            |          | _          |     | P42403 bacillus su |            |            | _<br>E     | 0         | 긆          | 4.        | S I        | P42332 bacillus li |
|-----------|----------------|--------------------|------------|------------|------------|------------|------------|------------|--------------------|------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------|-----------|------------|------------|------------|--------------------|------------|------------|----------|------------|-----|--------------------|------------|------------|------------|-----------|------------|-----------|------------|--------------------|
| SUMMAKIES | ID             | HIAF MACMU         | MDR3 CRIGR | RL17_CHLTR | CRTI_CERNC | BIOB_MYCTU | ATM1_YEAST | RPB1_YEAST | RPOH_METJA         | RNPA_MYCPN | G3P_CLOPA          | 1C28_PANTR         | HLAF_HUMAN         | CYDD_HAEIN         | MSBA_HAEIN         | YPHG_ECOLI | V187_BPT3 | YCD4_YEAST | TER4_ECOLI | TER8_PASPI | YHS5_CAEEL         | A2AB_CAVPO | A2AB_HUMAN | A2AB_RAT | A2AB_MOUSE | - 1 | BGL2_BACSU         | PGKD_TRYBB | YETI_SCHPO | RNPA_MYCGE | DP1_MOUSE | RPO6_VACCV | RPO6_VARV | NH10_YEAST | BCRA_BACLI         |
|           | DB             | ; -                | -          | ٦          | Н          | Н          | Н          | Н          | Н                  | Н          | Н                  | Н                  | Н                  | -                  | Н                  | Н          | 7         | Н          | Н          |            | Н                  | -          | -          | -        | <b>~</b> 1 | -   | -                  | Н          | ~4         |            | Н         | 1          | Н         | Н,         | -                  |
|           | Length         | 348                | 1281       | 122        | 621        | 349        | .069       | 1733       | 78                 | 118        | 334                | 346                | 362                | 286                | 287                | 1124       | 83        | 212        | 217        | 218        | 411                | 448        | 450        | 453      | 455        | 469 | 477                | 208        | 693        | 128        | 185       | 185        | 185       | 203        | 306                |
| dР        | Query<br>Match | 7.07               | m          | 62.1       | ~          | 8          | æ          | æ          | 9                  | 9          | 9                  | ø                  | ø                  | 9                  | 9                  | 9          | S         | S          | S          | S          | S                  | ທ          | S          | S        | S          | S   | S                  | S          | S          | 3          | e.        | 53.4       | m         | 53.4       | 53.4               |
|           | Score          | 41                 | 37         | 36         | 36         | 34         | 34         | 34         | 33                 | 33         | 33                 | 33                 | 33                 | 33                 | 33                 | 33         | 32        | 32         | 32         | 32         | 32                 | 32         | 32         | 32       | 32         | 32  | 32                 | 32         | 32         | 31         | 31        | 31         | 31        | 31         | 31                 |
|           | Result<br>No.  | 1                  | 7          | m          | 4          | ហ          | 9          | 7          | ω                  | თ          | 10                 | 11                 | 12                 | 13                 | 14                 | 15         | 16        | 17         | 18         | 19         | 20                 | 21         | 22         | 23       | 24         | 25  | 56                 | 27         | 28         | 53         | 30        | 31         | 32        | 33         | 34                 |

Score 41; DB 1; Length 348;

70.7%;

Query Match

| P31132 escherichia Q04630 herpes simp P52449 herpes simp P52449 herpes simp P24653 orgyia pseudomonas Q09842 schizosacch P22638 anabaena sp P27299 escherichia Q27707 nosema locu P74856 salmonella P45306 haemophilus |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| OPPB_ECOLI<br>VGLM_HSV6U<br>VGLM_HSV6Z<br>VGLM_HSV6Z<br>Y101_NPV0P<br>HRMA_PSESY<br>YAE1_SCHPO<br>MSBA_ECOLI<br>SYI_NOSLO<br>SSAV_SALTY<br>PRC_HAEIN                                                                   |
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## ALIGNMENTS

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 EMBL; 221819; CAL.

JR EMBL; 221819; CAL.

DR PIR; S29990; S29990;

DR PRSSP; P00399; 1163A.

DR PRAM; PF00129; MHC.1:

DR PFAM; PF00129; MHC.1:

THOMAL 1; Transmembrane; Glycoprotein; Signal.

KW MHC 1; Transmembrane; Glycoprotein; Signal.

FT SIGNAL 22 348 ALPA CHAIN F.

FT CHAIN 22 113 EXTRACELLULAR ALPHA-1.

THA 205 EXTRACELLULAR ALPHA-2.

CONNECTING PEPTIDE.
 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
115-JUL-1999 (Rel. 38, Last annotation update)
HIA CLEASI I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN F PRECURSOR (HLA F ANTIGEN) (LEUXOCYTE ANTIGEN F).
 OTIING N., BONTROP R.E.; "Characterization of the rhesus macaque (Macaca mulatta) equivalent of HLA-F.";
 ဝှု
 Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
 Immunogenetics 38:141-145(1993).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS 'TEL IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
 CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
 3A375142 CRC32;
 348 AA.
 PRT;
 39300 MW;
 STANDARD;
 22
114
206
308
332
124
109
348 AA;
 SEQUENCE FROM N.A. MEDLINE; 93246295.
HLAF_MACMU
ID HLAF_MACMU
AC P33617;
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 GULJ., WENMAN W.M., REMACHA M., MEUSER R.U., COFFIN J.M., KAUL R.; "Chlamydia trachomatis RNA polymerase alpha subunit: sequence and structural analysis.";
J. Bacteriol. 177:2594-2601(1995).
-! SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOWAL PROTEINS.
 Cercospora nicotianae.
Eukaryota: Fungi; Ascomycota; Euascomycetes; Loculoascomycetes;
Pleosporales; Leptosphaeriaceae; mitosporic Leptosphaeriaceae;
 "Isolation, sequence, and characterization of the Cercospora nicotianae phytoene dehydrogenase gene."; Appl. Environ. Microbiol. 60:2766-2771(1994).
 01-FEB-1996 (Rel. 33, Created)
1-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
PHYTOENE DEHYDROGENASE (EC 1.3.-.-) (PHYTOENE DESATURASE).
 Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
 Score 36; DB 1;
Pred. No. 1.7;
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 Last sequence update)
Last annotation update)
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 621 AA.
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 PRT;
 1;
 Created)
 62.1%;
54.5%;
 SEQUENCE FROM N.A.
STRAIN-434/BU / SEROVAR L2;
MEDLINE; 95247702.
 50S RIBOSOMAL PROTEIN L17.
 STRAIN-ATCC 18366;
MEDLINE; 94368091.
EHRENSHAFT M., DAUB M.E.;
 Conservative
 Conservative
 STANDARD;
 STANDARD;
 Chlamydia trachomatis.
 01-FEB-1996 (Rel. 33,
01-FEB-1996 (Rel. 33,
15-DEC-1998 (Rel. 37,
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1184 RLAIRRALIR 1193
 45 RLAVGRLMVRY 55
 2 RLAIRRILLRY 12
 2 RLAIRRILLR 11
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Best Local Similarity
 tein.
 SEQUENCE FROM N.A.
 (Rel
 Ribosomal pro
 RESULT 3
RL17_CHLTR
ID RL17_CHLTR
AC P47760;
 01-FEB-1996
15-DEC-1998
 CRTI_CERNC
P48537;
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6
 Cercospora.
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8
 SEQUENCE
 CRII_CERNC
 Matches
 Matches
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 ö
 DNA Seq. 2:89-101(1991).
-!- FUNCTION: ENERGY-DEPENDENT EFFLUX PUMP RESPONSIBLE FOR DECREASED DEUCTION: ENERGY-DEPENDENT EFFLUX PUMP CELLS.
--- SUBCELLULAR LOCATION IN MULTIDRUG-RESISTANT CELLS.
-!- SUBCELLULAR LOCATION: THEGRAL MEMBRANE PROTEIN.
-!- MISCELLANEOUS: PGP ISOPORMS DIFFER IN THEIR DRUG TRANSPORT CAPABILITIES: PGP1 AND PGP2 CAN MEDIATE MDR, WHILE PGP3 APPARENTLY
 Gaps
 MEDLINE; 92135896.
ENDICOTT J.A., SARANGI F., LING V.;
"Complete cDNA sequences encoding the Chinese hamster P-glycoprotein
 SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS). MOR SUBFAMILY.
 Cricetulus griseus (Chinese hamster).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.
 ATP-binding; Glycoprotein; Transmembrane; Transport; Duplication;
 ö
 Score 37; DB 1; Length 1281; Pred. No. 14;
 Indels
 CYTOPLASMIC (POTENTIAL)
 CYTOPLASMIC (POTENTIAL) POTENTIAL.
 CYTOPLASMIC (POTENTIAL)
 01-NOV-1991 (Rel. 20, Created)
1-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
MULTIDRUG RESISTANCE PROTEIN 3 (P-GLYCOPROTEIN 3).
 ö
 9FE9DF5C CRC32;
Pred. No. 0.52;
1; Mismatches
 1281 AA
 (POTENTIAL)
 (POTENTIAL
 POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
 POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
 PS00211; ABC_TRANSPORTER; 1.
 PFAM; PF00005; ABC_tran; 2.
PFAM; PF00664; ABC_membrane; 2.
 63.8%;
80.0%;
 EMBL; M60042; AAA68885.1; -.
 63.68;
 140866
 Conservative
 STANDARD;
 436
 429 43
1071 107
1281 AA;
 |:|:||:||||
98 RVALRKLLLRY 108
 2 RLAIRRILLRY 12
Best Local Similarity
Matches 7; Conserv
 Query Match
Best'Local Similarity
 1NBD
 SEQUENCE FROM N.A.
 Multigene family
 P13569;
 PGY3 OR PGP3
 gene family
 MDR3_CRIGR
P23174;
 CANNO
 NP_BIND
SEQUENCE
 TRANSMEM
TRANSMEM
```

ö

Gaps

ö

1; Indels

**FRANSMEM** RANSMEM

PROSITE;

FRANSMEM

**TRANSMEM FRANSMEM FRANSMEM** PRANSMEM FRANSMEM

PRANSMEN

NP\_BIND

RANSMEM

Length 122;

```
SEQUENCE FROM N.A
 homeostasis.
 ATM1_YEAST
P40416;
 METAL
SEQUENCE
 ATM1_YEAST
 SSSSSSS AND SELECTION OF SELECT
 ò
 P PAULINE, STRAIN-H37RV,
XX MEDLÎNE; 98295987.
XA COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D.,
A COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D.,
RA BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R.,
RA BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R.,
RA DAVIES R., DEVLIN K., FELTUREL T., GENTLES S., HARLIN N., HOLROYD S.,
RA HORNSBY T., JAGELS K., SKROGH A., RAJANDREAM M.A., ROGERS J.,
RA HORNSBY T., SEBGER K., SKELTON S., SQUARES S., SQARES R., SULSTON J.E.,
RA RYLOR K., WHITEHRAD S., BARREL B.G.; BC.; RACORD S.,
RA TAYLOR R., MILEHRAD S., BARREL B.G.; ROCEPHERING THE GENOME sequence.";
COMPLETE GENOME sequence.";
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 ö
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 THE
 SIMILARITY: TO BACTERIAL PHYTOENE DEHYDROGENASES AND TO BACTERIAL METHOXYNEUROSPORENE DEHYDROGENASE (CRTD).
 Gaps
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
FUNCTION: THIS ENZYME CONVERTS PHYTOENE INTO ZETA-CAROTENE VIA INTERMEDIARY OF PHYTOFLUENE BY THE SYMMETRICAL INTRODUCTION OF DOUBLE BONDS AT THE C-11 AND C-11' POSITIONS OF PHYTOENE.
 STRAIN-PASTEUR;
YU S., JACOBS W.R. JR.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-: CATALYTIC ACTIVITY: DETHIOBIOTIN + (S) = BIOTIN.
-:- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.
-:- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
 EMBL; U03903; AAB86988.1; -.
PROSITE; PS00982; PHYTOENE_DH; 1.
Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD;
 ö
 Score 36; DB 1; Length 621; Pred. No. 10;
 Indels
 FAD (ADP PART) (POTENTIAL).
 nnotation update) (BIOTIN SYNTHETASE).
 CDA97504 CRC32;
 349 AA.
 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update
BIOTIN SYNTHASE (EC 2.81.16) (BIOTIN SYNTHESI
BIOB OR RV1589 OR MICY336.15C.
 3; Mismatches
 COFACTOR: FAD (PROBABLE).
PATHWAY: CAROTENOID BIOSYNTHESIS.
 621 AA; 69529 MW;
 62.1%;
54.5%;
 Mycobacterium tuberculosis.
 Conservative
 STANDARD;
 140 YELSVREVLLR 150
 1 YRLAIRRILLR 11
 Ouery Match
Best Local Similarity
Matches 6; Conserv
 SEQUENCE FROM N.A.
 FROM N.A.
 Fransmembrane.
 BIOB_MYCTU
006601;
 NP_BIND
TRANSMEM
 SEQUENCE
 SEQUENCE
 between
 BIOB_MYCTU
 RESULT
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 ö
 STRAIN-S288C / AB972;
CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
SUDMITTED (APR.1995) to the EMBL/GenBank/DDBJ databases.
-I. FUNCTION: PROBABLE TRANSPORTER FOR A YET UNKNOWN SUBSTRATE.
REQUIRED FOR MITOCHONDRIAL IRON HOREOSTASIS.
-I. SUBBURIT: HOMODIMER ON HETEROSIMER (POTENTIAL).
-I. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 SEQUENCE FROM N.A.
STRAIN=JK9-12D ALPHA;
MEDILINE; 95129546.
LEIGHTON J., SCHATZ G.;
"An ABC transporter in the mitochondrial inner membrane is required for normal growth of yeast.";
EMBO J. 14:188-195(1995).
 -! - SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
 ö
 KISPAL G., CSERE P., GUIARD B., LILL R.; "The ABC transporter Atmlp is required for mitochondrial iron
 Score 34; DB 1; Length 349;
Pred. No. 14;
4; Mismatches 2; Indels
 EMBL; Z95200,
EMBL; AF041819; AAB96962.1; -.
EMBL; AF041819; AAB96962.1; -.
METAL 85
IRON-SULFUR (POTENTIAL).
TON-SULFUR (POTENTIAL).
TON-SULFUR (POTENTIAL).
 31B0B9DA CRC32;
 01-FEB-1996 (Rel. 33, Last sequence update)
115-UTL-1999 (Rel. 38, Last annotation update)
117-CHONDRIAL TRANSPORTER ATMI PRECURSOR.
ATMI OR MDY OR YMR301C OR YM9952.03C.
 690 AA
 (ABC TRANSPORTERS). MDR SUBFAMILY.
 PRT;
 92 IR
37550 MW;
 01-FEB-1995 (Rel. 31, Created)
 58.6%;
 FEBS Lett. 418:346-350(1997).
 EMBL; 295586; CAB09080.1; -. EMBL; AF041819; AAB96962.1; -
 EMBL; X82612; CAA57938.1; -.
 Conservative
 STANDARD;
 :|||: | :||:
280 FRLALPRIMLRF 291
 1 YRLAIRRILLRY 12
 349 AA;
 Query Match
Best Local Similarity
Matches 6; Conserv
 SEQUENCE FROM N.A. MEDLINE; 98089018.
 INNER MEMBRANE
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SUBUNIT IS THE LARGEST COMPONENT OF RNA POLYMERASE II.
 CONFLICT
 CONFLICT
 CONFLICT
 qq
 ö
 ö
 FEMS MIGTODIOL. Lett. 130:221-230(1995).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
 Transmembrane; Transport; Mitochondrion; Inner membrane;
 Gaps
 RPBI_YEAST STANDARD; PRT; 1733 AA.
P04050; Q12364; Q92315;
P04050; Q12364; Q92315;
O1-NOV-1986 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
DNA-DIRCCTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (B220).
RPB1 OR RPD21 OR RPB220 OR SUAB OR YDL140C OR D2150.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
 CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE
 STRAIN-A364A;
MEDLINE: 85282617.
ALLISON L.A., MOYLE M., SHALES M., INGLES C.J.;
Extensive homology among the largest subunits of eukaryotic and prokaryotic RNA polymerases.";
Cell 42:599-610(1985).
 MEDIINE; 95377607.
CRONAN J.E. JR., WALLACE J.C.;
"The gene encoding the biotin-apoprotein ligase of Saccharomyces
 RNA(N).
SUBUNIT: RNA POLYMERASE II CONSISTS OF 12 DIFFERENT SUBUNITS.
 ö
 MITOCHONDRION (POTENTIAL).
MITOCHONDRIAL TRANSPORTER ATM1.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
STR (POTENTIAL).
S -> SRNHS (IN REF. 1).
S -> SRNHS (IN REF. 1).
 WOELFL S., HANEMAN V., SALUZ H.P.; Analysis of a 26,756 bp segment from the left arm of yeast
 Score 34; DB 1; Length 690;
Pred. No. 29;
2; Mismatches 1; Indels
 SGD; L0000140; ATM1.
PROSITE; PS00014; ER_TARGET; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
 Saccharomycetaceae; Saccharomyces.
 PFAM; PF00005; ABC_tran; 1.
PFAM; PF00664; ABC_membrane; 1.
ATP-binding; Transmembrane; Tra
 SEQUENCE OF 1669-1733 FROM N.A.
 77522 MW;
 58.6%;
70.0%;
 EMBL; Z49212; CAA89134.1; -.
CAA57359.1;
 Ouery Match 58.6
Best Local Similarity 70.0
Matches 7; Conservative
 chromosome IV.";
Yeast 12:1549-1554(1996).
 STRAIN-S288C / FY1679;
MEDLINE; 97127826.
 ||||| |:||:
580 RLAIARVLLK 589
 27
690 AA;
 RLAIRRILLR 11
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Transit peptide
TRANSIT
 SUBSTRATES
 STRAIN-S288C;
 NP_BIND
CONFLICT
SEQUENCE
 TRANSMEM
 TRANSMEM
 TRANSMEM
 FRANSMEM
 FRANSMEM
 FRANSMEM
 RPB1_YEAST
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 ö
 -:- SUBCELLULAR LOCATION: NUCLEAR.
-:- PTM: THE TANDEM T RESIDUES REPEATS CAN BE HIGHLY PHOSPHORYLATED.
THE PHOSPHORYLATION ACTIVATES POLZ.
-:- MISCELLANGOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE FOUND IN EURARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE II FOR 5S AND TRIM GENES.
-:- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
 STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,

SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCANNE J.D.,

KERLAVAGE A.R., DOUGHBERTY B.A., TOMB J.-F., ADANS M.D., RELCH C.I.,

OVERBEER R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,

SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.E., FUHRMANN J.L., NGUYEN D.,

UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,

COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORDDOVSKY M.,

KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.,

"COMPLETE GENOME SEQUENCE Of the methanogenic archaeon, Methanococcus
 Gaps
 ;
 Length 1733;
 Methanococcus jannaschil.
Archaea: Euryarchaeota; Methanococcales; Methanococcaceae;
Methanococcus.
 3; Indels
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
DNA-DIRECTED RNA POLYMERASE SUBUNIT H (EC 2.7.7.6).
 A -> V (IN REF. 1).
G -> A (IN REF. 1).
T -> M (IN REF. 1).
MW; BB65D7EE CRC32;
 Score 34; DB 1;
Pred. No. 79;
1; Mismatches
 78 AA.
 POL_II_REPEAT; 22
 191610 MW;
 EMBL; X03128; CAA26904.1; -. EMBL; X96876; CAA65619.1; -. EMBL; Z74188; CAA98713.1; -. EMBL; UZ7182; AAC49058.1; -. PIR; A00692; RNBYZL.
 58.68;
63.68;
 jannaschii.";
Science 273:1058-1073(1996).
 Query Match 58.6
Best Local Similarity 63.6
Matches 7; Conservative
 STANDARD;
 SGD; L0001744; RPO21.
PROSITE; PS00115; RNA_
 ||| ||:| |
1025 RLATRRVLQEY 1035
 2 RLAIRRILLRY 12
 RPOH OR MJ1039
 RESULT
RPOH_METJA
RPOH_METJA
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PROSITE; PS00071; GAPDH; 1.
PFAM; PF00044; gpdh; 1.
Glycolysis; Oxidoreductase; NAD.
BINDING 150 GLY
ACT_SITE 177 177 ACT
 EMBL; X72219; CAA51020.1; -. HSSP; P00362; 2GD1.
 Query Match 56.9°
Best Local Similarity 54.5
Matches 6; Conservative
 PARTIAL SEQUENCE OF 1-26.
 STANDARD;
 |:||: | |:|
53 YKLAVERNLIR 63
 SEQUENCE FROM N.A. OSTER I., ASSOBHEI
 MEDLINE; 98291870.
 Clostridium.
 /CP 18).
 G3P_CLOPA
Q59309;
 RESULT 10
 G3P_CLOPA
 à
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 ö
 -:- CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE OF RNA, REMOVING
5'-EXTRA-NUCLEOTIDE FROM TRNA PRECURSOR
-:- MISCELLANBOUS: RNASE P CONSISTS OF A RNA MOIETY (M1, RNPB) AND THE
PROFIELN COMPONENT: BOTH ARE NECESSARY FOR FULL ENZYMATIC ACTIVITY.
HOWEVER, IT IS THE RNA THAT CARRIES THE CATALYTIC SITE (BY
 "RNA polymerase subunit H features a beta-ribbon motif within a novel fold that is present in archaea and eukaryotes.";
J. Mol. Biol. 287:753-760(1999).
-- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
 Transferase; Transcription; DNA-directed RNA polymerase; 3D-structure.
SEQUENCE 78 AA; 9001 MW; 9F10C0F3 CRC32;
 CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +
 'Complete sequence analysis of the genome of the bacterium Mycoplasma
 Gaps
 -!- SIMILARITY: TO OTHER ARCHAEBACTERIAL RPOH AND TO THE C-TERMINAL
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
RIBONUCLEASE P PROTEIN COMPONENT (EC 3.1.26.5) (PROTEIN C5) (RNASE
 OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.
 HODACH M., ELORANTA J.J., KOSTOUROU V., WEINZIERL R.O.,
 ö
 pneumoniae.";
Nucleic Acids Res. 24:4420-4449(1996).
-!- FUNCTION: RIBONUCLEASE P GENERATES MATURE TRNA MOLECULES
-L- FUNCTION: RIBONUCLEASE P GENERATES MATURE TRNA MOLECULES
-L- FUNCTION: RIBONUCLEASE P GENERATES MATURE TRNA MOLECULES
-L- FUNCTION: THEIR 5' ENDS. IT CAN CLEAVE ALSO THE 4.5S RNA
 Mycoplasma pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
 HIMMELREICH R., HILBERT H., PLAGENS H., PIRKL E., LI B.-C.,
 Query Match 56.9%; Score 33; DB 1; Length 78; Best Local Similarity 66.7%; Pred. No. 4.2; Matches 6; Conservative 2; Mismatches 1; Indels
 SIMILARITY).
SIMILARITY: BELONGS TO THE RNPA FAMILY.
 OF EUKARYOTIC SUBUNIT ABC27 (RPB5).
 PROSITE; PS01110; RNA_POL_H_23KD; 1.
PFAM; PF01191; RNA_POI_H; 1.
 EMBL; U67546; AAB99042.1; -. PDB; 1HMJ; U5-APR-99.
TIGR; MJ1039; -.
 SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE; 97105885.
 STANDARD;
 (BY SIMILARITY)
 ||| |:||:
70 YRLVIKRII 78
 1 YRLAIRRIL 9
[2]
STRUCTURE BY NMR
 THIRU A., HOI
MATTHEWS S.;
 HERRMANN R.;
 RNPA_MYCPN
P75111;
 RNPA_MYCPN
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96 RVALRNLLRRY 106
 RLAIRRILLRY 12
 HLAF_HUMAN
ID HLAF_HUMAN
AC P30511;
 DOMAIN
TRANSMEM
DOMAIN
 DISULFID
CARBOHYD
SEQUENCE
 DISULFID
 SIGNAL
 DOMAIN
 DOMAIN
 CHAIN
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 ö
 Gaps
 CLASS I HISTOCOMPATIBILITY ANTIGEN,
 01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CH28 ALPHA CHAIN PRECURSOR.
Pan troglodytes (Chimpanzee).
 Nature 335:268-271(1988).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
 MEDLINE; 88319000.
LAWLOR D.A., WARD F.E., ENNIS P.D., JACKSON A.P., PARHAM P.;
"HLA-A and B polymorphisms predate the divergence of humans and
 ö
 Chordata; Craniata; Vertebrata; Mammalia;
Catarrhini; Hominidae; Pan.
 SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
 Length 334;
 DB 1; Length 346;
 Indels
 LAWLOR D.A., WARREN E., WARD F.E., PARHAM P.; "Comparison of class I MHC alleles in humans and apes."; Immunol. Rev. 113:147-185(1990).
 CHLA CLASS I HISTOCOMPAY
CH28 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
 CONNECTING PEPTIDE
 DB 1;
21;
 EMBL; M30685; AAA87973.1; HSSP; P03989; 1HSA.
PROSITE; PS00290; IG_MHC; 1.
PFAM: PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
SIGNAL 12 2 346 CHLA CLASS I HIST
36078 MW; 9061EAF0 CRC32;
 CYTOPLASMIC TAIL.
 78B65140 CRC32;
 SIMILARITY.
SIMILARITY.
SIMILARITY.
 346 AA
 Mismatches
 Score 33;
Pred. No. 2
 Score 33;
Pred. No.
 PRT;
 BY
BY
BY
 01-APR-1990 (Rel. 14, Created)
 39084 MW;
 56.9%;
87.5%;
 Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
 Query Match
Best Local Similarity 8/...
7; Conservative
 STANDARD;
 Eukaryota; Metazoa;
Eutheria; Primates;
 224
107
346 AA;
334 AA;
 SEQUENCE FROM N.A. MEDLINE; 90201944.
 SEQUENCE FROM N.A.
 14 RLALRRIL 21
 2 RLAIRRIL 9
 chimpanzees."
 1C28_PANTR
P16215;
 DOMAIN
TRANSMEM
DOMAIN
 DISULFID
CARBOHYD
SEQUENCE
SECUENCE
 DISULFID
 RESULT 11
1C28_PANTR
 DOMAIN
 DOMAIN
 DOMAIN
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 ö
 01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN F PRECURSOR (HLA F
 SEQUENCE FROM N.A.
MEDLINE; 90111605.
GERAGHTY D.E., WEI X., ORR H.T., KOLLER B.H.;
"Human leukocyte antigen F (HLA-F). An expressed HLA gene composed of a class I coding sequence linked to a novel transcribed repetitive
 Gaps
 CLASS I HISTOCOMPATIBILITY ANTIGEN,
 SEQUENCE FROM N.A.
MEDLINE; 91197889.
LURY D., EPSTEIN H., HOLMES N.;
The human class I MHC gene HLA-F is expressed in lymphocytes.";
Int. Immunol. 2:531-537(1990).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE INMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
 ö
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Length 362;
 Indels
 HLA CLASS I HISTOCOMPATI
ALPHA CHAIN F.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
 CONNECTING PEPTIDE
 NY SIMILARITY.
NY SIMILARITY.
NY SIMILARITY.
E9B29521 CRC32;
 DB 1;
 CYTOPLASMIC TAIL
 362 AA.
 PIR; A60384; A60384.

PIR; JU0147; JL0147.

MIM; 143110; -.

PROSITE: PS00290; IG_MHC; 1.

PRAM; PF0047; 19; 1.

PFRAM; PF00129; MHC_I; 1.

MHC I; Transmembrane; Glycoprotein; Signal.
 Score 33; DB 1
Pred. No. 23;
3; Mismatches
 ANTIGEN) (LEUKOCYTE ANTIGEN F) (CDA12).
HLA-F OR HLAF OR HLA-5.4.
 BY
BY
BY
 .
X
 56.9%;
54.5%;
 EMBL; X17093; CAA34947.1; -.
 7. Exp. Med. 171:1-18(1990)
 40568
 Query Match 56.9
Best Local Similarity 54.5
Matches 6; Conservative
STANDARD;
 21
362
 362
185
280
107
 Homo sapiens (Human)
 22
112
204
206
3306
122
122
107
362 AA;
```

Gaps

ö

Indels

ed. No. 21; Mismatches

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491 RLAIARALLR 500
 STRAIN-RD / KW20;
MEDLINE; 95350630.
 SEQUENCE FROM N.A.
 influenzae Rd
 STRAIN-BC200;
 HI0060;
 VENTER J.C.;
 01-NOV-1995
 Haemophilus
 MSBA_HAEIN
P44407;
 NP_BIND
SEQUENCE
 RANSMEM
 FRANSMEM
 FRANSMEN
 RANSMEM
 FRANSMEM
 EMBL;
 RESULT 14
MSBA_HAEIN
 IGR;
 g
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 ó
 FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERLEAYAGE M.A., MERRICK J.M., MCKENNEY R., SULT C.J., TOMB J.-F., DOGGHERTY B.A., MERRICK J.M., MCKENNEY K., SUTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., FINE L.D., FRIFCHMAN J.L., FUHRWANN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
 SCIENCE 259:496-512(1995).
-!- FUNCTION: SOMEHOW INVOLVED IN THE CYTOCHROME D BRANCH OF AEROBIC RESPIRATION. SEEMS TO BE A COMPONENT OF A TRANSPORT SYSTEM
 Gaps
 (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
 (PROBABLE).
-!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
 ö
 Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 "Whole-genome random sequencing and assembly of Haemophilus influenzae \operatorname{Rd}\ ",
 DB 1; Length 586; 38;
 2; Indels
 Inner membrane.
 ATP (POTENTIAL).
80EB2DE1 CRC32;
 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
TRANSPORT AFP-BINDING PROTEIN CYDD.
CYDD OR HI1157.
 586 AA.
 0; Mismatches
 Score 33;
Pred. No.
 ATP-binding; Transport; Transmembrane;
 POTENTIAL.
 POTENTIAL
 POTENTIAL
 POTENTIAL
 POTENTIAL
 (ABC TRANSPORTERS). MDR SUBFAMILY.
 POTENTIAL
 PS00211; ABC_TRANSPORTER; 1.
 PFAM; PF00005; ABC_tran; 1.
PFAM; PF00664; ABC_membrane; 1.
 MM.
 56.9%;
80.0%;
 EMBL; U32795; AAC22812.1; -.
 390
65645
 Query Match 56.9
Best Local Similarity 80.0
Matches 8; Conservative
 STANDARD;
 Haemophilus influenzae.
 96 RVALRNLLRRY 106
 2 RLAIRRILLRY 12
 383
586 AA;
 SEQUENCE FROM N.A.
 STRAIN=RD / KW20;
MEDLINE; 95350630.
 (PROBABLE)
 VENTER J.C.;
 Haemophilus.
 TIGR; HI1157
PROSITE; PS0
 CYDD_HAEIN
P45082;
 TRANSMEM
 TRANSMEM
 TRANSMEM
 TRANSMEM
 TRANSMEM
 TRANSMEM
 RESULT 13
CYDD_HAEIN
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 (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
(ABC TRANSPORTERS). MSBA SUBFAMILY.
 KERISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERLAVAGE A.R., BULT C.J., TONB J.F., DOUGHERTY B.A., MERRICK J.M., MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIRELY R., LUU L.-I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.K., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., GINEN C.L., KUTERMAN J.L., FUHRMANN J.L., GEOCHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
 Gaps
 SIMILARITY).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
 ö
 Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 "Whole-genome random sequencing and assembly of Haemophilus
 1; Length 587;
 Transmembrane.
 ATP (POTENTIAL).
FC711A0B CRC32;
 01-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) PROBABLE TRANSPORT ATP-BINDING PROTEIN MSBA.
587 AA.
 Score 33; DB 1
Pred. No. 38;
0; Mismatches
 PROSITE; PS00211; ABC_TRANSPORTER; 1.
PFAM; PF00105; ABC_tran; 1.
PFAM; PF00644; ABC_membrane; 1.
ATP-binding; Transport; Inner membrane;
 POTENTIAL.
 POTENTIAL
PRT;
 ;
 (Rel. 32, Created)
 64912 MW;
 56.9%;
 EMBL; U32691; AAC21738.1; -.
 SEQUENCE OF 1-458 FROM N.A.
 Science 269:496-512(1995).
 L20805; AAC13734.1;
 Conservative
 MSBA OR MSH-1 OR HI0060.
STANDARD;
 Query Match
Best Local Similarity
Matches 8; Conserv
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2 RLAIRRILLR 11

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 ô
 SEQUENCE FROM N.A.
STRAIN+RIZ 'MG1655;
MEDLINE: 97426617.
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
MAU B., SHAO Y.;
 Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 ö
 976585;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 127.3 KD PROTEIN IN CSIE-GLYA INTERGENIC REGION.
 Query Match
Best Local Similarity 87.5%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 1; Indels
 "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
 EMBL; AE000341; AAC75602.1; -.
ECOGRNE; EG13468; yphG.
Hypothetical protein.
SEQUENCE 1124 AA, 127284 MW; 0A06B4C6 CRC32;
 PRT; 1124 AA.
 STANDARD;
1111 | 111
493 REAIARALLR 502
 1 YRLAIRRI 8
 Sscherichia.
 YPHG_ECOLI
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 qq
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